(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 31 October 2002 (31.10.2002)

(10) International Publication Number WO 02/086443 A2

- (51) International Patent Classification7:
- **G01N**
- (21) International Application Number:
- (22) International Filing Date: 18 April 2002 (18.04.2002)
- (25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/284,770	18 April 2001 (18.04.2001)	US
60/290,492	10 May 2001 (10.05.2001)	US
60/339,245	9 November 2001 (09.11.2001)	US
60/350,666	13 November 2001 (13.11.2001)	US
60/334,370	29 November 2001 (29.11.2001)	US
60/372,246	12 April 2002 (12.04.2002)	US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

of inventorship (Rule 4.17(iv)) for US only

Published:

without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MOD-**ULATORS OF LUNG CANCER**

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

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Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include onthe-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent can be undertaken. Hoever, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment.

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

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In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

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In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

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In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

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In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseases lung samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

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Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

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"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

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For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

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Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) <u>Current Protocols in Molecular Biology</u>.

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

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In this sense, purification does not require that the purified compound be homogeneous, e.g.,

100% pure.

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The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

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conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3rd ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, 5 etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A 10 Practical Approach Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing 15 one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring 20 nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence.

The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine

5 hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem, 30:407-412.

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An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

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The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

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A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at ٠5 higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) 10 at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 15 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. 20 Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 25 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions 30 are provided, e.g., in Innis, et al. (1990) PCR Protocols. A Guide to Methods and Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

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occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

WO 02/086443 PCT/US02/12476 preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, 5 anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) Culture of Animal Cells a Manual of Basic Technique pp. 231-241 (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

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"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

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Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'₂, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'₂ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'₂ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to downregulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant diseasemay be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

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In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in nonmalignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are downregulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

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Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets,

Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

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The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

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pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, genedisease causal linkages, identification of correlates of immunity and physiological status,
among others. Although the data generated from the assays of the invention is suited for
manual review and analysis, in a preferred embodiment, data processing using high-speed
computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5.953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5.295.261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) Biological

Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids (; Baxevanis and

Oeullette (eds., 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and

Proteins); Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological

Science and Medicine; Setubal, et al. (eds 1997) Introduction to Computational Molecular

Biology; Misener and Krawetz (eds, 2000) Bioinformatics: Methods and Protocols; Higgins
and Taylor (eds., 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical

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Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the

Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and

Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

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The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

file, which comprises a binary description of an assay result.

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MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

15 Characteristics of lung cancer-associated proteins

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Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322).

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In another embodiment, the lung cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

WO 02/086443 PCT/US02/12476 localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

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Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

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As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

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In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

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In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

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In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

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In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

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Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

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The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

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In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha,

Kluyveromyces fragilis and K. lactis, Pichia guillerimondii, and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

25 Variants of lung cancer proteins

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In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above.

However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per seneed not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

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Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

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Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987)

Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth.

Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-

15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) <u>Proc. Nat'l Acad. Sci. USA</u> 87:6393-6397).

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to lung cancer proteins

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In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 5 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

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By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

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In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

WO 02/086443 PCT/US02/12476 afflicted area, but also serves to reduce deleterious side effects that may be associated with

the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

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Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

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"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

PCT/US02/12476 WO 02/086443 normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChipTM expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

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Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

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In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, in situ hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

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Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

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In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

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In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) <u>J. Med. Chem.</u> 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA-90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

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In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

WO 02/086443 PCT/US02/12476 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

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A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697: Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

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Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

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Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

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Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique</u> (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

20 Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

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non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is
determined autoradiographically. See, Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) <u>J. Natl. Cancer Insti.</u> 37:167-175; Eagle, et al. (1970) <u>J. Exp. Med.</u> 131:836-879); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

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Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in <u>Sem Cancer Biol.</u>).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, see, Unkeless, et al. (1974) <u>J. Biol. Chem.</u> 249:4295-4305; Strickland and Beers (1976) <u>J. Biol. Chem.</u> 251:5694-5702; Whur, et al. (1980) <u>Br. J. Cancer</u> 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) <u>Biological Responses in Cancer</u>, pp. 178-184; Freshney <u>Anticancer Res.</u> 5:111-130 (1985).

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Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

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Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, , IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or intersugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.

Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

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is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al.
(1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

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Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

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Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety.

Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation

of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

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The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, com and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

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The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacologial Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis of Therapeutics, supra.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

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It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, <u>Guide to Molecular Cloning Techniques</u>, <u>Methods in Enzymology</u> volume 152 (Berger), Ausubel, et al. (eds. 1999) <u>Current Protocols</u> (supplemented through 1999), and Sambrook, et al. (1989) <u>Molecular Cloning - A Laboratory Manual</u> (2nd ed., Vol. 1-3).

In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

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Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) <u>J. Immunol. Methods</u> 192:25; Eldridge, et al. (1993) <u>Sem. Hematol.</u> 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

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Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zine; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) <u>Science</u> 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

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Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein.

Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

WO 02/086443 PCT/US02/12476 EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
•	Pkey	ExAcon	UnigenelD	Unigene Title	70% ctron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780 100971	HG3731-HT4001 J02874	Hs.83213	fatty acid binding protein 4; adipocyte	2.68 1.96	3.28 0.14
10	101088	L05568	Hs.553	solute carrier family 6 (neurotransmitte	0.79	0.07
	101102	L07594	Hs.79059	transforming growth factor, beta recepto	2.55	1
	101168 101277	L15388 L38486	Hs.211569 Hs.118223	G protein-coupled receptor kinase 5 microfibrillar-associated protein 4	0.88 0.89	0.27 0.26
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.59	0.29
15	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	1.15	0.41
	101345	L76380 M62505	Hs.152175 Hs.2161	calcitonin receptor-like	0.81	0.31
	101678 101764	M80563	Hs.81256	complement component 5 receptor 1 (C5a I S100 calcium-binding protein A4 (calcium	1.31 1.44	0.77 0.82
00	101771	M81750	Hs.153837	myeloid cell nuclear differentiation ent	0.96	0.45
20	101842	M93221	Hs.75182	mannose receptor, C type 1	1.27	0.37
	102283 102363	U31384 U39447	Hs.83381 Hs.198241	guarine nucleotide binding protein 11 arnine oxidase; copper containing 3 (vasc	1.04 0.96	0.3 0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
25	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95	0.23
25	103025 103280	X54131 X79981	Hs.123641 Hs.76206	protein tyrosine phosphatase; receptor t cadherin 5; VE-cadherin (vascular epithe	1.62 0.9	0.21 0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; i	1.86	1
30	103554 104212	Z18951	Hs.74034 Hs.173035	caveolin 1; caveolae protein; 22kD	1.27 1.17	0.47 0.16
50	104691	AB002298 AA011176	Hs.37744	KIAA0300 protein ESTs	1.08	0.16
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
35	104865 104989	AA045136 AA102098	Hs.22575 Hs.118615	ESTs ESTs	1.23 0.63	0.49 0.32
	105729	AA292694	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894 106490	AA400979 AA451861	Hs.25691 Hs.115537	calcitonin receptor-like receptor activi ESTs; Weakly similar to dipeptidase prec	0.78 1.2	0.28 0.47
40	106536	AA453997	Hs.23804	ESTs	0.82	0.15
	106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667 106773	AA461086 AA478109	Hs.16578 Hs.188833	ESTs ESTs	1.17 1.46	0.4 0.43
	106797	AA478962	Hs.169943	ESTs	1.18	0.32
45	106844	AA485055	Hs.158213	sperm associated antigen 6	0.98	0.51
	106870 106954	AA487576 AA496980	Hs.26530 Hs.204038	serum deprivation response (phosphatidyl ESTs	1.05 1.25	0.14 0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292	T30407	Hs.4789	ESTs; Wealdy similar to oxidative-stress	1.07	2.58
50	107994 107997		Hs.165030	ESTS	0.7 1.02	0.21 0.48
	108041	AA037388 AA041552	Hs.82223 Hs.61957	Human DNA sequence from clone 141H5 on c ESTs	1.44	0.40
	108087	AA045709	Hs.40545	ESTs	1.98	1
55	108382	AA074885		macrophage receptor with collagenous str	1.52	0.72
33	108435 108480		Hs.194101 Hs.68055	ESTs ,	2.53 1.56	1.53 0.48
	109252	AA194830	Hs.85944	ESTs	2.69	3.18
	109550			ESTs	1.19	0.65
60	109613 109837			ESTs ESTs	1.01 0.81	0.29 0.15
	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984			ESTs	0.62	0.14
	110099 110837			ESTs ESTs; Weakly similar to semaphorin F (H.	1.01 1.1	0.28 0.22
65	111247			Homo sapiens mRNA; cDNA DXFZp564B2062 (f	1.26	0.26
	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510 111737			ESTs ESTs	3.95 0.97	1 0.24
~ ^	113195		11010210	""yc20g11.s1 Stratagene lung (#937210) .	1.22	0.35
70				EST ₆	2.27	0.45
				ESTs ESTs	1.06 · 1.16	0.22 0.42
	113506			ESTs .	1.48	0.7
75	113695	T96965	Hs.17948	ESTs	1.54	0.28
75	113946 114251			ESTs ESTs	1.79 1.95	0.72 0.25
	114359	Z41589		ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300	Hs.182980	ESTs	2.62	0.42
80				ESTs ESTs	1.79 0.86	0.91 0.2
50				ESTS	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
				ESTs ESTs	2.27 1.36	0.78
	117023	1100101	Hs.41105	ESTs	1.30	0.16

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	117209	H99959	Hs.42768	ESTs	1.46	0.48
	118901	N90719	Hs.94445 ·	ESTs	1.51	1
	118981	. N93839	Hs.39288	ESTs	1.34	0.48
5	119073 119221	R32894 R98105	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14 1.32	0.27 0.53
,	119824	W74536	Hs.184	"yr30g11.s1 Soares fetal liver spleen advanced glycosylation end product-speci	1.32	0.53
	119861	W80715	10.101	ESTs; Moderately similar to IIII ALU SUB	1.83	0.45
	120041	W92775	Hs.59368	ESTs	1.23	0.55
	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37
10	120467	AA251579	Hs.187628	ESTs	1.87	1.91
	121314	AA402799	Hs.182538	ESTs	1.3	0.31
	121643	AA417078	Hs.193767	ESTs	2.31	0.68
	121690	AA418074	Hs.110286 Hs.34853	ESTs	1.47	0.51
15	122633 123978	AA454080 C20653	Hs.170278	inhibitor of DNA binding 4; dominant neg ESTs	1.31 1.52	0.63 0.32
13	124214	H58608	Hs.151323	ESTs	0.93	0.35
	124357	N22401	120.000	"yw37g07.s1 Morton Fetzl Cochtea Homo	1.29	1
	124438	N40188	Hs.102550	ESTs	1.36	0.7
00	125167	W45560	Hs.102541	ESTs	1.46	0.69
20	125174	W51835	Hs.231082	EST	3.07	3.76
	125422	AA903229	Hs.153717	ESTs	1.34	0.3
	125561	Al417667	Hs.22978	ESTS	1.89	0.63
	125831 127002	D60988 R35380	Hs.24979	***HUM145B09B Clontech human fetal bratn ESTs	0.94 3.02	0.36 4.06
25	127307	AA369367	Hs.126712	ESTs; Wealdy similar to plL2 hypothetica	1.01	0.69
	127609	AA622559	Hs.150318	ESTs	1.21	0.32
	127959	Al302471	Hs.124292	ESTs	2.5	1
	128458	D52193	Hs.56340	ESTs	1.13	0.33
20	128624	AA479209	Hs.102647	ESTs	1.45	0.58
30	128789	AA486567	Hs.105695	ESTs	1.1	0.34
	128798	AF014958	Hs.105938	chemokine (C-C motif) receptor-like 2	1.16	0.55
	128952	R51076	Hs.107361	ESTs; Highly similar to Rap2 Interacting	2.04	24
	129057 129210	X62466 AA401654	Hs.214742 Hs.202949	CDW52 antigen (CAMPATH-1 antigen) KIAA1102 protein	1.77 1.11	0.73 0.36
35	129240	W24360	Hs.237868	interleukin 7 receptor	0.91	0.41
-	129402	T63781	1000	"'yc21g01.s1 Stratagene lung (#937210)	1.36	0.43
	129565	хтт	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08
	129593	AA487015	Hs.98314	Homo sepiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42
40	129626	AA447410	Hs.11712	ESTs; Weakly similar to !!!! ALU SUBFAMI	1.28	0.46
40	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ublqu	1.58	1
	129898	N48595	Hs.13256	ESTs	1.13	0.53
	129958	L20591	Hs.1378	annexin A3	0.81	0.31
	130273 130655	U59914 N92934	Hs.153863 Hs.17409	MAD (mothers against decapentaplegic; Dr cysteine-rich protein 1 (intestinal)	0.59 1.44	0.22 0.76
45	130657	T94452	Hs.201591	ESTs	0.96	0.42
7.5	131061	N54328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45
	131066	F09006	Hs.22588	ESTs	0.97	0.37
	131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.34	. 2.82
50	131589	U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62
50	131686	AA157428	Hs.30687	Grb2-essociated binder 2	0.95	0.38
	131751	H18335	Hs.31562	ESTs	1.47	0.52
	132430	T23630	Hs.258675	EST	1.86	2.09
	132476 132836	N67192 F09557	Hs.49476 Hs.57929	Homo sapians clone TUA8 Cri-du-chat regi slit (Drosophila) homolog 3	1.73 0.91	0.58 0.29
55	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	0.82	0.2
-	133488	D45370	Hs.74120	adipose specific 2	1.29	0.48
	133565	H57056	Hs.204831	ESTs	2.25	0.57
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62
·c0	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg	1.16	0.34
60	133978	W73859	Hs.78061	transcription factor 21	0.79	0.27
	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.99	0.28
	134299	AA487558	Hs.8135	ESTs	1.02	0.46
	134300 134323	U81984 AA028976	Hs.166082 Hs.8175	endothelial PAS domain protein 1, Homo saplens mRNA; cDNA DKFZp564M0763 ff	0.86 1.19	0.42 0. <i>2</i> 7
65	134343	D50683	Hs.82028	transforming growth factor, beta recepto	1.21	0.27
•	134417	D87969	Hs.82921	solute carrier family 35 (CMP-static aci	1.28	1
	134561	U76421	Hs.85302	adenosine deaminase; RNA-specific; B1 (h	2.12	0.55
	134624	W67147	Hs.8700	deleted in liver cancer 1	2.35	2.74
70	134696	H88354	Hs.8861	ESTs	1.35	. 0.33
70	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous	0.48	0.21
	134869	T35288	Hs.90421	ESTs; Moderately similar to IIII ALU SUB	214	2.64
	135346 100113	M21056 D00591	Hs.992 Hs.84746	phospholipase A2; group IB (pancreas) Chromosome condensation 1	0.63 1	0.13 2.15
75	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5	2 13
	100280	D42085	Hs.155314	KIAA0095 gene product	1.02	1.39
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrola	1	5.58
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04
00	100372	D79997	Hs.184339	KIAA0175 gene product	0.75	2.03
80	100486	HG1112-HT1112		TIGR: ras-like protein TC4	1.09	1.93
	100559	HG2197-HT2267		*collagen, type VII, alpha 1*	0.97	3.6
	100576	HG2290-HT2386		*calcitorin/alpha-CGRP, all transcript	1	1.
	100668	HG2981-HT3938		TIGR: CD44 (epican, all. transcript 12	0.85	1.9
85	100906 100930	HG4716-HT5158 HG721-HT4827		Guanosine 5'-Monophosphate Synthase "TIGR: placental protein 14, endometrial	1.1B 1	2.29 1.45
-	100300	119121-014027		TOTA protest protest 14, Citationia	•	1.40

	W	O 02/0864	143			
	100960	J00124	Hs.117729	keratin 14 (epidarmolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute comptex (Orosophila) hornol	1	1
	101124	L10343	Hs.112341	"Protease Inhibitor 3, skin-derived (SKA	0.62	2.67
5	101175	L18920	Hs.36980	"Melanoma antigen, family A, 2"	1	1
_	101204	L24203	Hs.82237	Ataxia-telangiectasia group D-associated	0.74	4.1
	101431	M19888	Hs.1076	Small proline-rich protein 18 (comitin)	0.85	2.51
					. 0.61	8.83
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex		
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
10	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	"Guartine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		"Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	M86757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
	101809	M86849	120112100	"Homo sapiens connexin 26 (GJB2) mRNA, c	1	7
20	101845	M93426	Hs.78867		i	i
20				*Protein tyrosine phosphatase, receptor-		
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	26
	102083	U10323	Hs.75117	"Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
0.5	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
25	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77258	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
	102623	U66083	Hs.37110	"Melanoma antigen, family A, 9 (MAGE-9)"	1	1
30	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	i	i
50				Forthead box M1	1.06	2.77
	102696	U74612	Hs.239			
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888	X04741	Hs.76118	Ubłquifin carboxyl-terminal esterase L1	1.13	2.59
0.5	102913	X07696	Hs.80342	kerafin 15	0.7	4.72
35	102915	X07820	Hs.2258 .	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	*Calcitorin/calcitonin-related potypepti	1	1
	103021	X53587	Hs.85266	"integrin, beta 4"	1.3B	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
	103058	X57348	Hs.184510	Stratifin	1.25	4.17
40	103050				1	1.72
TU		X57766	Hs.155324	matrix metalloprotetnase 11 (stromelysin		
	103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	"Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	XB2693	Hs.3185	*Lymphocyte antigen 6 complex, locus D;	0.92	1.28
45	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083 ,	Hs.82128	5T4 Oncofetal antigen	1	3.93
	103594	Z31560	Hs.816	*SRY (sex determining region Y)-box 2, p	0.71	7.23
50			NS.010		0.99	1.8
50	103768	AA089997	11-0407	"ESTs, Highly similar to integral membra		
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
	104733	AA019498	Hs.23071	ESTs	1.18	1.88
55	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Wealdy similar to !!!! ALU SUBFAMI	1.64	2.89
	105012	AA116036	Hs.9329 ·	"Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Wealdy similar to unknown [S.cerev	0.9	4.63
	105263	AA227926 '	Hs.6682	EST6	0.95	2.87
60	105298	AA233459	Hs.26369	ESTs	1	1.13
••	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1.20	1
					0.94	
65		AA411621	Hs.8895	ESTs; same as BFH6?		2.04
O.S	105231	AA429571	Hs.38002	KIAA1355 protein .	1.04	1.5
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
70	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
		S74039	Hs.291904		1.15	3.65
75	107284			Accessory proteins BAP31/BAP29		
1 5	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	lg superfamily receptor LNIR precursor	1	2.48
	107932	AA029317	Hs.18878	Hypothetical protein FLJ21620	1	1
	108695	AA121315	Hs.70823	KIAA1077 protein	0.91	3.53
00	108857	AA133250	Hs.62180	ESTs	1	1
80	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	i	4.55
		AA227919			i	1.28
	109424		Hs.85962	Hyahronan synthase 3		
85	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
93	109970	H09281	Hs.13234	ESTs	1.13	2.16
					•	

	w	O 02/0864	43			
	110015	H10998	Hs.7164	A disintegrin and metalloproteinase doma	0.84	1.95
	110156	H18957	Hs.4213	ESTs	0.94	1.41
	110561	H59617	Hs.5199	HSPC150 protein similar to ubiquitin-con	0.91	3.18
_	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13
5	111345		Hs.14559	Hypothetical protein FLJ 10540	1	1.25
	111876		Hs.293246 Hs.109445	*ESTs, Wealdy similar to putative p150 [0.83 0.91	1.27 0.91
	111902 112244	R39191 R51309	Hs.70823	KIAA1020 protein KIAA1077 protein	0.77	3.01
	112973	T17271	11011 0100	CDNA FLJ13308 fis, clone OVARC1001436,	1	1
10	112989	T23482	Hs.89981	"Diacylglycerol kinase, zeta (104kD)"	0.55	1.03
	113047	T25867	Hs.7549	ESTs .	0.87	2
	113095	T40920	Hs.126733	ESTs	1	1
	113531	T90345	Hs.16740 Hs.8109	Hypothetical protein FLJ11036 ESTs	0.42 1.17	1.44 1.73
15	113970 114346	W86748 Z41450	Hs.130489	"ATPase, aminophospholipid transporter-I	0.86	0.82
13	114407	AA010188	Hs.103305	ESTs	0.8	1.88
	114471	AA028074	Hs.104613	RP42 homolog	1.05	1.34
	114509	AA043551	Hs.101799	KIAA1350 protein	1.82	2.32
20	115060	AA253214	Hs.198249	"Gap junction protein, beta 5 (connexin	0.79	1.49
20	115091	AA255900 AA256642	Hs.184523 Hs.236894	KIAA0965 protein "ESTs, High sim to LRP1_hu low density I	0.72 0.59	1.92 1.97
	115123 115291	AA279943	Hs.122579	ESTs	1	1.25
	115506	AA292537	Hs.45207	Hypothetical protein KIAA1335	1.15	1.48
~ -	115522		Hs.47378	ESTs	0.5	3.29
25	115536	AA347193	Hs.62180	ESTs	1	1
	115697	AA411502	Hs.63325	Homo sapiens type (I membrane serine pro	1	6.53 6.98
	115909 115978	AA436666 AA447522	Hs.59761 Hs.69517	ESTs Differentially expressed in Fanconi anem	1	2.31
	116028		Hs.42644	thioredoxin-like	0.99	1.68
30	116107	AA456958	Hs.92030	ESTs	1.14	1.8
	116134		Hs.50441	CGI-04 protein -	1.11	1.86
	116157	AA461063	Hs.44298	Hypothetical protein	0.99	1.9
	116158		Hs.61762	Hypoxia-inducible protein 2	0.44	0.86 3.89
35	116335 116483	AA495830 C14092	Hs.87013 Hs.76118	"Homo sapiens cDNA FLJ10238 fis, clone H Ubiquitin carboxyl-terminal esterase L1	0.62 1.04	2.36
55	117320	N23239	Hs.211092	LUNX protein; PLUNC(palate lung & nasal	0.51	0.64
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63
	117693		Hs.112110	PTD007 protein	0.98	1.79
40	117881	N50073	Hs.260622	Butyrate-induced transcript 1	1	1.43
40	118368 118566	N64339 N68558	Hs.48956 Hs.42824	ESTs Hypothetical protein FLJ10718	0.67 1.21	2.86 0.83
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88	1.63
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	1	1
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1	1
45	120102	W95428	Hs.132927	*ESTs, Moderately similar to p53 regulat	1	1
	120104	W95477	Hs.180479	ESTS Turner controls 63 kDs with stress beganing	0.69 1.08	3.07 12.05
	120486 120859	AA253400 AA350158	Hs.137569 Hs.1619	Tumor protein 63 kDa with strong homolog Achaete-scute complex (Drosophila) homol	1.00	1
	120880	AA360240	Hs.97019	EST	i	i
50	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292	1.04	2.15
	120983		Hs.97587	EST	1	1
	121362	AA405500 AA405657	Hs.97932	Chondromodulin I precursor	1	1 1.8
	121369 121791	AA423978	Hs.128791 Hs.293317	CGI-09 protein "ESTs, Wealthy similar to JM27 (H.sapiens	i	1.0
55	123005	AA479726	Hs.105577	ESTs	1	i
	123044	AA481549	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88
	123160	AA488687	Hs.284235	ESTs	1.59	4.98
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20 "ESTs, Weakly similar to PQ0109 Purkinje	1.19 1.03	1.64 1.14
60	1235/1	AA608956 AA620697	Hs.112619 Hs.112208	XAGE-1 protein	1.39	2.2
•	124006	D60302	Hs.108977	ESTs	1	4.85
	124059	F13673	Hs.99769	ESTs	1.49	8.62
	124960	T15386	Hs.194766	Salzure related gene 6 (mouse)-like	0.76	0.77
65	125218	W73561	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33 0.8	1.77 1.42
05	125453 125759	R05041 AA425587	Hs.18048 Hs.82226	"Melanoma antigen, family A, 10" Givcoprotein (transmembrane) nmb	1.52	2.26
	125972	AA434562	Hs.35406	"ESTs, Highly similar to unnamed protein	1.05	2.48
	125994	H55782	Hs.270799	EST	1	1.95
70	126395	N70192	Hs.278956	Hypothetical protein FLJ12929	1	1.35
70	126645	Al167942	Hs.61635	STEAP1 (Homo sapiens BAC clone RG041D11	1 0.73	2.23 3.27
	127221 127479	Al354332 AA513722	Hs.72365 Hs.179729	ESTs collagen; type X; alpha 1 (Schmid metaph	0.51	1.94
	128192		· ==. 11 01 23	KIAA1085 protein	1.8	3.16
75	128610	L3850B	Hs.10247	activated leucocyte cell adhesion molecu	0.89	0.97
75	128777	U46006	Hs.10526	Cysteine and glycine-rich protein 2	1.	1
	128924	AA234962	Hs.26557	Plakophilin 3	1.3	2.97
	129041 129099	H58873 H50398	Hs.169902 Hs.108660	*Solute carrier family 2 (facilitated gl *ATP-binding cassette, sub-family C (CFT	0.84 0.87	2.04 1.04
	129404	AA172056	Hs.111128	ESTs	1	1
80	129466	L42583		"Genbank Homo sapiens keratin 6 isoform	0.72	12.67
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5
	129628	U26727	Hs.1174	*Cyclin-dependent kinase inhibitor 2A (m	0.85	1.93
	130023 130080	X13461 X14850	Hs.239600	Calmodulin-like 3 "H2A histone family, member X"	0.84 0.98	1.22 1.96
85	130385	AA126474	Hs.147097 Hs.155223	stannincalcin 2	1	1.50

	w	O 02/086	443			
	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63
	130441	U35835	Hs.301387	"Human DNA-PK mRNA, partial cds"	1.15	3.65
	130482	L32866	Hs.1578	Bacutoviral IAP repeat-containing 5 (sur	1	1.88
_	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.98
5	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7
	130627 130800	L23808	Hs.1695	Matrix metalloproteinase 12 (macrophage	0.69	4.05
	130939	AA223386 AA598689	Hs.19574 Hs.21400	ESTs; Weakly similar to katanin p80 subu ESTs	1.13 0.8	2.41 0.89
	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS		1.15
10	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85
	131877	J04088	Hs.156346	Topoisomerase (DNA) (I alpha (170kD)	1	1
	131927	AA461549	Hs.34780	*Doublecortex; lissencephaly, X-linked (0.81	0.62
	131965	W90146	Hs.35962	ESTs	0.74	3.27
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1
13	132354	L05187	Hs.211913	Small proline-rich protein 1A	0.69	1.43
	132543 132632	AA417152 N59764	Hs.5101 Hs.5398	ESTs; Highly similar to protein regulati guanine-monophosphate synthetase	0.79 1	4.27 1.08
	132653	U31201	Hs.54451	"laminin gamma2 chain gene (LAMC2), exon	i	1.00
	132659	Z75190	Hs.54481	*Low density Epoprotein receptor-relate	0.89	0.89
20	132710	W93726	Hs.55279	"Serine (or cysteine) proteinase inhibit	0.64	4.41
	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08
	132767	L05188	Hs.231622	Small proline-rich protein 28	0.83	1.66
	132816	M74542	Hs.575	Aldehyde dehydrogenase 3	0.55	0.55
25	132990 133070	AA458761 U69611	Hs.18387	transcription factor AP-2 alpha (activat	1	3.53
23	133282	U52960	Hs.64311 Hs.286145	"A disintegrin and metalloproteinase dom "SRB7 (suppressor of RNA polymerase B, y	1.16 1	2 2.7
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	0.95	1.42
	133370	AA156897	Hs.72157	Homo sapiens mRNA; cDNA DKFZp564l1922	1.12	2.55
	133391	X57579	Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76
30	133832	H03387	Hs.241305	estrogen-responsive 8 box protein (EBBP)	1.02	1.39
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase inhibit	1	1
	134168	AA398908	Hs.181634	"Homo sapiens cDNA: FLJ23602 fis, clone	0.95	1.53
	134218	AA227480	Hs.80205	Pim-2 oncogene	1.36	2.48
35	134405 134453	R67275 X70683	Hs.82772 Hs.83484	""collagen, type XI, alpha 1"" SRY (sex determining region Y)-box 4	0.76	2.86
55	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.89 1.82	3.78 4.11
	134645	U87459	Hs.167379	"Cancer/lestis antigen (NY-ESO-1, CTAG1,	0.82	0.83
	134781	M17183	Hs.89626	Paralhyroid hormone-like hormone	1	1
40	135002	U19147	Hs.272484	G antigen 6	1	1
40	100040	M97935		AFFX control: STAT1	0.92	1.25
	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	2.92	8.5
	101664	M60752	Hs.121017	H2A histone family; member A	1	1
	102025 102031	U03911 U04898	Hs.78934 Hs.2156	mutS (E. coll) homolog 2 (colon cancer; RAR-related orphan receptor A	0.8 1	1.61 1
45	102221	U24576	113.2150	LIM domain only 4	i	i
•••	102270	U30255	Hs.75888		1.08	1.43
	102339	U37022	Hs.95577		0.88	1.32
	102391	U41668	Hs.77494		1.07	1.58
50	103000	X51956	Hs.146580		0.91	1.49
50	103395	X94754	Hs.119503		0.89	1.32
	105638	AA281599	Hs.20418		0.91	1.25
	105726 114841	AA29232B AA234722	Hs.9754 Hs.55408		0.94 0.78	1.48 1.56
	115206	AA262491	Hs.186572		1	1
55	115906	AA436616	Hs.82302		0.74	2.52
	119132	R49046	Hs.107911		1.1	1.51
	124163	H30539	Hs.189838		1	1
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46
60	127141	AA307960	Hs.75478		0.85	1.4
60	128034	AA905754	Hs.75103		1	1.18
	128609 128895	AA234365 R37753	Hs.102456 Hs.106985	survival of motor neuron protein interac ESTs	1 1.7	1.5 2
	130199	Z48579	Hs.172028		1.7	1
	130524	U89995	Hs.159234		i	i .
65	133000	U24152	Hs.62402		İ	1
	133558	M25758	Hs.75426		1	1
	135047	AA460466	Hs.93597	ESTs	1	1
	100053	M27830			0.88	1.53
70	100114	D00596	Hs.82962		0.68	1.86
70	100128 100154	D11094 D14657	Hs.61153		1.29	2.03
	100154	D14694	Hs.81832 Hs.77329		0.71 1.02	4.28 1.56
	100168	D14874	Hs.394		0.46	1.17
	100187	D17793	Hs.78183		1	1
75	100188	D21063	Hs.57101		0.97	1.4
	100217	D26600	Hs.89545	proteasome (prosome; macropain) subunit;	1.13	1.9
	100220	D28364		Human mRNA for annextn II, 5UTR (seq	1.11	1.53
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09
80	100297	D49489	Hs.182429		0.92	1.78
30	100330 100355	D55716 D78129	Hs.77152		1.07 n.os	1.61 1.87
	100364	078586	Hs.154868		0.96 1.49	2.46
	100368	D79987	Hs.153479		0.59	1.32
0.5	100398	D84557	Hs.155462		1.08	1.9
85	100438	D87448	Hs.91417		1	2.15

WO 02/086443 100455 D87953 N-myc downstream regulated Nucleoside Diphosphate Kinase Nm23-H2s Hs,75789 HG1153-HT1153 1.41 100491 1.28 100518 HG174-HT174 Desmoplakin I 3.17 "Nexin, Glia-Derived" 100528 HG1828-HT1857 0.68 1.9 Ribosomal Protein L39 Homolog 5.44 5 100661 HG2874-HT3018 0.8 1.97 "Epican, Alt. Splice 11" 100667 HG2981-HT3127 212 HG4074-HT4344 Rad2 100830 101061 K03515 Hs.944 glucose phosphate isomerase 0.91 1.79 splicing factor, arginine/serine-rich 3 solute carrier family 1 (glutamate/neutr macrophage migration inhibitory factor (Hs.167460 1.87 101131 L10838 1 23 10 Hs.174203 1.35 273 101162 1.14595 Hs.73798 1.03 101181 L19688 H2A histone family; member O 1.3 L19779 Hs.795 101183 cyclin-dependent kinase inhibitor 3 (CDX 1.25876 Hs.84113 0.7 22 101216 101228 127706 Hs.82916 chaperonin containing TCP1; subunit 6A (0.99 1.99 sorbild dehydrogenase glycogen synthase kinase 3 beta 15 211 0.82 101233 1 29008 Hs 878 Hs.78802 1.2 L33801 101247 101332 L47276 "Homo sapiens (cell line HL-6) alpha t 2.78 Hs.182018 interleukin-1 receptor-associated kinase 1 04 1.84 101342 L76191 3.55 101396 M15796 Hs.78996 proliferating cell nuclear antigen 0.95 20 EphA1 1.5 101423 M18391 Hs 89839 small nuclear ribonucleoprotein polypept 1.21 101445 M21259 Hs.1066 M27396 Hs.75692 asparagine synthetase 1.6 101505 eukaryotic translation initiation factor 101525 M29536 Hs.12163 1.19 1.93 101535 M30448 Hs.251669 casein kinase 2; beta polypeptide 0.96 1.42 CD9 antigen (p24) —Human alpha-1 collagen type I gene, 3 1.25 25 Hs.1244 1.11 101607 M38690 1.98 101624 M55998 Hs.79217 pyrroline-5-carboxytate reductase 1 3.45 101758 M77836 membrane component; chromosomal 4; surfa 101839 M93036 Hs.692 0.71 1.45 Hs.76084 1.19 101853 M94362 lamin B2 0.84 30 0.89 putative Rab5-interacting protein (cl 101977 SR3364 polo (Drosophia)-like kinase 1.46 U01038 Hs.77597 101992 protein tyrosine kinase 9 singed (Drosophila)-like (sea urchin fas aldo-keto reductase family 1; member C1 Hs.82643 1.23 3.35 102009 U02680 1.88 102012 U03057 Hs.118400 0.85 2.32 102039 U05861 Hs.201967 0.93 centromere protein A (17kD) smati nuclear ribonucteoprotein D3 polyp 35 4.28 1114518 102123 Hs.1594 0.89 1.42 U15009 Hs.1575 102130 Hs.75823 ALL1-fused gene from chromosome 1q 0.8 2.95 102148 U16954 1.34 eukaryotic translation initiation factor 102210 U23028 Hs.2437 1.01 2.34 lysyl oxidase-like 1 Hs.65436 1.15 102220 U24389 40 2.69 Hs.159557 karyopherin aipha 2 (RAG cohort 1; impor 102260 U28386 U35451 Hs.77254 chromobox homolog 1 (Drosophila HP1 beta 1.7 102330 2.99 102423 U44754 Hs.179312 small nuclear RNA activating complex; po 1.14 discondin domain receptor family; member ATPase; Na+/K+ transporting; beta 3 poly 2.01 1.05 102455 U48705 Hs.75562 Hs.76941 1.27 1.92 1151478 102499 45 Hs.183556 solute carrier family 1 (neutral amino a 0.84 1.31 102522 U53347 102590 U62136 "Homo sapiens enterocyte differential 1.11 1.6 102676 U72514 Hs.12045 putative protein 1 04 2.17 ubiquitin carrier protein E2-C BRCA1 associated RING domain 1 2.28 Hs.93002 0.86 102687 U73379 Hs.54089 1.12 102704 U76638 50 "Human HIV-1 Nef interacting protein (1.39 102781 U83843 0.98 102784 U85658 Hs.61796 transcription factor AP-2 gamma (activat 2.16 chaperonin containing TCP1; subunil 2 (b small nuclear ribonucleoprotein polypept 102827 U91327 Hs.6456 0.96 1.62 4.2 1.21 102935 X13482 Hs.80506 annexin A8 X16662 Hs.87268 102972 55 non-metastatic cells 1; protein (NM23A) 1.03 1.83 102983 X17620 Hs.118638 103023 Hs.117950 multifunctional polypeptide similar to S 1.58 5.44 X53793 CDC28 protein kinase 1 ribonucleofide reductase M1 polypeplide 3.79 1.32 103038 X54941 Hs.77550 Hs.2934 1.11 2.58 103075 X59543 glutathione peroxidase 2 (gastrointestin 3.05 103168 X68314 Hs.2704 60 Hs.74368 transmembrene protein (63kD); endoplasmi 1.01 1.97 103185 X69910 phosphorytase kinase; alpha 1 (muscle) chaperonin containing TCP1; subunit 3 (g 103212 X73874 Hs.2393 0.95 1.72 X74801 0.97 1.77 103223 Hs.1708 X78416 casein; alpha 103260 Hs.3155 Hs.204133 hexabrachion (tenascin C; cytotactin) 1.23 3.09 103262 X78565 65 Hs.77496 103330 small nuclear ribonucleoprotein polypept 1.12 2 25 4.62 X90872 X91868 SULT1C sufforensferase sine oculis homeobox (Drosophila) homolo 103364 Hs.75854 2.85 Hs.54416 103375 Hs.114366 pyrroline-5-carboxylate synthetase (glut 1.53 103391 X94453 103404 X95586 Hs.78596 proteasome (prosome; macropain) subunit; 0.92 1.53 1.54 70 103437 103448 M-phase phosphoprotein 11 lipocalin 2 (oncogene 24p3) cadherin 1; E-cadherin (epithellal) X98260 Hs.82254 0.92 0.96 X99133 Hs.204238 0.55 Z35402 1.32 103605 Hs.194657 2.51 103646 Z68228 Hs.2340 junction plakoglobin 1.28 103658 2 98 **Z74615** Hs.172928 collagen; type I; alpha 1 1.06 conlagent type i, aprila i ESTs; Wealdy similar to R07G3.8 [C.elega RNA polymerase I subunit ESTs; Wealdy similar to R27090_2 [H.sapi 75 4.66 103774 AA092898 Hs.92918 1.88 217 104261 AF008442 Hs.5409 0.87 Hs.85222 2.49 104276 C02193 KIAA0956 protein 1.15 1.68 104289 C162B1 Hs.75478 collagen; type VII; alpha 1 (epidermolys 104434 104453 1.49 L02870 Hs.1640 1.04 80 0.76 Hs.123114 0.38 M19169 cystatin SN ribulose-5-phosphate-3-epimerase 1.08 104611 R98280 Hs.125845 AA024561 ESTs; Wealthy similar to ACYL-COA DEHYDRO 1.65 104758 Hs.7010 AA156532 adenosine A2b receptor pseudogene 0.91 1.38 105114 Hs.11801 105132 AA159501 Hs.247280 **HBV** associated factor 1.08 1.7 85 2.05 105174 AA186613 Hs.34744 **ESTs**

	W	O 02/086	5443			
	105280	AA232215	Hs.14500	ESTs	1	1.4
	105344	AA235303	Hs.8645	ESTs	0.72	2.02
	105516 105621	AA257971 AA280865	Hs.21214 Hs.6375	ESTs Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.35 1.23	3.56 1.82
5	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98	1.28
	105705	AA290767	Hs.101282	Homo saplens mRNA; cDNA DKFZp434B102 (fr	0.92	1.32
	105724	AA292098	Hs.22934 Hs.21580	ESTs; Weakly similar to ZINC FINGER PROT	0.99 1	1.41 1
	105782 105799	AA350215 AA372018	Hs.24743	ESTs ESTs	1.08	1.78
10	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN ALP	0.95	1.34
	105891	AA400768	Hs.26562	ESTs; Wealthy similar to tumor necrosis f	0.87	2.25
	105936 106069	AA404338 AA417741	Hs.29899	ESTs ESTs; Wealthy similar to ZINC FINGER PROT	1,14 1	1.46 1
	106103	AA421104	Hs.12094	ESTs	1.04	1.44
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11
	106149	AA424881	Hs.256301 Hs.6994	ESTs ESTs	0.83 0.77	1.48 2.05
	106154 106182	AA425304 AA426609	Hs.10862	ESTs	0.74	2.23
	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97	1.99
20	106228	AA429290	Hs.17719	ESTs	0.99	1.54
	106318 106341	AA436570 AA441798	Hs.9605 Hs.5243	pre-mRNA cleavage factor Im (25kD) ESTs; Moderately similar to plL2 hypothe	0.95 0.98	2.09 2.66
	106432	AA448850	Hs.17138	ESTs	0.95	1.93
25	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	1.	1
25	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29
	106599 106611	AA457235 AA458904	Hs.12842 Hs.26267	ESTs; Moderately similar to non-function ESTs; Wealdy similar to torsinA [H.sapie	1.49	1.82 2.78
	106654	AA460449	Hs.3784	ESTs; Highly similar to phosphoserine am	1	1.4
20	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49
30	107115	AA610108	Hs.27693	ESTs; Highly similar to CGI-124 protein	1 1.13	1.03 3.63
	107129 107159	AA620553 AA621340	Hs.4756 Hs.10600	flap structure-specific endonuclease 1 ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18	1.9
25	107481	W58247	Hs.27437	Homo sapiens kinesin superfamily motor K	0.99	2.74
35	107516 107529	X56597 Y12065	Hs.99853 Hs.5092	fibrillarin nucleolar protein (KKE/D repeat)	0.94 1.05	1.77 2.29
	107525	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	1.06	1.62
	107801	AA019433	Hs.173100	ESTs	1.03	1.4
40	107957	AA031948	Hs.57548	ESTs	0.95	1.46
40	108565 108780	AA085342 AA128561	Hs.1526 Hs.117938	ATPase; Ca++ transporting; cardiac muscl collagen; type XVII; alpha 1	0.59 1	1.35 7.63
	108828	AA131584	Hs.71435	DKFZP564O0463 protein	1.33	2.56
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42
45	109112 109344	AA169379	Hs.72865 Hs.86559	ESTs	1.03 0.97	2.31 1.55
73	109344	AA213696 AA227145	Hs.209473	poly(A)-binding protein-like 1 ESTs; Wealty similar to REGULATOR OF MIT	0.76	1.87
•	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9	0.95
	110958	N50550	Hs.24587	signal transduction protein (SH3 contain	1.17 1.21	2.26
50	111018 111337	N54067 N79512	Hs.3628 Hs.16607	mitogen-activated protein kinase kinase ESTs; Highly similar to Myosin heavy cha	1	1.85 1.45
•	112305	R54822	Hs.26244	ESTs	1	1
	112401	R61279	Hs.237536	ESTs; Wealty similar to F25B5.3 [C.elega	1.24	1.64
	112853 112869	T02843 T03313	Hs.4351 Hs.4747	EST dyskeratosis congenita 1; dyskertn	1.56 1.03	1.96 1.57
55	112992	T23513	Hs.7147	ESTs	1	1
	113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26
	113063	T32438	Hs.5027	ESTS	1 1.33	1 27
	113179 113573	T55182 T91166	Hs.152571 Hs.15990	ESTs; Highly similar to IGF-II mRNA-bind ESTs	0.76	1.47
60	113811	W44928	Hs.4878	ESTs	0.79	1.51
	114086	Z38266	Hs.12770	Homo saptens PAC clone DJ0777023 from 7p	0.9	1.34
	114587 114846	AA070827 AA234929	Hs.180320 Hs.44343	ESTs; Wealthy similar to GOLGI 4-TRANSMEM ESTs	1.02 1.32	1.76 2.36
	114964	AA243873	Hs.82184	ring finger protein 3	1.1	1.84
65	115047	AA252627	Hs.22554	homeo box 85	1.01	2.36
	115166	AA258409	Hs.198907	myelin protein zero-like 1	1.05	2.31
	115167 115239	AA258421 AA278650	Hs.43728 Hs.73291	hypothetical protein ESTs; Weakly similar to similar to the b	1.52 0.7	2.52 2.57
a 0	115278	AA279757	Hs.67466	ESTs; Wealdy similar to BACN32G11.d [D.m	1.14	2.12
70	115652	AA405098	Hs.38178	ESTs	0.82	4.67
	115875 116004	AA433943 AA449122	Hs.43946 Hs.76086	ESTs; Wealdy similar to Weak similarity ESTs; Highly similar to small zinc finge	1.2 0.96	1.98 1.31
	116121	AA459254	Hs.48855	ESTs	0.97	1.55
75	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73
75	116190	AA464963	Hs.67776	ESTs ESTs	0.8 1.37	1.57 2.65
	116312 116732	AA490494 F13779	Hs.65403 Hs.165909	ESTs ESTs	0.92	1.8
	117602	N35020	Hs.44585	ESTs; Wealthy similar to GOLIATH PROTEIN	1.15	1.84
QΛ	117950	N51394	Hs.75478	KIAA0956 protein	1.04	2.36
80	117992 118785	N52000 N75386	Hs.172089 Hs.111867	Homo sapiens mRNA; cDNA DKFZp58680222 (f GLI-Kruppel family member GLI2	0.62 1	1.29 1
	119717	W69134	Hs.57987	ESTs	i	1.4
	119814	W74069	Hs.58350	ESTs	0.78	1.77
85	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86 0.83	1.46
05	120242	Z98443	Hs.86366	ESTs	0.83	2.01

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	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64
	121054 121326	AA398604 AA404246	Hs.97387 Hs.97031	ESTs ESTs: Weakly similar to Similar to phyto	1.05 0.98	1.93 1.3
_	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83
5	121457 121780	AA411448 AA422086	Hs.208985 Hs.124660	ESTs ESTs	0.91 0.46	1.59 0.55
	121781	AA422150	Hs.98370	cytochrome P540 family member predicted	1.07	1.54
	121844	AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4
10	122059 122338	AA431737 AA443311	Hs.98749 Hs.98998	EST ESTs	1.93 1	2.33 1
10	122354	AA443772	Hs.186892	ESTs ·	0.88	1.39
	122591	AA453265	Hs.99311	ESTs; Wealty similar to MRJ [H.sapiens]	2.28	2.93
	122790 123398	AA460156 AA521265	Hs.99556 Hs.105514	ESTs :	0.88 1	1.3 1.93
15	123518	AA508531	Hs.170313	ESTs	1	1
	123673	AA609471	Hs.112712 Hs.74861	ESTs activated RNA polymerase II transcriptio	1 0.74	1.15 1.12
	124000 124367	D57317 N24006	Hs.99348	distal-less homeo box 5	0.67	1.1
20	124447	N48000	Hs.140945	Homo sapiens mRNA; cDNA DXFZp586L141 (fr	1.19	1.7
20	125756 125769	W25498 Al382972	Hs.81634 Hs.82128	ATP synthase; H+ transporting; mitochond 5T4 oncofetal trophoblast glycoprotein	0.93 1.65	1.59 6.76
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp56481264 (f	0.72	2.26
	125924	AA526849	Hs.82109	syndecan 1	1.22 1.36	2.25 1.63
25	126037 126214	M85772 N29455	Hs.6066 Hs.74316	KIAA1112 protein desmoplakin (DPI; DPII)	1.93	3.55
	126414	N78770	Hs.223439	ESTs	1.21	1.66
	126737 126743	AA488132 AA179253	Hs.62741 Hs.172182	ESTs poly(A)-binding protein; cytoplasmic 1	1 1.3	1 2.16
	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8
30	127432	AA501734	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.57	2.12
	128218 128527	H02682 M31523	Hs.99189 Hs.101047	ESTs; Moderately similar to recombinatio transcription factor 3 (E2A immunoglobul	1.24 1.08	2.09 _. 1.78
	128568	X60673	Hs.247568	adenytate kinase 3	1.23	3.48
35	128584	M11433	Hs.101850	retinol-binding protein 1; cellular	0.87 1.22	2.42 1.9
33	128628 128691	C14037 W27939	Hs.251978 Hs.103834	EST ESTs	1.1	1.73
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17
	128733 128781	AA328993 X85372	Hs.104558 Hs.105465	ESTs small nuclear ribonucleoprolein polypept	1.34 0.9	1.94 1.34
40	129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19
	129095	L12350	Hs.108523	thrombospondin 2	1.04	3.2
	129241 129665	AA435665 M88458	Hs.109706 Hs.118778	ESTs; Moderately similar to HN1 [M.muscu KDEL (Lys-Asp-Gtu-Leu) endoplasmic retic	0.95 1.28	1.61 2.63
40	129703	AA401348	Hs.179999	ESTs	0.97	1.63
45	129720 129850	AA476582	Hs.12152 Hs.56845	ESTs; Moderately similar to SIGNAL RECOG GDP dissociation inhibitor 2	1.09 0.74	1.79 1.68
	129896	N20593 AA043021	Hs.13225	UDP-Gal:betaGlcNAc beta 1;4- galactosytt	1.43	4.19
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98
50	130405 130541	H88359 X05608	Hs.155396 Hs.211584	nuclear factor (erythroid-derived 2)-lik neurofilament; light polypeptide (68kD)	1.26 1	1.79 1
50	130599	M91670	Hs.174070	ubiquitin carrier protein	1.07	1.66
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1 0.93	4.8 1.05
	131009 131028	AA063596 U20240	Hs.22142 Hs.2227	ESTs; Weakly similar to NADH-CYTOCHROME CCAAT/enhancer binding protein (C/EBP);	1	1.23
55	131083	U66661	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.1	1.8
	131091 131144	T35341 C14412	Hs.22880 Hs.23528	ESTs; Highly similar to dipeptidyl pepti ESTs; Highly similar to HSPC038 protein	1.28 1.43	1.98 2.06
	131148	C00038	Hs.23579	ESTs	0.88	3.38
60	131164	Y00503	Hs.182265	keratin 19	1.19	2.77
UU	131185 131219	M25753 C00476	Hs.23960 Hs.24395	cyclin B1 small inducible cytokine subfamily B (Cy	0.86 0.65	3.84 2.96
	131454	AA455896	Hs.2699	glypican 1	0.99	1.54
	131687 131689	L11066 AA599653	Hs.3069 Hs.30696	heat shock 70kD protein 9B (mortalin-2) transcription factor-like 5 (basic helix	1	1.18 1.95
65	131692	D50914	Hs.30736	KIAA0124 protein	1.55	2.39
	131786	AA135554	Hs.32125	ESTs	1	1.33
1	131843 131860	AA195893 U02082	Hs.184062 Hs.334	ESTs; Moderately similar to putative Rab Oncogene TIM	0.83 1.08	1.63 2.2
5 0	131884	H90124	Hs.3463	ribosomal protein \$23	1.23	1.24
70	131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog) replication factor C (activator 1) 4 (37	0.91 1	1.18 2.8
	131945 131958	M87339 AA093998	Hs.35120 Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36
	131954	W42508	Hs.3593	ESTs	1	1.25
75	132001 132040	J00277 AA146843	Hs.37003 Hs.172894	v-Ha-ras Harvey rat sarcoma viral oncoge BH3 interacting domain death agonist	1.12 1	1.43 1.55
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89	1.27
	132109	AA599801	Hs.40098	ESTs	1 0.99	1.05 1.44
	132112 132123	AA150661 AA447123	Hs.40154 Hs.250705	jumonji (mouse) hornolog ESTs	1.05	2.45
80	132162	H89551	Hs.41241	ESTs	1.08	2.46
	132180 132309	AA405569 AA460917	Hs.418 Hs.2780	fibroblast activation protein; alpha; se Jun D proto-oncogene	1.02 1.16	4.56 1.8
	132371	AA235448	Hs.46677	ESTs	0.8	1.26
95	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.5	1.49
85	132736	U68019	Hs.211578	MAD (mothers against decapentaplegic; Dr	1.21	1.81

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	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3	
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43	
		T23641	Hs.6066	KIAA1112 protein	1.16	1.53	
		AA028103	Hs.61472	ESTs; Wealty similar to unknown [S.cerev	1.02	1.88	
5	132994	AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97	
_	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34	
		X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23	
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76	
		L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43	
10	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8	
	133195		Hs.181409	KIAA1007 protein	2.29	2.69	
		AA249427	Hs.70704	ESTs	1.07	1.68	
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18	
	133438		Hs.73722	APEX nuclease (multifunctional DNA repair	0.91	1.45	
15		T99303	Hs.73797	quanine nucleotide binding protein (G pr	0.94	1.68	
	133483	X52426	Hs.74070	keratin 13	0.85	1.14	
		L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69	
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	0.7	6.21	
	133517		Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3	
20	133540		Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25	
	133594	L07758	Hs.172589	nuclear phosphoprotein similar to S. cer	0.84	1.29	
	133627	U09587	Hs.75280	glycyl-IRNA synthetase	1.09	1.99	
	133671		Hs.75471	zinc finger protein 146	1.02	1.5	
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33	
25	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7	
23			NS.170230	calumenin	1.15	1.86	
	133963	W84712	Hs.7753		1.3	1.91	
		L34587	Hs.184693	transcription elongation factor B (SiII)	1.3	1.99	
	133982		Hs.207251	nucleolar autoantigen (55kD) similar to	0.72	1.65	
30	134100		Hs.171075	replication factor C (activator 1) 5 (36	1.04	1.62	
50	134110		Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.55	
	134158	U15174	Hs.79428	BCL2/adenovirus E18 19kD-interacting pro	0.82	1.95	
		U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.98		
	134193	F09570	Hs.7980	ESTs		1.48	
35		X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8	
33	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2	
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1	1.47	
		X17567	Hs.83753	small nuclear ribonucleoprotein polypept	0.94	1.57	
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2	2.64	
40	134501		Hs.211568	eukaryotic translation initiation factor	0.84	1.36	
40	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.93	
	134548		Hs.85215	Deleted in split-hand/split-foot 1 regio	1.46	2.73	
		X99226	Hs.86297	Fanconi anemia; complementation group A	1.36	2.22	
	134692	R73567	Hs.8850	a disintegrin and metalloproteinase doma	0.77	1.64	
4.5	134693	N70361	Hs.8854	ESTs	1.09	1.82	
45		Z49099	Hs.89718	spermine synthase	0.98	1.35	
	134821	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4	
		Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42	
		U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.16	1.29	
	134953	L10678	Hs.91747	profilin 2	0.95	1.76	
50	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73	
	135051	C15324	Hs.93668	ESTs	1.35	2.11	
	135158	U51711		Human desmocollin-2 mRNA; 3' UTR	0.86	1.16	
55	Table 18	shows the acc	ession numbers	for those pkeys in Table 1A lacking unigenelD's. For	or each probeset we ha	ave listed the gene ch	uster number from which the
ככ	ougonuc	eodoes were de	sgnea, Gene a	lusters were compiled using sequences derived from	II ∪enDank 25 IS 200 I	itiranas. Idese segl	icinces were ciusteieu dased on sequei

55 of Strows the accession numbers for times preys in table I/L access ungestions. The earlier process we have itself to table interest on sequences of the strower of the strong control of the stron

	Pkey:	Unique Eos probeset identifier number
60	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

	Pkey	CAT	Accessions
65	100661 100667	23182_1 26401_3	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA332714 AA572695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA278047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153
70			BES46944 T69221 AW377441 AA907406 H50799 AW051416 A420712 BE620922 AL7979161 AA992549 W47198 BE005241 AI342598 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675981 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AIZ78771 BE454018 AI081503 AI824195 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668	26401_3	AUG4333 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27385 AAS32714 AA972695 AW377728 AI632506 T29066 AI783934 AW3777727 BE163715 ALD47291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE548944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700
80			A1969974 A1853855 AA374490 AW130675 A1950633 AA146867 H99482 X55150 BED05414 BED05339 N28294 A1573068 A1887890 AW804171 A1675961 AW804172 AA778841 AL048050 A1127757 AX995568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N56010 AW589527 A160414 AA2633090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW795025 AW382768 BE565571 C00444 AAD54555
85	101332	25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AJ471482 AJ970337 AA737616 AJ827444 AW003286 AJ742333 AJ344044 AJ765634

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AI948838 AW235336 AW172827 AA095289 BE046383 AI734240 W16699 AI660329 AI289433 AA933778 AW469242 AA468838 AA806983

			A1948838 AW235336 AW172827 AA095289 BE046383 A1734240 W16699 A1660329 A1289433 AA933778 AW469242 AA468838 AA806983 AA625873 W78031 BE206307 AA550803 A1743147 A1990075 AA948274 AA129533 A1636399 AA605313 A1624669 AW594319 A1221834 A1337434 AA307706 BE550282 A1760467 A1630636 A1221521 AW674314 AW078889 A1933732 A1686969 A1186928 AW074595 A1127486 A1079644
5			AJ910815 H17814 AA310903 AW137854 T19279 AA026682 AA306035 AW383390 AW383389 AW383422 AW383427 AW383395 H09977 AA306247 AA352501 AW403639 F05421 AA224473 AA306321 H93904 AA089612 AW391543 AW402915 AW173382 AW402701 AW403113 R94438 N73126 H93466 AA090928 AA095051 T29025 AW951071 L47277 L47276 AJ375913 BE384156 W24652 AA746288 AA568223 BE090591
10			H93033 N57027 AA504348 AA327653 AW959913 N53767 AA843715 AI453437 AW263710 AI076594 AA583483 AW873194 AW575166 AI128799 AI803319 AL042776 AW0714313 AI8877722 AI032284 AA447521 AI123885 N29334 AI354911 AW09087 AA236763 AA435535 AA236910 AA047124 AA236734 AW514610 H93457 AA965200 AI446783 AA172759 AI613495 AI686720 AI3567374 AA336731 AA702453 AI859757 AA246736 AI354914 AI467274 AA2687874 AA2687874 AA2687874 AA367874 AA2687874 AA268787
			AA216786 Al251819 Al469227 AA806022 Al092324 N71868 AA958782 AA236919 AA809450 AA227220 AA765284 A1192007 AA768810 AA805794 AA729280 AA806238 AW768817 N71879 Al050686 AA505822 AA668974 Al688160 BE045915 AW466315 AA731314 AA649568 AA834316 AW591901 AW063876 AW294770 Al300266 Al336094 Al560380 AA721755 H09978 D20305 D29155 AW821790 BE150864 F01675 A457474 AW466316 AA550989 AA630788
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85			R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849590 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467

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5			AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092137 BE092137 BE092136 AW177784 Al022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 A1190590 C03378 A1554403 A1205263 AA128470 AX392926 AF139065 AW370813 AW370873 AW798477 AW79870 AW798883 AW798569 R335590 C03378 A1554403 A1205263 AA128470 AW370829 AA247685 BE002273 A1760816 AW39101 AW879451 A1700963 AA451923 A1340326 A1590975 T48793 A1568096 A1142882 AA039975 A470146 AA946336 BE067737 BE057786 W19287 AA644381 AA702424 A1417612 A1306554 A1588859 A1568892 AW190555 A1571075 A1220573 AA056527 A1471874 A1304772 AW517828 A1915596 A1627383 A1270345 AW021347 AW166807 AW105614 A1346078 AA552300 W95070
10			AM94059 AI911702 AA149191 AA026864 AI830049 AI887258 AW760435 AI910434 AI819984 AI858282 AI078449 AI025932 AI660584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243915 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771855 AI270027 AA951816 AA283207 AI076962 AM98487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW850878
15	100528	45979_1	BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE2774163 BE277479 BE408180 BE274874 C15000 AA047476 NZ7099 AI359165 AI638794 A1151283 AI863925 AW444977 AI207392 AA931263 AA443112 R40138 AW088538 AA351008 AA676972 R62503 AA916492 AW001865 H42334 H38280 AA121497 AA114137 A1750938 M17783 AA383786 BE274462 A1753182 C05975 AA347404 AW069298 A1754351 A1754044 AA188808 AA186879 AA565243 AU040655 AA456177 A1750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 M44761 R58560 R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591
20	100559	2260_1	BE389677 A7752233 AI568195 AA668004 AI424523 AW753720 AA652159 BE366803 NM_000094 L02870 D13694 S51236 M96994 AW946220 M65158 AI285422 D29523 AL119986 AW630655 L06862 AI884355 AW168737 T29085 AW797005 AW801340 AI355504 AW079048 AW601337 AI690455 AI972063 AW266565 W66588 AA587326 AA883498 AI033523 AW510356 AW591998 H98463 AL043852 AI150055 AI566239 AI624803 AA844717 H40670 AA922334 AI864424 AW615094 AW451233 AI302203 F31221 AI872170 W68589 AA904478 AI917631 AW014208 AW450759 AA847625 AI284033 AA848176 AA598507
25	100576 124357 101624 101625 135158	9986_1 genbank_N22 entrez_M5599 entrez_M5729 57963_1	X00356 NM_001741 M26095 X03662 M12667 X02330 X02330 AA716058 AW296074 X04861 Al695720 AA719597 401 N22401 8 M55998

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic normalignant lung diseases such as fibrosis, emphysema, and bronchibs. These genes were selected from 59660 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

•	wpi wood		, processi vs	and don't one diagon new expression as arrange		,,			,			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
	Pkey: ExAcon: Unigenell	Exempla		identifier number number, Genbank accession number								
10	Unigene ' R1:	Title: Unigene		or normal lung samples divided by the 80th percent	ile of All for a	denocarcir	oma and	squamous	cell carc	inoma lunç	j tumor	
	R2: R3:	median median	of Al for norm of Al for norm	al lung samples divided by 90th percentile of Al for al lung samples minus the 15th percentile of Al for	ell normal lun	ng, chronic	ally diseas	ed lung a	nd turnor	samples d	ivided by	
15				Al for adenocarcinoma and squamous cell carcino	ma tung tumo	or samples	minus the	15th pen	centile of	Al for all n	amal	
	· R4:			ased lung and tumor samples. nal lung samples divided by average Al for squamo	us cell carcin	oma and a	denocarc	inoma lun	g turnors.			
	R5: R6:	median	of Al for norm	ral lung samples divided by the 90th percentile of Al ral lung samples minus the 15th percentile of Al for	for adenocal	rcinomas. M. chronic	ally dicase	ed hma a	nd himor	samnles d	ivided by II	ne GOZh
20		percenti	le of Al for ad	enocarcinomas minus the 15th percentile of Al for a	di normal lun	g, chronica	dly diseas	ed lung at	d tumor	samples.		
	R7: R8:	average	of All for norm	nal lung samples divided by the 90th percentile of A hal lung samples minus the 15th percentile of Al for	l for squamo all normal lun	us cell car no. chronic	cinomas. aliv disea:	sed lung a	nd turnor	samples d	ivided by th	ne 90th
	-	percenti	ile of Al for sq	uamous cell carcinomas minus the 15th percentile o	of All for all no	ormal lung,	chronical	ly disease	d lung an	d tumor sa	mples.	
25	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4	R5	R6	R7	R8
	100095 100115	Z97171 NM_002084	Hs.78454	myocilin; trabecular meshwork inducible glutathione peroxidase 3 (plasma)	40.20							3.46
	100138	U8350B	Hs.2463	angiopoletin 1			2.30					
30	100299		Hs.2171 Hs.80598	growth differentiation factor 10		11.00				3.06		
	100306 100447			transcription elongation factor A (SII); KIAA0275 gene product						0.00		3.16
	100458	S74019	Hs.247979	Vpre-B	42.40					4.43		
35		AA005247 AA359129	Hs.285754 Hs.118127	Hapatocyte Growth Factor Receptor actin; alpha; cardiac muscle				125.60		4.13		
	101032	BE205854	Hs.46039	phosphoglycerate mutase 2 (muscle)	36.40							
	101081 101088	AF047347 X70697	Hs.4880 Hs.553	arrylold beta (A4) precursor protein-bind solute carrier family 6 (neurotransmitte				34.60 193.20				
40	101125	AJ250562	Hs.82749	transmembrane 4 superfamily member 2						3.10		
40	101180 101308	U11874	Hs.846	interleukin 8 receptor; beta "Homo sapiens core 2 beta-1,6-N-acetylgi	33.20			54.86				
	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				36.40				
		NM_005795 Al738616	Hs.152175 Hs.77348	Calcitonin receptor-like hydroxyprostaglandin dehydrogenase 15-(N			2.29	70.55				
45	101397		Hs.180878	lipoprotein lipase					•		6 0.	3.54
73	101414			complement component 8; beta polypeptide				34.60			3.81	
	101507	NM_001100 X16896	Hs.82112	actin; alpha 1; skeletal muscle interteukin 1 receptor; type I				37.60				
50	101530		Hs.1360	cytochrome P450; subfamily IIB (phenobar			2.54					4.25
30	101537 101542	AI469059 NM_000102	Hs.184915 Hs.1363	zinc finger protein; Y-linked cytochrome P450; subfamily XVII (steroid		5.50	2.04					
	101545		Hs.154210	EDG1; endothetial differentiation, sphin	39.40	13.00						
	101554 101560		Hs.123078 Hs.83733	thyroid stimulating hormone receptor Intercellular adhesion molecule 2, exon		13.00						3.38
55	101574	M34182	Hs.158029	protein kinase; cAMP-dependent; catalyti						4.37		3.80
	101621	M37984 BE391804	Hs.118845 Hs.62661	troponin C; slow guanylate binding protein 1; interferon-	30.20							0.00
	101680	AA299330	Hs.1042	Sjogren syndrome antigen A1 (52kD; ribon					ŧ	3.37	2.75	
60	101829 101842	AW452398 M93221	Hs.129763 Hs.75182	solute carrier family 8 (sodium/calcium mannose receptor; C type 1				38.20		3.31		
	101961	AW004056	Hs.168357	"Hs-TBX2=T-box gene (T-box region) [huma			2.32					6.85
	101994 102020	T92248 AU077315	Hs.2240 Hs.154970	uteroglobin transcription factor CP2			2.45					
65	102091	BE280901	Hs.83155	aldehyde dehydrogenase 7	C4 C0							6.75
05	102112 102190	AW025430 AA723157	Hs.155591 Hs.73769	forkhead box F1 folate receptor 1 (adult)	54.60							3.98
	102202	NM_000507	Hs.574	fructose-bisphosphatase 1			2.32					3.62
	102241 102310	NM_007351 U33839	HS.268107	Multimenta Accession not listed in Genbank		7.00	2.32					
70	102397		11. 000000	"Human sodium cotransporter RKST1 mRNA,	29.40							3.75
	102571 102620	U60115 AA976427	Hs.239069 Hs.121513	"Homo sapiens skeletal muscle LIM-protei Human clone W2-6 mRNA from chromosome X						3.07		3.73
	102636	U67092		"Human ataxia-lelangiectasia locus prote			2.40 3.15					
75	102667 102675	U70867 U72512	Hs.83974 Hs.7771	solute carrier family 21 (prostaglandin "Human B-cell receptor associated protei			J. 10			3.56		
	102698	M18667	Hs.1867	propastricsin (pepsinogen C)					12.00			4.51
	102727 102852	U79251 V00571	Hs.99902 Hs.75294	opioid-binding protein/cell adhesion mol conficotropin releasing hormons	37.40							
80	103026	X54162	Hs.79386	thyroid and eye muscle autoantigen D1 (6					13.00			
ου	103028 103098	X54380 M86361	Hs.74094	pregnancy-zone protein Human mRNA for T cell receptor; clone IG	28.80				10.00			
	103117	X63578	Hs.295449	parvalbumin		6.00	2.47					
	103241 103280	X76223 U84722	Hs.76206	H.sapiens MAL gene exon 4 Cadherin 5, VE-cadherin (vascular epilhe			2.47 2.69					
85	103360	Y16791	Hs.73082	keratin; hair, acidic; 5							2.16	

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		Y09267	Hs.132821	flavin containing monooxygenase 2							05021	5.97
	103508 103561	Y10141 NM 001843	Lie 142424	"H.sapiens DAT1 gene, partial, VNTR" contactin 1			2.40			3.27		
_	103569	NM_005512		glycoprotein A repetitions predominant			2.99					
5	103575			"H.sapiens isoform 1 gene for L-type cal						4.18 3.44		
	103627 103767	Z48513 BE244667	Hs.298155	H.sapiens XG mRNA (clone PEP6) CGI-100 protein						U.77	2.25	
	103850	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR				46.55		3.05		
10	104078 104326		Hs.303276 Hs.143067	ESTs ESTs						3.54		
	104352	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	C4 00					3.16		
	104398 104473	AJ423930 AJ904823	Hs.36790 Hs.31297	ESTs; Wealdy similar to putative p150 (H ESTs	64.80							3.38
16	104493		Hs.79059	ESTs; Moderately similar to TGF-BETA REC	00.00		2.47					
15	104495 104595	AW975687 AI799603	Hs.292979 Hs.271568	ESTs ESTs	28.60					3.42		
	104597	Al364504	Hs.93967	ESTs; Weakly similar to Slit-1 protein (6.00						
	104659 104686	AW969769 AA010539	Hs.105201 Hs.18912	ESTs ·	34.00	11.00						
20	104691	U29690	Hs.37744	ESTs; Beta-1-adrenergic receptor	56.80							
	104764 104776	A1039243 AA026349	Hs.278585	ESTs ESTs	34.20			60.40				
	104825	AA035613	Hs.141883	ESTs			3.03					
25	104865 104942	T79340 NM_016348	Hs.22575 Hs 10235	Homo sapiens cDNA: FLJ21042 fis, clone C ESTs	41.20							3.27
25	104989	R65998	Hs.285243	ESTs				40.00				
	105062 105101	AW954355 H63202	Hs.36529 Hs.38163	ESTs ESTs	34.20							3.20
••	105173	U54617	Hs.8364	ESTs	07.20							4.17
30	105194 105226	R06780 R58958	Hs.19800 Hs.26608	ESTs ESTs		16.00	2.34					
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr			2.72					
	105394	BE245812	Hs.8941	ESTs	33.60		2.61					
35	105647 105789	Y09306 AF106941	Hs.30148 Hs.18142	homeodomain-interacting protein kinase 3 arrestin; beta 2	33.00						٠	3.59
	105817	AA397825	11- 22044	synaptopodin				35.40		4.46		
	105847 105894	AW964490 Al904740	Hs.32241 Hs.25691	ESTs calcitonin receptor-like receptor activi			3.43	33.40				
40	105999	BE268786	Hs.21543	ESTs		7.00		42.60				
40	106075 106178	AA045290 AL049935	Hs.25930 Hs.301763	ESTs KIAA0554 protein	34.80			42.00				
	105381	AB040916	Hs.24106	ESTs					12.00	2 60		
	106467 106536	AA450040 AA329648	Hs.154162 Hs.23804	ADP-ribosylation factor-like 2 ESTs				96.40		3.69		
45	106569	R20909	Hs.300741	sorcin				47.20		•		
	106605 106842	AW772298 AF124251	Hs.21103 Hs.26054	Homo sapiens mRNA; cDNA DKFZp564B076 (fr novel SH2-containing protein 3			2.55	220.40				
	105844	AA485055	Hs.158213	sperm associated antigen 6	39.20							
50	106870 106943	A1983730 AW888222	Hs.26530 Hs.9973	serum deprivation response (phosphalidy) ESTs			2.28					4.28
-	106954	AF128847	Hs.204038	ESTs -					45.45			4.32
	107106 107163	AA862496 AF233588	Hs.28482 Hs.27018	ESTs ·			2.57		10.45			
c c	107201	D20378	Hs.30731	EST						3.84		
55	107238 107376	D59362 U90545	Hs.330777 Hs.327179	EST solute carrier family 17 (sodlum phospha		8.00 10.67						
	107530	Y13622	Hs.85087	latent transforming growth factor beta b			2.32					
	107688 1077 0 6	AW082221 AA015579	Hs.60536 Hs.29276	ESTs ESTs	28.40			34.60	•			
60	107723	AA015967		EST	•					3.29		
	107727 107750	AA149707 AA017291	Hs.173091 Hs.60781	DKFZP434K151 protein ESTs				80.80 51.40				
	107751	AA017301	Hs.235390	ESTs				•		3.14	•	
65	107873 107899		Hs.143811 Hs.83869	ESTs ESTs; Wealtly similar to IIII ALU SUBFAMI		9.00				3.65		
00	107994	AA036811	Hs.48469	ESTs				44.60				
	107997 108041	AL049176 AW204712	Hs.82223 Hs.61957	Human DNA sequence from clone 141H5 on c ESTs				32.00 30.80				
70	108048	AJ797341	Hs.165195	ESTs				33.33			4.75	
70	108338 108434	AA070773 AA078899		"zm53g11.s1 Stratagene fibroblast (#9372 "zm94b1.s1 Stratagene colon HT29 (#93722			2.33				2.92	
	108447	AA079126		"zm92a11.s1 Stratagene ovarian cancer (#						3.06		
	108480 108499	AL133092 AA083103	Hs.68055	ESTs *zn1b12.s1 Stratagene hNT neuron (#93723				34.00				3.36
75	108535	R13949	Hs.226440	Homo sapiens clone 24881 mRNA sequence					19.00			
	108550 108604	AA084867 AA934589	Hs.49696	*zn11f6.s1 Stratagene hNT neuron (#93723			2.33		12.00			
	108625		Hs.283022	ESTS ESTS								5.82
80	108629 108655	AA102425 AA099960		*zn24c6.s1 Stratagene neuroepithelium NT *zm65c6.s1 Stratagene libroblast (#93721		7.00					3.42	
50	108756	AA127221	Hs.117037	Homo sapiens mRNA; cDNA DKFZp564N1164 (f		6.05						
	108864	AI733852	Hs.199957	ESTs	28.80							
0-	108895 108921	AL138272 Al568801	Hs.62713 Hs.71721	ESTs	32.80		•	57.80				
85	108967	AA142989	Hs.71730	ESTs	28.80							

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	109001	AI056548	Hs.72116	ESTs, Moderately similar to hedgehog-int			2.57					
	109003 109004	AA147497 AA156235	Hs.71825 Hs.139077	ESTs EST		5.60					2.11	
_	109065	AA161125	Hs.252739	EST					10.00			
5	109250 109490	H83784 AA233416	Hs.62113 Hs.139202	ESTs; Wealdy similar to PHOSPHATIDYLETHA ESTs							3.44 2.92	
	109510	A1798863	Hs.87191	ESTs			2.40					
	109578 109601	F02208 F02695	Hs.27214 Hs.311662	ESTs EST		10.00		40.80				
10	109613	H47315	Hs.27519 ·	ESTs				54.40				
	109650	R31770	Hs.23540 Hs.22869	ESTs ESTs	31.20	8.40						
	109682 109724	H18017 D59899	Hs.127842	ESTs		0.40		29.40				
15	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene		10.00			8.00			
13	109833 109837	R79864 H00656	Hs.29889 Hs.29792	ESTs ESTs		10.00	6.49					
	109977	T64183	Hs.282982	ESTs				107.00			2.75	
	109984 110146	Al796320 H41324	Hs.10299 Hs.31581	ESTs ESTs; Moderately similar to SYNTAXIN 1B				107.00			2.22	
20	110271	H28985	Hs.31330	ESTs						3.48		
	110280	AW874263 R93141	Hs.32468 Hs.184261	ESTs ESTs	44.20			32.00				
	110420 110578	T62507	Hs.11038	ESTs	28.40			02.00				
25	110634	R98905	Hs.35992	ESTs					20.00			4.15
23	110726 110837	AW961818 H03109	Hs.24379 Hs.108920	potassium voltage-gated channet; shaker- ESTs; Weakly similar to semaphorin F (H.				56.80				4.13
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfami			3.13					
	110894 110971	R92356 Al760098	Hs.66881 Hs.21411	ESTs; Moderately similar to cytoplasmic ESTs		5.33		44.60	•			
30	111023	AV655386	Hs.7645	ESTs	32.40							
	111057 111247	T79639 AW058350	Hs.14629 Hs.16762	ESTs Homo sapiens mRNA; cDNA DKFZp564B2062 (f					17.14		4.58	
	111330	BE247767	Hs.18166	KIAA0870 protein							4.00	3.42
35	111374	BE250726	Hs.283724 Hs.181003	ESTs; Moderately similar to HYA22 (H.sap				33.20				3.91
33	111442 111737		Hs.9218	ESTS ESTS				53.00				
	111747	AI741471	Hs.23666	ESTs	46.20	40.00						
	111807 111862	R33508 R37472	Hs.18827 Hs.21559	ESTs EST		16.00				3.91		
40	112045	Al372588	Hs.8022	TU3A protein							2.74	
	112057 112214	R43713 AW148652	Hs.22945 Hs.167398	EST ESTs					13.00		4.92	
	112263	R52393	Hs.25917	ESTs			2.43					
45 ·	112314 112324	AW206093 R55965	Hs.748 Hs.26479	ESTs limbic system-associated membrane protei		9.00			14.00			
73	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H			2.49		14.00			
	112380	H63010 AA324998	Hs.5740	ESTS		8.00	2.34					
	112425 112473	R65993	Hs.321677 Hs.279798	ESTs; Wealdy similar to !!!! ALU SUBFAMI pregnancy specific beta-1-glycoprotein 9		0.00				4.53		
50	112492	N51620	Hs.28694	ESTs				29.80		3.62		
	112541 112620	AF038392 R80552	Hs.116674 Hs.29040	ESTs ESTs			2.37			3.02		
	112623	AW373104	Hs.25094	ESTs			2.26		40.00			
55	112867 112894	T03254 T08188	Hs.167393 Hs.3770	ESTs ESTs		6.50			12.00			
	112954	AA928953	Hs.6655	ESTs		7.00						4 00
	113029 113086	AW081710 AA346839	Hs.7369 Hs.209100	ESTs; Weakly similar to IIII ALU SUBFAMI DKFZP434C171 protein								4.39 4.47
<i>c</i> 0	113140	T50405	Hs.175967	ESTs					10.00			
60	113252 113257	NM_004469 AJ821378	Hs.11392 Hs.159367	c-fos induced growth factor (vascular en ESTs		14.00				3.72		
	113394	T81473	Hs.177894	ESTs						3.60		
	113437 113454	T85349 Al022166	Hs.15923	EST	35.00	6.00						
65	113502	T89130	Hs.16188	ESTs ESTs	39.60	0.00						
	113552	A1654223	Hs.16026	ESTs							2.58	3.88
	113645 113691	T95358 T96935	Hs.333181 Hs.17932	ESTs EST				38.20			230	
70	113706	AA004693	Hs.269192	ESTs			0.24			3.09		
70	113883 113924	U89281 BE178285	Hs.11958 Hs.170056	oxidative 3 alpha hydroxysteroid dehydro Homo sapiens mRNA; cDNA DXFZp586B0220 ff	30.40		2.31					
	114035	W92798	Hs.269181	ESTs					13.00		-	r 00
	114058 114084	AK002016 AA708035	Hs.114727 Hs.12248	ESTs ESTs				40.60				5.00
75	114121	H05785	Hs.25425	ESTs			2.31					
	114124 114275	W57554 AW515443	Hs.125019 Hs.306117	Human lymphoid nuclear protein (LAF-4) interleukin 13 receptor; alpha 1		7.00 6.00						
	114297	AA149707	Hs.173091	DKFZP434K151 protein				48.80		- 1-		
80	114427 114449	AA017176 AA020736	Hs.33532	ESTs; Highly similar to Miz-1 protein (H ze63b11.s1 Soares retina N2b4HR Homo sa					10.00	3.45		•
	114452	Al369275	Hs.243010	ESTs, Moderately similar to RTCO_HUMAN G		14.00						
	114609	AA079505 AA101056		"zm97a5.s1 Stratagene colon HT29 (#93722 "zn25b3.s1 Stratagene neuroepithelium NT				35.40		3.13		
0.5	114648 114731	BE094291	Hs.155651	Homo sapiens HNF-3beta mRNA for hepatocy				JJ.40		•		3.42
85	114762	AA146979	Hs.288464	ESTs	33.00							

	w	O 02/08	5443							PCT/	US02/1	12476
		AA151719	Hs.95834	ESTs	34.40						0002	
	115009	AA251561	Hs.48689	ESTs	30.20 32.60							
	115272	AW015947 AW964897	Hs.290825	ESTs; Wealthy similar to hypothetical L1 ESTs	32.00	6.00						
5		AL109719	Hs.47578	ESTs					12.00			
	115365		Hs.268391	ESTs				40.00		3.32		
	115559 115566	AL079707 Al142336	Hs.207443 Hs.43977	ESTs ESTs				48.00 56.20				
	115683	AF255910	Hs.54650	ESTs, Weakly similar to (defline not ava	31.40			50025				
10	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.sa				33.60				
	115819 115949		Hs.41135 Hs.43125	Endomucin 2 ESTs			3.18	74.40		•		
	115965	AA001732	Hs.173233	ESTs			w.10	388.80				
1.5	116035	AA621405	Hs.184664	ESTs .				33.20				
15	116049		Hs.41644	ESTs				45.80		3.57		
	116081 116082	Al190071 AB029496	Hs.55278 Hs.59729	ESTs ESTs			3.06			3.37		
	116213	AA292105	Hs.326740	leucine rich repeat (in FLII) interactin	50.60							
20	116228	A1767947	Hs.50841	ESTs; Wealdy similar to tuftelin [M.musc		6.00	3.85					
20	116250 116419	N76712 Al613480	Hs.44829 Hs.47152	ESTs ESTs; Weakly similar to testicular tekti		0.00		30.00				
	116617	D80761	Hs.45220	EST		•	2.27					
	116784	AB007979	Hs.301281	tenascin R (restrictin; janusin)	47.20			41.20				
25	116835 116970		Hs.38218 Hs.9059	ESTs KIAA0962 protein				41.20	11.00			
	117023	AW070211	Hs.102415	ESTs				91.00				
	117027	AW085208	Hs.130093	ESTs	49.40			32.60				
	117036 117110		Hs.41192 Hs.172932	EST .		8.67		32.00				
30	117209		Hs.306881	ESTs				30.60				
	117325	N23599	Hs.43396	ESTs					9.29	2.40		
	117454 117475	N29569 N30205	Hs.44055 Hs.93740	ESTs ESTs	44.00					3.19		
	117543	BE219453	Hs.42722	ESTs		16.00						
35	117567		Hs.44565	ESTs					12.00			
	117570 117600	N48649 N34963	Hs.44583 Hs.44676	ESTs EST					11.00	3.74		
	117730	N45513	Hs.46608	ESTs		6.00						
40	117791		Hs.93956	EST		9.00		~~ ~~				
40	117929 11 79 90	N51075 AA446167	Hs.47191 Hs.47385	ESTs ESTs		8.00		29.20				
	118224	N62275	Hs.48503	EST	31.40	0.00						
	118244	N62516	Hs.48556	ESTs	32_80		0.40				•	
45	118357 118446	AL109667 N66361	Hs.124154 Hs.269121	Homo sapiens mRNA full length insert cDN ESTs			2.40 2.28					
73	118447	N66399	Hs.49193	EST	30.80							
	118530	N67900	Hs.118446	ESTs						3.10		
	118549 118823	N68163 W03754	Hs.322954 Hs.50813	EST ESTs; Weakly similar to long chain fatty			3.94			3.41		
50	118862	W17065	Hs.54522	ESTs			5.5 1			3.58		
	118935	AI979247	Hs.247043	KIAA0525 protein				33.00	44.40			
	118944 118995	AI734233 N94591	Hs.226142 Hs.323056	ESTs; Weakly similar to IIII ALU SUBFAMI ESTs		14.00			11.43			
	119073	BE245360	Hs.279477	ERG-2/ERG-1; V-ets avian erythroblastosi		14.00		52.60				
55	119268	T16335	Hs.65325	EST	31.40			•		2.50		
	119514 119824	W37937 W74536	Hs.184	Accession not listed in Genbank advanced glycosylation end product-speci			2.75			3.50		
	119831	AL117664	Hs.58419	DKFZP586L2024 protein								3.21
60	119861	W78816	Hs.49943	ESTs; Moderately similar to IIII ALU SUB				33.80				
60	119889 119921	W84346 W86192	Hs.58671 Hs.58815	ESTs ESTs	29.00			30.03				
	120082	H80286	Hs.40111	ESTs	20.00					3.80		
	120094	AA811339	Hs.124049	ESTs		6.00		20.00				
65	120132 120378	W57554 AA223249	Hs.125019 Hs.285728	Human lymphoid nuclear protein (LAF-4) ESTs		12.00		36.60				
03	120404	AB023230	Hs.96427	KIAA1013 protein	39.40	12.00						
	120504			ESTs					8.00			
	120512	N55761 AA287740	Hs.194718 Hs.78335	ESTs microtubute-associated protein; RP/EB fa	33.00							4.18
70		AA287702	Hs.10031	KIAA0955 protein				46.60				
	121082	AA398722		ESTs				39.00				
	121191 121248		Hs.104447 Hs.97827	ESTs EST	41.60						5.08	
		Al287280	Hs.97933	ESTs					12.00			
75	121366	AI743515		ESTs					20.00	2 20		
	121483 121518	A1660332 AA412155	Hs.25274	ESTs; Moderately similar to putative sev ESTs				30.20		3.32		
		AA412442	Hs.98132	ESTs			2.29	V-1.20				
0Λ	121622	AA416931	Hs.126065	ESTs		9.00		94.00				
80	121665 121709	AA416556 AI338247	Hs.98234 Hs.98314	ESTs Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80			34.80				•
	121730		Hs.98328	ESTs	38.80							
	121740	AA421138	Hs.98334	EST		7.00						
85		Al590770 Al040235	Hs.110347 Hs.3346	Homo saplens mRNA for alpha integrin bin ESTs	36.20							3.61
00	14.1041		100000									

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		AB033030	Hs.300670	ESTs			2.34			- 0 - 7	05027	12470
	121841	AA427794	Hs.104864	ESTs			2.61					
	121885	AA934883	Hs.98467	ESTs							2.25	
_	121888	AA426429	Hs.98463	ESTs							2.92	
5	121938 121950	AA428659 AA429515	Hs.98610	ESTs EST				46.80 31.40				
	122030	AA431310	Hs.98724	ESTs	34.40			31.40				
	122054	AA431725	Hs.98745	EST	01.40						3.58	
	122211	AA300900	Hs.98849	ESTs; Moderately similar to bilhoraxoid-	49.40							
10	122233	AA436455	Hs.98872	EST	29.60							
	122247	AA436676	Hs.98890	EST		0.00		39.80				
	122253 122266	AA435703 AA435840	Hs.104938 Hs.98907	ESTs; Wealdy similar to hypothetical pro EST		9.00				3.60		
	122285	AA436981	Hs.121602	EST						3.14		
15	122409	AA446830	Hs.99081	ESTs	30.80							
	122485	AA524547	Hs.160318	phospholemman			2.65					
	122697	AA420683	Hs.98321	Homo saptens cDNA FLJ14103 fis, clone MA		15.00						
	122772 122831	AW117452 AIB57570	Hs.99489 Hs.5120	ESTs ESTs		6.67				3.37		
20	122913	A1638774	Hs.105328	ESTs				32.20		4.07		
	123049	BE047680	Hs.211869	ESTs				41.80				
	123076	AI345569	Hs.190046	ESTs	35.80							
	123136	AW451999	Hs.194024	ESTs					40.00		2.58	
25	123309 123455	N52937 AA353113	Hs.102679 Hs.112497	ESTs ESTs				82.80	19.00			
23	123691	AA609579	Hs.112724	ESTs				02.00		3.95		
	123756	AA609971	Hs.112795	EST	35.40				•			
	123802	AA620448		Homo sapiens clone 24760 mRNA sequence	58.00							
30	123837	AI807243	Hs.112893	ESTs			2 62	32.40				
50	123844 123936	AA938905 NM_004673	Hs.120017	olfactory receptor; family 7; subfamily ESTs	29.00		2.63					
	123987	C21171	Hs.95497	ESTs: Weakly similar to GLUCOSE TRANSPOR	20.00			70.60				
	124013	Al521936	Hs.107149	ESTs; Wealthy similar to PTB-ASSOCIATED S	28.40							
25	124160	R40290	Hs.124685	ESTs					13.00	4		
35	124205	H77570	Hs.108135	ESTs			2 25			4.74		•
	124226 124246	AA618527 H67680	Hs.190266 Hs.270962	ESTS ESTS			2.35	29.40				
	124348	AI796320	Hs.10299	ESTs		17.00		20.10				
40	124358	AW070211	Hs.102415	"yw35g11.s1 Morton Fetal Cochlea Homo sa			3.07					
40	124409	AI814166	Hs.107197	ESTs			0.40			3.14		
	124442 124468	AW663632 N51413	Hs.285625 Hs.109284	TATA box binding protein (TBP)-essociate ESTs			2.48	30.80				
	124479	AB011130	Hs.127436	calcium channel; voltage-dependent; alph				00.00				6.03
	124519	A1670056	Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO			2.50					
45	124711	NM_004657		serum deprivation response (phosphalidy)	59.20							
	124866 124874	AJ768289 BE550182	Hs.304389 Hs.127826	ESTS ESTS		8.00		37.60				
	125097	AW576389	Hs.335774	ESTs				31.00	10.00			
	125179	AW206468	Hs.103118	ESTs						3.12		
50	125200	AW836591	Hs.103156	ESTs							2.79	
	125299	T32982	Hs.102720	ESTs	20.00			34 <i>.2</i> 0				
	125400 125810	AL110151 H00083	Hs.128797	DKFZP586D0824 protein aryl hydrocarbon receptor-interacting pr	29.00 32.20							
	126176	BE242256	Hs.2441	KIAA0022 gene product	02.20	12.00						
55	126303	D78841		HUM525A05B Human placenta polyA+ (TFuji				33.60				
	126403	AW629054	Hs.125976	ESTs; Wealty similar to metalloprotease/	35.80							
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF [M.muscu	39.60			29.80				
	126773 127307	AA648284 AW962712	Hs.187584 Hs.126712	ESTs ESTs; Weakly similar to plL2 hypothetica	28.80							
60	127462	AA760776	Hs.293977	aa59b04.s1 NCL_CGAP_GCB1 Homo sapiens c				34.40				
	127486	AW002846	Hs.105468	ESTs ·		9.00						
	127572	AA594027	Hs.191788	EST8			2.36	20.40				
	127609 127832	X80031 AW976035	Hs.530 Hs.292396	ESTs ESTs				29.40 37.20				•
65	127898	AA774725	Hs.128970	ESTs				07.20			4.42	
	128073	AW340720	Hs.125983	ESTs				38.40				
	128101	AA905730	Hs.128254	ESTs		7.33					0.50	
	128149 128212	NM_012214 W27411	Hs.177576 Hs.336920	mannosyl (alpha-1;3-)-glycoprotein beta- glutathione peroxidase 3 (plasma)			3.09				2.58	
70	128333	W68800	Hs.12126	ESTs; Weakly similar to LRS [H.sapiens]			3.03	34.40				
	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00						
	128426	Al265784	Hs.145197	ESTs							4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20			#4 CD				
75	128534 128587	AA464918 AW271273	Hs.23767	ESTs; Moderately similar to IIII ALU SUB ESTs				41.60 87.00				
. •	128726	Al311238	Hs.104476	ESTs				07.00				4.02
	128773	NM_004131		granzyme B (granzyme 2; cytotoxic T-lymp					9.00			
	128833	W26667	Hs.184581	ESTs			0.00					3.76
80	128870 128878	H39537 R25513	Hs.75309 Hs.10683	eukaryotic translation elongation factor ESTs			2.66			3.10		
-	128885	AF134803	Hs.180141	cofilin 2 (muscle)					11.00	w.,0		
	128998	W04245	Hs.107761	ESTs; Weakly similar to PUTATIVE RHO/RAC					-		3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CeM-KII inhi						2 47		3.68
85	129038 129098	AW156903 AW580945	Hs.108124	ribosomai protein L41 ESTs	34.60					3.17		
	123030	300340	. 6.000400	20.3	U-1.00							

	W	O 02/08	5443						•	PCT/	US02/	12476
		AL039940	Hs.202949	KIAA1102 protein			2.29					4.09
	129240 129262	AA361258 BE222198	Hs.237868 Hs.109843	interleukin 7 receptor ESTs			LES			3.30		
_	129301	AF182277	Hs.330780	Human cytochrome P450-tiB (hilB3) mRNA;								4.05
5	129331 129381	AW167668 AW245805		ESTs; Highly similar to CGI-38 protein (claudin 5 (transmembrane protein deleted			2.93					4.09
	129565	X77777	Hs.198726	vasoactive intestinal paptide receptor 1			255	160.80				
	129595	U09550	Hs.1154	oviductal glycoprotein 1; 120kD					10.00			
10	129613 129782	AW978517 AW016932	Hs.172847 Hs.104105	ESTs; Wealdy similar to collagen alpha 1 EST		9.00				3.40		
10	129950	F07783	Hs.1369	decay accelerating factor for complement		3.00		87.80				
	129958	R27496	Hs.1378	annexin A3			0.70	44.60				
	129959 130160	AL036554 AA305688	Hs.274463 Hs.267695	defensin; atpha 1; myeloid-related seque UDP-Gal:belaGicNAc beta 1;3-galactosyltr			272	42.20				
15	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator			2.54					
	130273 130312	AW972422 AF056195	Hs.153863 Hs.15430	MAD (mothers against decapentaplegic; Dr				51.60		3.16		
	130436	NM_001928		DKFZP586G1219 protein D component of complement (adipsin)						3.10		4.11
20	130523	AA999702	Hs.214507	ESTs						4.77		
20	130799 130885	AB028945 NM_005883	Hs.12698 Hs.20912	ESTs adenomatous polyposis coli like		6.00				3.54		
	131002	AL050295	Hs.22039	KIAA0758 protein						0.0		3.50
	131012		Hs.202949	KIAA1102 protein	41.20	20.00						
25	131031 131061	NM_001650 N64328	Hs.268744	aquaporin 4 ESTs; Moderately similar to KIAA0273 [H.	41.20			31.40				
	131066	AW169287	Hs.22588	ESTs				29.60				
	131082 131087	AJ091121 AF147709	Hs.246218 Hs.22824	ESTs; Weakly similar to zinc finger prot ESTs; Weakly similar to p160 myb-binding					9.00			3.86
••	131161		Hs.23735	potassium voltage-gated channel; subfami						3.14		0.00
30	131179	AA171388	Hs.184482	DKFZP586D0624 protein						3.80		
	131182 131205	AI824144 NM_003102	Hs.23912 Hs.2420	ESTs superoxide dismutase 3; extracellular			2.98					3.67
	131277	AA131466	Hs.23767	ESTs			3.15					
35	131281 131282	AA251716	Hs.25227	ESTS				32.20				3.44
33	131285	X03350 Al567943	Hs.4 Hs.25274	alcohol dehydrogenase 3 (class I); gamma ESTs; Moderately similar to putative sev						6.40		3.44
	131355	R52804	Hs.25956	DKFZP564D206 protein		8.00						
	131391 131461	AW085781 AA992841	Hs.26270 Hs.27263	ESTs butyrate response factor 2 (EGF-response	28.80	10.00						
40	131487		Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	20.00				•		4.03	
	131517		Hs.263395	ESTs; Highly similar to semaphorin Via [39.00				44.00			
	131545 131583	AL137432 AK000383	Hs.28564 Hs.323092	ESTs ESTs; Wealdy similar to dual specificity					11.00 10.00			
4.5	131647	AA359615	Hs.30089	ESTs		•	2.47					
45	131675 131676	H15205 Al126821	Hs.30509 Hs.30514	ESTs ESTs	45.80					3.06		
	131708	S60415	Hs.30941	calcium channel; voltage-dependent; beta	טטנטר		2.28					
	131717	X94630	Hs.3107	CD97 antigen				40.00				3.78
50	131756	AA443966 AA744902	Hs.31595 Hs.107767	ESTs ESTs; Moderately similar to CaM-KII inhi				40.60				3,67
	131821	AA017247	Hs.164577	ESTs			2.87					
	131839 131861	AB014533 AL096858	Hs.33010 Hs.184245	KIAA0633 protein KIAA0929 protein Msx2 interacting mudea	54.00						3.48	
	132015	Al418006	Hs.3731	ESTs	07.00			49.20				
55	132070	BE622641	Hs.38489	ESTs			0.00	34.80				
	132242 132334	AA332697 AW080704	Hs.42721 Hs.45033	ESTs lacrimal proline rich protein			2.68 4.66					
	132476	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	34.20							
60	132490 132533	NM_001290 Al922988	Hs.4980 Hs.172510	LIM binding domain 2 ESTs		13.00	2.66					
00	132598	X80031	Hs.530	collagen; type IV; alpha 3 (Goodpasture		10.00		30.60				
	132619	H28855	Hs.53447	ESTs; Moderately similar to kinesin ligh						4.02		
	132652 132726	N41739 N52298	Hs.61260 Hs.55608	ESTs ESTs; Wealdy similar to cONA EST yk484g1					11.43	3.18		
65	133028	R51604	Hs.300842	ESTs			2.37					
	133071 133120	BE384932	Hs.64313	ESTS			2.27 2.63					
	133129	NM_003278 AA428580	Hs.65551	tetranectin (plasminogen-binding protein ESTs			203					5.49
70	133147	AA026533	Hs.66	Interleukin 1 receptor-like 1			6.20					
70	133151	NM_014051 AA903424	Hs.94896 Hs.6786	ESTs ESTs				31.40		3.69		
	133276	AW978439	Hs.69504	ESTs				01.40	9.00			
		AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famili	41.20	•						
75		AF017987 AL134030	Hs.7306 Hs.284180	secreted frizzled-related protein 1 protocadherin 2 (cadherin-like 2)	50.20					3.72		
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr								3.35
	133656 133689	BE149455 NM_001872	Hs.75415	Accession not listed in Genbank carboxypeptidase B2 (plasma)			2.65	90.80				
0.0	133779	T58486	Hs.222566	ESTs				50.00		3.05		
80	133978	AF035718	Hs.78061	transcription factor 21			2.92					0.45
	133985 134000	L34657 AW175787	Hs.78146 Hs.334841	platelet/endothelial cell adhesion molec selenium binding protein 1								3.45 4.05
	134111	A1372588	Hs.8022	TU3A protein			4.49					
85	134185	AA285136	Hs.301914	Homo sapiens mRNA; cDNA DKFZp586K1220 (f				40 PA			3.27	
99	134204	A1873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein (40.80				

	W	O 02/086	443					PCT/US02/124		
	134641	AI092634	Hs.156114	protein tyrosine phosphatase; non-recept					3.76	
	134677 134745	AA251363 NM_000685	Hs.177711	ESTs		45.00		32.20		
	134749	T28499	Hs.89472 Hs.89485	angiotensin receptor 1B carbonic anhydrase IV		15.00	3.05			
5	134786	T29618	Hs.89640	angiopoletin 1 receptor, TEK tyrosine ki			3.05	57.80		
•	134825	U33749	Hs.197764	thyroid transcription factor 1				01.00		3.73
	134978	AI829008	Hs.333383	ficolin (collagen/fibrinogen domain-cont			2.52			
	135010	N50465	Hs.92927	ESTs				31.60		
10	135053	AW796190	Hs.93678	ESTs					3.21	
10	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80					
	135091	AA493650 AA775910	Hs.94367	ESTs						4.24
	135135 135203	C15737	Hs.95011 Hs.269386	syntrophin; beta 1 (dystrophin-associate ESTs		8.00			4 24	
	135236	Al636208	Hs.96901	ESTs	43.00				4.31	
15	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial cd	74.00					6.42
	135346	NM_000928	Hs.992	phospholipase A2; group (8 (pancreas)			3.82			0.12
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-			4.15			
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20					
20	135388	W27965	Hs.99865	EST	38.80					
20	135402	L12398	Hs.99922	doparnine receptor D4					4.21	

TABLE 2B shows the accession numbers for those primekeys tacking unigenelD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

30		Unique Eos probeset Ider ber: Gene duster number r: Genbank accession numb	
	Pkey	CAT number Accession	ns
35	108447 108550 108655 102397		16 17 AA084996 10 AA113013
40	126303 125810 103627 121366 114609		R81062
45	115272 108338 108434 123802 102310	172113_1 AWD1594 112185_1 AA07077: 114012_1 AA07889: genbank_AA620448 NOT_FOUND_entrez_U33	47 AA211890 AA279425 3 AA070774 9 AA078782 AA075788 AA620448 839 U33839
50	102638 104776 120504 113502 108499	entrez_U67092 U67092 genbank_AA026349 genbank_AA256837 genbank_T89130T89130 genbank_AA083103	AA026349 AA256837 AA083103
55	101308 108629 103098 103241 103508	entrez_X76223 X76223 entrez_Y10141 Y10141	AA102425 126593 X02850 D13070 AE000559 M17649 M87859 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
60	103575 119514 121082 128634 105817	entrez_Z26256 Z26256 NOT_FOUND_entrez_W37: genbank_AA398722 AA464918_at AA464918 genbank_AA397825	AA398722
65	121518 114449 114648 121950 107723	genbank_AA412155 genbank_AA020736 genbank_AA101056 genbank_AA429515 genbank_AA015967	AA12155 AA020736 AA101056 AA429515 AA015967

Table 3A shows 452 genes up-regulated in chronically diseased tung relative to normal tung. Chronically diseased tung samples represent chronic non-malignant tung diseases such as fibrosis, emphysema, and bronchilis. These genes were selected from 59580 probesets on the Eos/Afrymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

	process	CONTRICT DOM	and disciplina at	क व्यक्तिकारका क इत्रवादीय तात्रांशति दिनी, व त्रवातात्रांस्त्रा	AGEND (CHOPATI)	nie icimiec	iere a mater expression.
5	Pkey:	Unious	Eos arabesei	identifier number			
_	ExAcon			number, Genbank accession number			
	Unigene		ne number				
	Unigene	Title: Unige:	ne gene title				
10	R1:			for chronically diseased lung samples divided by the S			
10	R2:			for chronically diseased lung samples divided by the !	90th percentile	of normal tu	ng samples, squamous cell carcinomas and
			carcinomas				
	R3:						al lung, chronically diseased lung and tumor samples
					momas and ad	enocarcinon	as minus the 15th percentile of Al for all normal lung,
15		Guou	any diseased	lung and tumor samples			
13							•
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2	R3
			•			•-	· -
~~	135423	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	12.40		
20	135378	AW961818	Hs.24379	MUM2 protein			2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)			
	135235	AW298244	Hs.293507	ESTs	12.40		
	135057 134951	U90268 BE305081	Hs.93810	cerebral cavernous malformations 1	11.67	8.00	
25	134799	M36821	Hs.169358 Hs.89690	hypothetical protein GRO3 oncogene		8.20	
~~	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous		0.20	
	134772	NM_000829	Hs.163597	glutarnate receptor, ionotrophic, AMPA 4	29.80		
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
20	134749	T28499	Hs.89485	carbonic anhydrase IV			2.07
30	134696	BE326276	Hs.8851	ESTs			
	134636	NM_005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		400
	134627 . 134622	AI018768 AW975159	Hs.12482 Hs.293097	glyceronephosphate O-acyltransferase			1.92 1.92
	134570	U66615	Hs.172280	ESTs, Weakly similar to A55380 faciogeni SWI/SNF related, matrix associated, acti	13.20		1.32
35	134561	U76421	Hs.85302	adenosine dearninase, RNA-specific, B1 (h	13.20		1.78
-	134468	NM_001772	Hs.83731	CD33 antigen (gp67)		6.20	.,,,
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci			
	134343	D50683	Hs.82028	transforming growth factor, beta recepto			
40	134323	BE170651	Hs.8700	deleted in liver cancer 1			
40.	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939 X52075	Hs.97199	complement component C1q receptor	20.60		
	134253 134182	D52059	Hs.80738 Hs.7972	sialophorin (gpl.115, leukosialin, CD43) KIAA0871 protein	12.20		
	133985	L34657	Hs.78146	platelet/endothetial cell adhesion molec	12.20		
45	133978	AF035718	Hs.78061	transcription factor 21			
	133835	A1677897	Hs.76640	RGC32 protein			•
•	133651	Al301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleotar and coiled-body phosphprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A			477
50	133548 133488	AW946384 AA335295	Hs.178112 Hs.74120	DNA segment, single copy probe LNS-CAI/L adipose specific 2			1.77
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
	133200	AB037715	Hs.183639	hypothetical protein FLJ10210			1.77
55	133153	AF070592	Hs.66170	HSKM-B protein	30.60		
	133130	AJ128606	Hs.6557	zinc finger protein 161	22.60		
	133120	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	40.00		
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		•
60	132836 132799	AB023177 W73311	Hs.29900 Hs.169407	KIAA0960 protein SAC2 (suppressor of actin mutations 2,	41.60		
00	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40		
	132548	X12830	Hs.193400	interleukin 6 receptor	40.40	7.20	
	132476	AL119844	Hs.49476	Homo saciens clone TUAS Crl-du-chat regi		4.76	
65	132439	AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
65	132240		Hs.42676	KIAA0781 protein	21.20		4 🚣
	132210		Hs.42322	A kinase (PRKA) anchor protein 2	45.00		1.99
	132199 131751	AL041299 T96555	Hs.165084 Hs.31562	ESTs ESTs	15.20		1.76
	131745	AJ828559	Hs.31447	ESTs, Moderately similar to A46010 X-II	27.80		1.10
70	131694	NM_000246	Hs.3076	MHC class II transactivator	2120	4.00	
	131686		Hs.30687	GRB2-associated binding protein 2		•	
	131676	Al126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589		Hs.29191	epithelial membrane protein 2		0.40	
15	131536		Hs.269210	ESTs		9.40	
	131517 131355		Hs.263395 Hs.25956	sema domain, transmembrane domain (TM), DKFZP564D206 protein		3.59 4.48	
		R71802	Hs.24853	ESTs	15.00	7.70	
		AF104266	Hs.24212	latrophilin			1.75
80	131156	AJ472209	Hs.323117	ESTs			1.84
	131066	AW169287	Hs.22588	EST8		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein			400
	131053	AA348541	Hs.296261	guardine nucleotide binding protein (G pr	. 40.60		1.93
85	130895 130762		Hs.21015 Hs.1898	hypothetical protein DKFZp564L0864 simil paraoxonase 1	16.60 12.00		
55	.50.02	201011	, 10, 1000	parameters 1	.2.00		

		/O 02/086					
	130657	AW337575	Hs.201591	ESTs			
	130655 130589	AJ831962 AL110226	Hs.17409 Hs.16441	cysteine-rich protein 1 (intestinal) DKFZP434H204 protein			2.08
	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled			1.91
5	130555	R69743	Hs.116774			9.60	
	130365	W56119	Hs.155103	eukaryotic translation Initiation factor	11.60		
	130273	AW972422	Hs.153863			6.60	
	130259 130090	NM_000328 H97878	Hs.153614 Hs.132390	retinitis pigmentosa GTPase regulator zinc tinger protein 36 (KOX 18)	~ ^		1.91
10	129958	R27496	Hs.1378	annexin A3	21.20	5.05	
	129898	AI672731	Hs.13256	ESTs		u.w	
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60		
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas			
1.5	129626	F13272	Hs.111334	ferritin, light polypeptide			
15	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	22.63		
	129593 129565	Al338247	Hs.98314 Hs.198726	Homo sapiens mRNA; cDNA DKFZp586L0120 (f vasoactive intestinal peptide receptor 1			2 52
	129527	X77777 AA769221	Hs.270847	della-lubulin	39.20		2.53
	129402	W72062	Hs.11112	ESTs	00.20		2.11
20	129385	AA172106	Hs.110950	Rag C protein	15.20		
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40		
	129312	T97579	Hs.110334	ESTs, Wealdy similar to 178885 serine/th	20.83		
	129240 129210	AA361258 AL039940	Hs.237868 Hs.202949	interleukin 7 receptor KIAA1102 protein			1.95
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi		4.20	
	129057	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)		7.20	
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3		5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2			
20	128789	AW368576	Hs.139851	caveolin 2			2.24
30	128778	AA504776	Hs.186709	ESTs, Weakly similar to 138022 hypothet	12.20		
	128766 128631	AW160432 R44238	Hs.296460 Hs.155546	craniofacial development protein 1 KIAA1080 protein; Golgi-associated, gamm	26.40		1 70
	128624	BE154765	Hs.102647	ESTs, Wealdy similar to TRHY_HUMAN TRICH			1.78 2.51
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00		2.01
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80		
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s		4.00	
•	128458	H55864	Hs.56340	ESTs	47.00		
	128061 127968	AF150882 AA830201	Hs.186877 Hs.124347	sodium channel, voltage-gated, type XII, ESTs	17.20 21.30		
40	127959	Al302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	21.30		
	127944	Al557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60		
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40		
	127896	AI669586	Hs.222194	ESTs		7.00	
45	127859	AA761802	Hs.291559	ESTs	14.00		
43	127817 127742	AA836641 AW293496	Hs.163085 Hs.160138	ESTs ESTs	14.00		
	127628	A1240102	Hs.322430	NDRG family, member 4	11.00 11.10		
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			
50	127582	AA908954	Hs.130844	ESTS	19.60		
50	127543	AK000787	Hs.157392	Homo saptens cDNA FLJ20780 fis, clone CO	15.40		
	127535	AA568424	Hs.164450	ESTs	17.50		
	127404 127396	AJ379920 L31968	Hs.270224 Hs.187991	ESTs DKFZP564A122 protein	14.60 15.40		
	127374	AA442797	Hs.312110	ESTs, Wealthy similar to 138022 hypothet	14.60		
55	127346	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily 8, membe	21.00		
	127340	BE047653	Hs.119183	ESTs, Wealty similar to ZN91_HUMAN ZINC	15.80		
	127307	AW962712	Hs.126712	ESTs, Wealty similar to AF191020 1 E21G5			
	127242	AW390395 AA625690	Hs.181301	cathepsin S	22.60		
60	127167 127046	AA321948	Hs.190272 Hs.293968	ESTS ESTS	21.40 41.20		
00	126928	AA480902	Hs.137401	ESTs	11.00		
	126900	AF137386	Hs.12701	plasmolipin			1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap		5.60	
65	126816	AA248234		gb:csg2228.seq.F Human fetal heart, Lamb	12.20		
U.J	126812	AB037860	Hs.173933	nuclear factor I/A	17.19		
	126666 126645	AA648886 AA316181	Hs.151999 Hs.61635	ESTs sbx transmembrane epithelial antigen of	13.57 15.40		
	126592	AI611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	13.40	4.67	
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00		
70	126433	AA325606		gb:EST28707 Cerebellum II Homo saplens c	16.77		
	126299	AW979155	Hs.298275	arnino acid transporter 2	14.60		
	126218	AL049801	Hs.13649	Novel human gene mapping to chomosome 13	40.40	3.50	
	126182 126177	AA721331 AW752782	Hs.293771 Hs.129750	ESTS	13.40		
75	126142	H86261	Hs.40568	hypothetical protein FLJ10546 ESTs	18.20 14.00		
. •	126077	M78772	Hs.210836	ESTs	16.59		
	125994	A1990529	Hs.270799	ESTs	17.40		
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	13.00		
80	125847	AW161885	Hs.249034	EST _B	49.57		
80	125831 125731	H04043 R61771	Hs_26912	gbryj45c03.r1 Soares placenta Nb2HP Homo	42.00		
	125/31	BE612918	Hs.151973	ESTs hypothetical protein FLJ23511	13.20 11.20		
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	11.20		
0.5	125552	H09701	Hs.278366	ESTs, Wealty similar to 138022 hypotheti	12.60		
85	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40		

	W	O 02/086	443					PCT/US02/12476
		AA903229	Hs.153717	ESTs			1.80	
	125331	AJ422996	Hs.161378	ESTs	38.00			
	125309	T12411	Hs.183745	hypothetical protein FLJ13456	18.20			
_	125167	AL137540	Hs.102541	netrin 4			1.95	
5	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to	04.00		1.84	
	125042	178906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	10.00		
	124711	NM_004657	Hs.26530	serum deprivation response (phosphatidy)	22.20	10.60		
	124631 124578	NM_014053 N58321	Hs.270594 Hs.231500	FLVCR protein EST	23.20 21.43			•
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	21.43		1.77	
10	124472	N52517	Hs.102670	EST	37.20		,	
	124438	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	J			
	124357	N22401		gb:yw37g07.s1 Morton Fetal Cochlea Homo	14.64			
	124306	AW973078	Hs.293039	ESTs		4.00		
15	124214	H58608	Hs.151323	ESTs				
	124097	AW298235	Hs.101689	ESTs		27.20		
	123978	T89832	Hs.170278	ESTs			2.03	
	123972	T46848	Hs.70337	Immunoglobulin superfamily, member 4		6.00	4 300	
20	123961	AL050184	Hs.21610	DKFZP434B203 protein		45.00	1.79	
20	123936 123802	NM_004673 AA620448	Hs.241519	engiopoletin-like 1		15.80 4.23		
	123734	AA609861	Hs.312447	gb:ae58c09.s1 Stratagene lung carcinoma ESTs		4.20		
	123619	AA602964	10.012441	gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60	7.20		
	123596	AA421130	Hs.112640	EST	10.93			
25	123476	AA384564	Hs.108829	ESTs			2.18	
	123340	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	11.20			
	123190	AA489212	Hs.105228	EST	14.20			
	123136	AW451999	Hs.194024	EST8		7.00		
20	123073	AA485061	Hs.105652	ESTs	31.20			
30	123055	AA482005	Hs.105102	ESTs, Wealthy similar to reverse transcri		4.80		
	122699	AA456130	Hs.301721	KIAA1255 protein	14.40	5.00		
	122679 122633	AA811286	Hs.192837 Hs.34853	ESTs, Weakly similar to ALU5_HUMAN ALU S	14.40			
	122553	NM_001546 AA451884	Hs.190121	Inhibitor of DNA binding 4, dominant neg ESTs	40.00			
35	122544	AW973253	Hs.292689	ESTs	15.40			
33	122485	AA524547	Hs.160318	FXYD domain-containing ion transport reg			1.81	
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H		12.10		
	122127	AW207175	Hs.106771	ESTs			1.95	
40	122011	AA431082		gb:zw78a10.s1 Soares_testis_NHT Homo sap			1.89	
40	121992	AI860775	Hs.98506	ESTs		3.60		
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f			2.01	
	121835	AB033030	Hs.300670	KIAA1204 protein	40.40		1.85	
	121726	AF241254 AV660305	Hs.178098	anglotensin I converting enzyme (peptidy ESTs	12.43		1.82	•
45	121690 121643	AA640987	Hs.110286 Hs.193767	ESTs			1.02	
43	121633	AA417011	Hs.98175	EST	14.00			
	121622	AA416931	Hs.126065	ESTs		16.40		
	121497	AA412031	Hs.97901	EST	11.20			
	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20			
50	121314	W07343	Hs.182538	phospholipid scramblase 4			1.83	
	121242		Hs.97509	ESTs	22.40			
	121059	AA393283		gb:zt74e03.r1 Soares_testis_NHT Homo sap	14.80			
	120934	AA226198	Un 400745	gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens Homo sapiens cDNA: FLJ21326 fis, clone	21.20		1.79	
55	120755 120637	AA312934 AA811804	Hs.190745	gb:ob39a05.s1 NOI_CGAP_GCB1 Homo saptens	20.00		1.75	
55	120484	AA253170	Hs.95473	EST	40.20			
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60		
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80			
	120132	W57554	Hs.125019	ESTs		4.73		
60	120041	AA830882	Hs.59368	ESTs			1.75	•
	119996	W88996	Hs.59134	EST	44.00	7.20		
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	2.70		
	119861	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-		3.78		
65	119824 119740	W74536 AW021407	Hs.184 Hs.21068	advanced glycosylation end product-speci hypothetical protein	20.20			
05	119271	AU061118	Hs.65328	Fanconi anemia, complementation group F	15.20			
	119221	C14322	Hs.250700	tryptase beta 1	,0.20			
	119126		Hs.117183	ESTs	12.60			
	119073	BE245360	Hs.279477	ESTs				
70	118928	AA312799	Hs.283689	activator of CREM in testis		10.00		
	118901	AW292577	Hs.94445	ESTs		3.96		
	118661	AL137554	Hs.49927	protein kinase NYD-SP15	40.40	9.60		
	118607	A1377444 ·	Hs.54245	ESTs, Wealthy similar to \$65824 reverse t	10.40		4 00	
75	118449	AIB13865	Hs.164478	hypothetical protein FLJ21939 similar to	16 20		1.90	
13	118416 118379	N66028 N64491	Hs.49105	FKBP-associated protein ESTs	16.20	4.00		
	118379	N63520	Hs.48990	gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60		
	118329	N63451	Hs.141600	ESTs, Weakly similar to alternatively s		3.80		
	118253	AA497044	Hs.20887	hypothetical protein FLJ10392	17.60			
80	118124	N56968	Hs.46707	chromosome 21 open reading frame 37	14.00			
	118056	AB037746	Hs.42768	hypothetical protein DKFZp76100113			1.86	
	118032	N52802	Hs.47544	EST		5.00		
	117840	T26379	Hs.48802	Homo saptens clone 23632 mRNA sequence		4.00	4	
85	117404	N39725	Hs.15220	zinc finger protein 106	44.00		1.90	
95	117314	N32498	Hs.42829	ESTs	14.20			

	W	O 02/086	5443				
	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	20.20		231
	115814 116784	H50834 AB007979	Hs.301281	gb:yp86a10.s1 Soares fetal liver spteen Homo sapiens mRNA, chromosome 1 specific	20.20	3.51	
5	116768	Al608657	Hs.95097	ESTs	16.20		
	115712	AW901618	Hs.61935	Homo sepiens mRNA; cDNA DKFZp7611071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Wealthy similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	19.40		
10	116279 116165	AW971248 AL039940	Hs.291289 Hs.202949	ESTs, Weakly similar to ALU1_HUMAN ALU S KIAA1102 protein			2.13
10	116152	AL040521	Hs.15220	zinc finger protein 106			1.75
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	13.20		,,,,,
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	30.11		
1.5	115965	AA001732	Hs.173233	hypothetical protein FLJ10970			2.36
15	115955	AF263613	Hs.44198	intracellular membrane-associated calclu	18.20		
	115844 115683	Al373062	Hs.332938 Hs.54650	hypothetical protein MGC5370	18.57	22.00	
•	115673	AF255910 AA406341	Hs.269908	junctional adhesion molecule 2 Homo saplens cDNA FLJ11991 fis, clone HE	11.82	23.00	
	115672	AIB89110	Hs.73251	ESTs	10.60		
20	115566	Al142336	Hs.43977	Human DNA sequence from clone RP11-196N1			1.76
	115313	AA808001	Hs.184411	albumin	25.20		
	115279	AW964897	Hs.290825	ESTs		8.00	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	44.00		1.80
25	115110 114999	AK001671 BE246481	Hs.11387 Hs.87856	KIAA1453 protein ESTs	14.20 19.20		
	114930	AA237022	Hs.188717	ESTs	10.20	5.60	
	114922	AA235672	Hs.87491	ESTs ·		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70		
20	114769	AA149060	Hs.296100	ESTs	11.00		
30	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
	114736 114596	AI610347 AA310162	Hs.103812 Hs.169248	ESTs, Moderately similar to ALU1_HUMAN A	10.71	4.20	
	114518	AW163267	Hs.106469	cytochrome c suppressor of var1 (S.cerevisiae) 3-like	20.40		
	114455	H37908	Hs.271616	ESTs, Weakly similar to ALUS_HUMAN ALU S	20.40		
35	114452	Al369275	Hs.243010	Homo saplens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5			2.09
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
	114251 114138	H15261 AW384793	Hs.21948 Hs.15740	ESTs Homo saplens mRNA; cDNA DKFZp434E033 (fr		11.40	2.00
40	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, done PL		4.07	1.82
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN !!!!			
	113606	NM_013343	Hs.278951	NAG-7 protein			2.15
45	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
43	113560 113552	T91015 Al654223	Hs.268626 Hs.16026	ESTs	32.00		
	113540	AW152618	Hs.16757	hypothetical protein FLJ23191 ESTs			
	113502	TB9130	12010101	gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
	113288	A1076838	Hs.12967	ESTs	12,40		
50	113252	NM_004469	Hs.11392	c-fos induced growth factor (vascular en		4.27	
	113238	R45467	Hs.189813	ESTs	04.00		
	113203 113195	AA743563 H83265	Hs.10305 Hs.8881	ESTs ESTs, Weakly similar to S41044 chromosom	21.20		1.92
	113089	T40707	Hs.270862	ESTs	14.33		1.52
55	113076	AF033199	Hs.8198	zinc finger protein 204		6.00	
	113009	T23699	Hs.7246	ESTs		9.40	
	112937	Al694320	Hs.6295	ESTs, Wealty similar to T17248 hypotheti		12.20	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-li	10.57		
60	112794 112691	R97018 R88708	Hs.220647	gb:yq74b08.s1 Soares fetal liver spleen ESTs	26.60 15.33		
••	112602	AW004045	Hs.203365	ESTs	15.60		
	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	15.40		
	112210	R49645	Hs.7004	ESTs	14.00		
65	112064	AL049390	Hs.22689	Homo saplens mRNA; cDNA DKFZp586O1318 (1	13.00		
05	111998	R42379	Hs.138283	ESTs	11.00		
	111987 111803	NM_015310 AA593731	Hs.6763 Hs.325823	KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A	22.40		1.77
	111737	H04607	Hs.9218	ESTs			1.86
70	111605	T91061	Hs.194178	ESTs, Moderately similar to PC4259 femi	23.00		
70	111510	R07856	Hs.16355	ESTs	11.02		
	111341	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr			1.88
	111280	AA373527	Hs.19385	CGI-58 protein	18.40		
	111247 111232	AW058350 Al247763	Hs.16762 Hs.16928	Homo sapiens mRNA; cDNA DKFZp564B2062 (f ESTs	27.60		
75	110942	R63503	Hs.28419	ESTs	14.80		
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	24.71		
	110837	H03109	Hs.108920	HT018 protein			2.18
	110824	AI767183	Hs.26942	ESTs	12.20		4
80	110776 110576	AB032417 H60869	Hs.19545 Hs.37889	frizzled (Drosophila) homolog 4	13.00		1.75
55	110376	AK000768	Hs.107872	ESTs hypothetical protein FLJ20761	19.00	5.60	
	110099	R44557	Hs.23748	ESTs			2.31
	109984	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL			
95	109958	AA001266	Hs.133521	ESTs	11.25		
85	109893	AA884208	Hs.30484	ESTs			2.68

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	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		
	109837	H00656	Hs.29792	ESTs, Weakly similar to 138022 hypotheti		47.00	3.91
	109798	AI800515	Hs.12024	ESTS		17.20 9.60	
5	109688 109648	R41900 H17800	Hs.22245 Hs.7154	ESTs ESTs	22.80	2.00	
•	109613	H47315	Hs.27519	ESTs			
	109550	AW021488	Hs.26981	ESTs			4.00
	109523 109472	AW193342 AK001989	Hs.24144 Hs.91165	ESTs hypothetical protein		6.00	1.89
10	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00	w.00	
	109260	AW978515	Hs.131915	KIAA0863 protein	25.60		
	108781	AA128654		gbzn98g07.s1 Stratagene fetal relina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Wealdy similar to T26845 hypotheti obz184c04.s1 Stratagene colon (937204)	11,00 26,00		
15	108573 108480	AA086005 AL133092	Hs.68055	hypothetical protein OKFZp434I0428	20.00		
~~	108382	NM_006770	Hs.67726	macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20	2.00	
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	15.44	3.60	
20	108087 108048	AA045708 Al797341	Hs.40545 Hs.165195	ESTs Homo sapiens cDNA FLJ14237 fis, clone NT	10.44	11.40	
	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469	LIM domains containing 1 Ig superfamily receptor LNIR	14.20		
25	107922 107681	BE153855 BE379594	Hs.61460 Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST	29.20		
	107332	T87750	Hs.183297	DKFZP566F2124 protein	10.73		
	107292 107230	BE166479 AI034467	Hs.4789 Hs.34650	Homo saplens serologically defined breas ESTs	32.00 17.40		
30	107230	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
	107160	AA314490	Hs.27669	KIAA1563 protein	11.40		
	107054	AI076459	Hs.15978	KIAA1272 protein	04.40		
	107029	AF264750	Hs.288971 Hs.10710	myeloid/lymphoid or mixed-lineage leukem	21.40 35.80		
35	106999 106954	H93281 AF128847	Hs.204038	hypothelical protein FLJ20417 indolethylamine N-methyltransferase	Q.00		1.76
	106870	Al983730	Hs.26530	serum deprivation response (phosphatidy)			
	106865	AW192535	Hs.19479	ESTs C	13.40	7.40	
	106844 106820	AA485055 NM_016831	Hs.158213 Hs.12592	sperm associated antigen 6 period (Drosophila) homolog 3		7.13 7.00	
40	106818	AK002135	Hs.3542	hypothetical protein FLJ11273	13.00	1.00	
	106797	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL			2.05
	106773	AA478109	Hs.188833	ESTs	12.00		
	106747 106743	NM_007118 8E613328	Hs.171957 Hs.21938	triple functional domain (PTPRF interact hypothetical protein FLJ12492	12.60 10.60		
45	106667	AW360847	Hs.16578	ESTs	10.00		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5			1.78 1.76
	106562 106536	AL031846 AA329648	Hs.152151 Hs.23804	ptakophilin 4 ESTs, Weakly similar to PN0099 son3 prot			2.19
50	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068	Hs.267819	protein phosphatase 1, regulatory (Inhib	15.20		
	106490	AA404265	Hs.115537	putative dipeptidase	10.44		
	106474 106211	BE383668 AA428240	Hs.42484 Hs.126083	hypothetical protein FLJ10618 ESTs	10.44	29.80	
55	105986	AB037722	Hs.8707	KIAA1301 protein		3.70	
	105894	Al904740	Hs.25691	receptor (calcitonin) activity modifying			1.94
	105847 105803	AW964490 AW747996	Hs.32241 Hs.160999	ESTs, Wealdy similar to S65657 alpha-1C- ESTs, Moderately similar to A56194 throm			1.75 2.47
	105731	AAR34664	Hs.29131	nuclear recentor coactivator 2	10.71	•	
60	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105688	Al299139	Hs.17517	ESTs	23.40		
	105510 105101	Z42047 H63202	Hs.283978 Hs.38163	Homo sapiens PRO2751 mRNA, complete cds ESTs	37.20	8.30	
	104989	R65998	Hs.285243	hypothetical protein FLJ22029		8.09	
65	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
	104969	A1670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903 104896	Al436323 AW015318	Hs.31141 Hs.23165	Horno saptens mRNA for KIAA1568 protein, ESTs	13.80	7.60	
	104865	179340	Hs.22575	Homo saplens cDNA: FLJ21042 fis, clone C	10.00		
70	104825	AA035613	Hs.141883	ESTs			1.87
	104781	AA099904	Hs.21610	DKFZP434B203 protein		10.20	1.93
	104776 104591	AA026349 U29690	Hs.37744	gb:zj99f01.s1 Soares_pregnant_uterus_NbH Homo saplens beta-1 adrenergic receptor		5.69	
	104667	Al239923	Hs.30098	ESTs		3.82	
75	104404	H58762		gb:EST00057 HE6W Homo sapiens cDNA clone		4.20	
	104392	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	27.20		1.91
	104212 104074	AB002298 AL162039	Hs.173035 Hs.31422	KIAA0300 protein Homo saptens mRNA; cDNA DKFZp434M229 (fr	11.20		1.31
	103749	AL135301	Hs.8768	hypothetical protein FLJ10849	10.86		
80	103645	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	12.00		4.00
	103554 103541	A1878826 A1815601	Hs.323469 Hs.79197	caveolin 1, caveolae protein, 22kD CD83 antigen (activated B lymphocytes, i			· 1.80
	103541	Y09267	Hs.132821	flavin containing monooxygenase 2			
0.5	103428	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	11.20		
85	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

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	W	O 02/086	443					PCT/US02/12476
	103295	X81479	Hs.2375	egf-like module containing, mucin-like,		3.60		
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula				
	103100	NM_005574	Hs.184585	LiM domain only 2 (rhombolin-like 1)			1.76	
_	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t			2.15	
5	102698	M18567	Hs.1867	progastricsin (pepsinogen C)				
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00			
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40			
	102417		Hs.153487	signal transducing adaptor molecule (SH3	14.00			
10		NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	10.86			
10	102302	AA306342	Hs.69171	protein kinase C-like 2	10.00			
	102283	AW161552	Hs.83381 Hs.78913	guarine nucleotide binding protein 11		7.40	•	
	102188 102151	U20350 T27013	Hs.3132	chemokine (C-X3-C) receptor 1 steroidogenic acute regulatory protein	16,40	7.40		
	102151	L28824	Hs.74101	spisen tyrosine kinase	15.40			
15	101842		Hs.75182	mannose receptor, C type 1	15.40			
13	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				
	101764	Al198550	Hs.81256	S100 calcium-binding protein A4 (calcium			1.78	
	101716		Hs.2563	tachykinin, precursor 1 (substance K, su	18.80		0	
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a)			2.22	
20	101447	M21305	113-2101	gbd-tuman alpha satellite and satellite 3	504.80			
	101383		Hs.79345	coagulation factor VIII, procoagulant co		31.00		
	101346	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N			1.75	
		NM 005795	Hs.152175	calcitonin receptor-like				
	101336	NM_005732	Hs.75678	FBJ murine osteosarcoma viral oncogene h			2.24	
25	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4				
		L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00			
	101168		Hs.211569	G protein-coupled receptor kinase 5			2.01	
20		NM_003243	Hs.79059	transforming growth factor, beta recepto				
30	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte		7.52		
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38		4.04	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	45.40		1.91	
	100893		Hs.180789	S164 protein	15.40			
35	100770	W25797.comp		amyloid beta (A4) precursor protein (pro	11.20 14.80			
22	100716 100555	X89887 M69181	Hs.172350	HiR (histone cell cycle regulation defec	33.00			
	100333	NM_014747	Hs.78748	gb:Human nonmuscle myosin heavy chain-B KIAA0237 gene product	16.20			
	100423	D86640	Hs.56045	src homology three (SH3) and cysteine ri	10.20	4.00		
	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		4.24		
40	100351	D64158	113.150007	DOWN Synthetic Grides region gold 1-1x		6.20		
	100299	D49493	Hs.2171	growth differentiation factor 10		21.20		
	100134	AA305746	Hs.49	macrophage scavenger receptor 1				
	100108	U09577	Hs.76873	hyaluronoglucosaminidase 2			1.79	•
	100095	Z97171	Hs.78454	myocilin, trabecular meshwork inducible		5.40		
45	100066				11.29			

TABLE 3B shows the accession numbers for those primakeys tacking uniquenelD's for Table 3A. For each probaset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 50

Pkey: Unique Eos probeset identifier number CAT number: Gene duster number Accession: Genbank accession numbers 55

60	Pkey	CAT unuper	Accessions	
00	123619	371681_1	AA602964 A	A609200
	126433	127143_1	AA325606 A	A099517 N89423
	125831	1522905_1	H04043 D60	988 D60337
		122973_1		
65	126852	136135_1	AA399961 A	A128347
	121059			
	120637	200885_1	AAB11B04 A	A809404 AA286907 AW977624
		76172	AA431082	
=-	120934			A226513 AA383773
70	123802	genbank_AA620	1448	AA620448
	116814	genbank_H5083	14	H50834
	118329		.0	N63520
	104404	H58762_at	H58762	
	104776			AA026349
75	113502	genbank_T8913	0T89130	
	101262	entrez_L35854	L35854	
	108573	genbank_AA086	5005	AA086005
	101447			
00	124357			N22401
80	108781			
	112794			R97018
	100351			
	100555	tigr_HT2245	M69181 M81	105 U51039

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Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59560 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Ptey: Unique Eos probeset identifier number

ExAccr: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gans title

d by the average of Al for normal lung samples.

		Title: Unigene g		a from a strong to stand with the small account of the	
10	R1:	average o	Al tor sample:	s from patients treated with chemotherapy or radiother	apy aivided
	Pkey	ExAcon	UnigenelD	Unigene Title	R1
	100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
1 5	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	20.60
15	100210	D26361	Hs.3104	KIAA0042 gene product	- 20.40
	100225	D28539	Hs.167185	glutamate receptor, metabotropic 5 E2F transcription factor 3	20.60 29.40
	100269 100438	NM_001949 AA013051	Hs.1189 Hs.91417	topoisomerase (DNA) Il binding protein	23.50
	100877	X80821	Hs.27973	KIAA0874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	21.80
	101447	M21305	11. 4000	gb:Human alpha satellite and satellite 3	193.60
	101649 101724	AW959908 L11690	Hs.1690 Hs.620	heparin-binding growth factor binding pr bullous pemphigoid antigen 1 (230/240kD)	38.40 198.80
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
	101809	MB6849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	50.00
	101915	AF207881	Hs.155185	cytosolic ovarlan carcinoma antigen 1	26.00
30	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
30	102025 102031	U04045 U04898	Hs.78934 Hs.2156	mutS (E. coli) homolog 2 (colon cancer, RAR-related orphan receptor A	32.00
	102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20
	102391	AA296874	Hs.77494	deoxyguanosine kinase	13.90
26	102420	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
	102829	NM_006183	Hs.80962	neurotensin	116.80 2.30
	103000 103036	NM_001975 M13509	Hs.146580 Hs.83169	enolase 2, (gamma, neuronal) matrix metalloprotelnase 1 (interstitial	181.40
	103507	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	49.20
40	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
	104896	AW015318	Hs.23165	ESTs	29.40
	105038 105298	AW503733 BE387790	Hs.9414 Hs.26369	KIAA1488 protein hypothetical protein FLJ20287	21.50 32.80
45	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	20.20
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	28.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
	106205	AW965058	Hs.111583	ESTs, Weakly similar to 138022 hypotheti	32.00
50	106516 106533	AL137311 AL134708	Hs.234074 Hs.145998	Homo sapiens mRNA; cDNA DKFZp761G02121 (ESTs	40.60 59.80
50	106575	AW970602	Hs.105421	ESTs	43.40
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
	106851	Al458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
55	106995	AB023139	Hs.37892	KIAA0922 protein	20.88
55	107332 107532	T87750 AA443473	Hs.183297 Hs.173684	DKFZP566F2124 protein Homo sapiens mRNA; cDNA DKFZp762G207 (fr	23.60 57.20
	107922	BE153855	Hs.61460	lg superfamily receptor LNIR	49.00
	108609	BE409857	Hs.69499	hypothetical protein	19.67
C 0	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17
60	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	59.20
	109260 109280	AW978515 AK001355	Hs.131915 Hs.279610	KIAA0863 protein hypothetical protein FLJ10493	28.60 22.80
	109292	AW975746	Hs.188662	KIAA1702 protein	
	109384	AA219172	Hs.86849	ESTs	21.00
65	109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60
	109445	AA232103	Hs.189915	ESTS	24.20
	109502 109633	AW967069 AW003785	Hs.211556 Hs.170267	hypothetical protein MGC5487 ESTs	21.40 20.40
	109786	A1989482	Hs.146286	kinesin family member 13A	19.60
70 ·	109958	AA001266	Hs.133521	ESTs	24.00
	110920	N47224	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	28.40
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	36.00
	111084 111132	H44186 AB037807	Hs.15456 Hs.83293	PDZ domain containing 1	61.20 24.60
75	111229	AW389845	Hs.110855	hypothetical protein ESTs	27.20
. •	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00
	111987	NM_015310	Hs.6763	KIAA0942 protein	37.80
	112046	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	26.80
80	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	63.80
30	112685 112871	R87650 AL110216	Hs.33439 Hs.12285	ESTs, Wealdy similar to ALU1_HUMAN ALU ESTs, Wealdy similar to I55214 salivary	26.40 47.64
	112897	AW206453	Hs.3782	ESTs, Weardy Similar to 155214 Salivary	22.00
	112973	AB033023	Hs.318127	hypothetical protein FLJ 10201	65.00
05	112992	AL157425	Hs.133315	Homo saplens mRNA; cDNA DKFZp761J1324 (f	42.00
85	113073	N39342	Hs.103042	microtubute-associated protein 1B	55.40

	W	O 02/086	443		
	113494	T91451	Hs.86538	ESTs	22.80
	113560	T91015	Hs.268626	ESTs	22.80
	113849	AA457211	Hs.8858 Hs.30504	bromodomain adjacent to zinc finger doma	51.80 28.20
5	113950 114339	A1267652 AA782845	Hs.22790	Homo sapiens mRNA; cDNA DKFZp434E082 (fr ESTs	20.20
9	114365	H42169	Hs.18653	hypothetical protein FLJ14627	21.00
	114455	H37908	Hs.271616	ESTs, Weathy similar to ALU8_HUMAN ALU S	25.80
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	23.60
	114824	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	27.20
10	114837	BE244930	Hs.166895	ESTs	30.20
	114974	AW966931	Hs.179862	nucleosome assembly protein 1-like 1	20.80
	115075	AA814043	Hs.88045	ESTs	30.60
	115084	BE383668	Hs.42484	hypothetical protein FLJ10618	28.86
15	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	38.00
IJ	115313 115697	AA808001 D31382	Hs.184411 Hs.63325	albumin	22.60 173.60
	115909	AW872527	Hs.59761	transmembrane protease, serine 4 ESTs, Wealthy similar to DAP1_HUMAN DEATH	27.77
	116090	AL591147	Hs.61232	ESTs	20.80
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	164.20
20	116399	AA889120	Hs.110637	homeo box A10	38.00
	117099	H93699		gb:yv16a11.s1 Soares fetal liver spleen	21.60
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	49.40
	118091	AW005054	Hs.47883	ESTs, Wealthy strntlar to KCC1_HUMAN CALCI	22.40
25	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	22.00
25	118720	N73515	Un 44577	gb:za49d07.s1 Soares fetal liver spleen	20.00 19.40
	118873 119126	AI824009 R45175	Hs.44577 Hs.117183	ESTs ESTs	111.20
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	33.00
	119940	AL050097	Hs.272531	DKFZP586B0319 protein	31.00
30	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	20.20
	120515	AA258356		gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi	25.00
	120859	AA826434	Hs.1619	achaete-scute comptex (Drosophila) homol	95.40
	120983	AA398209	Hs.97587	EST	105.20
25	121054	AW976570	Hs.97387	ESTs	38.80
35	121369	AW450737	Hs.128791	CGI-09 protein	41.60
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	30.80 19.60
	122612 123130	AA974832 AA487200	Hs.128708	ESTs gb:ab19f02.s1 Stratagene lung (937210) H	33.20
	123440	A1733692	Hs.112488	ESTs	23.17
40	123596	AA421130	Hs.112640	EST	23.00
	123619	AA602954		gb:no97c02.s1 NCI_OGAP_Pr2 Homo sepiens	28.80
	124005	Al147155	Hs.270016	ESTs .	77.60
	124169	BE079334	Hs.271630	ESTs	22.20
4.5	124281	A1333756	Hs.111801	arsenate resistance protein ARS2	42.20
45	124472	N52517	Hs.102670	EST	32.60
	124617	AW628168	Hs.152684	ESTs	21.80
	124631 124839	NM_014053	Hs.270594	FLVCR protein	30.40 21.20
	125186	R55784 AA610620	Hs.140942 Hs.181244	ESTs major histocompatibility complex, class	42.80
50	125321	T86652	Hs.178294	ESTs	27.00
	125535	NM_013243	Hs.22215	secretogranin III	23.80
	125646	AA628962	Hs.75209	protein kinase (cAMP-dependent, catalyti	23.20
	125684	AW589427	Hs.158849	Homo saplens cDNA: FLJ21663 fis, clone C	21.20
	125724	AL360190	Hs.295978	Homo sapiens mRNA full length insert cDN	48.80
55	125847	AW161885	Hs.249034		31.00
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	21.20
	126077	M78772	Hs.210836	ESTs	49.80
	126299 126395	AW979155 Al468004	Hs.298275 Hs.278956	amino acid transporter 2 hypothetical protein FLJ12929	21.80 71.00
60	126433	AA325606	113.27 0530	gb:EST28707 Cerebellum II Homo sapiens c	23.20
00	126509	R47400	Hs.23850	ESTs	23.80
	126538	AB030656	Hs.17377	coronin, actin-binding protein, 1C	23.10
	126666	AA648886	Hs.151999	ESTs	36.00
	126812	AB037860	Hs.173933	nuclear factor I/A	20.80
65	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	46.29
	127046	AA321948	Hs.293968	ESTs	22.80
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	30.00
	127489 127521	AA650250	Hs.272076 Hs.164018	ESTs ESTs	20.80 25.20
70	127742	AW297206 AW293496	Hs.180138	ESTs ·	28.00
. •	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	21.20
	127930	AA809672	Hs.123304	ESTs	20.54
	127968	AA830201	Hs.124347	ESTs	28.20
~~	127987	AI022103	Hs.124511	ESTs	19.60
75	128116	H07103	Hs.285014	Horno sapiens, ctone IMAGE:3857243, mRNA	20.40
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	34.40
	128777	Al878918	Hs.10526	cysteine and glycine-rich protein 2	53.80
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	23.00
80	129168	Al132988	Hs.109052	chromosome 14 open reading frame 2	37.60
30	129404	Al257700 AA760221	Hs.317584	ESTs	28.60
	129527 129574	AA769221 AA026815	Hs.270847 Hs.11463	delta-lubulin UMP-CMP kinase	40.80
	129574	N30436	Hs.11463 Hs.11556	Home sapiens cDNA FLJ12566 fis, clone NT	31.20 29.60
	129785	H19006	Hs.184780	ESTs	72.20
85	129970	AV655806	Hs.296198	chromosome 12 open reading frame 4	22.20

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	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60	
	130199	Z48579	Hs.17202B	a disintegrin and metalloproteinase doma	27.60	
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36	
_		W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20	
5		AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	22.40	
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60	
	130703	R77776	Hs.18103	ESTs ·	19.40	
		AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40	
10	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00	
10	131028	Al879165	Hs.2227 Hs.2281	OCAAT/enhancer binding protein (C/EBP).	25.20 40.60	
	131086	AL035461		chromogranin B (secretogranin 1)	24.60	
	131284	NM_001429	Hs.25272 Hs.31921	E1A binding protein p300 KIAA0648 protein	21.00	
	131850	AB014548 BE383576	Hs.334	Rho quanine nucleotide exchange factor (33.40	
15		NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80	
13	132040	NM 001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	20.40	•
		NM_002267	Hs.3886	karyopherin alpha 3 (Importin alpha 4)	29.40	
	132389	AA310393	Hs.190044	ESTs	32.40	
	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40	
20		AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60	
		AF037335	Hs.5338	carbonic anhydrase XII	31.36	
		AU076916	Hs.5398	guarrine monphosphate synthetase	32.40	
		W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40	
	132742	AA025480	Hs.292812	ESTs, Wealdy similar to T33468 hypotheti	61.20	
25	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33	
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50	
		AF070 5 92	Hs.66170	HSKM-B protein	30.00	
		X91662	Hs.66744	bvist (Drosophila) homolog (acrocephalos	23.80	
20		AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60	
30	133350	AJ499220	Hs.71573	hypothetical protein FLJ 10074	33.00	
		AV652066	Hs.75113	general transcription factor IIIA	82.00	
	133658	AA319146	Hs.75426	secretogramin II (chromogramin C)	69.33	
		AB011155	Hs.170290	discs, large (Drosophila) homolog 5	33.20	
35	134032	NM_005025	Hs.78589 Hs.50421	serine (or cysteine) proteinase inhibito KIAA0203 gene product	31.60	
33	134125 134158	NM_014781 U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60	
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40	
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20	
	134570	U66615	Hs. 172280	SWI/SNF related, matrix associated, acti	20.20	
40	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.80	
		AA448542	Hs.251677	G antigen 78	37.60	•
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40	
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	31.60	
	135345	X53655	Hs.99171	neurotrophin 3	28.80	
45						

TABLE 4B shows the accession numbers for those primekeys lacking unigenelD's for Table 4A. For each probeset we have listed the gene cluster number from which the ofigonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

	Pkey	CAT number	Accessions
60	123619 126433 126872	127143_1 142696_1	AA602964 AA609200 AA325606 AA099517 N89423 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
65	106851 118720 120515 117099 101447 123130	322947_1 genbank_N73515 genbank_AA2583	A458623 AA639708 AA485409 R22065 AA485570 5 N73516 156 AA258356 HB3699 H97976 H80036 M21305

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Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5	Pkey:	Unique Eos probeset identifier number
	ExAcon:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene fille
•	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung turnor samples divided by the 90th percentile of AI for normal and chronically
10		diseased tung samples.
	R2:	80th percentile of Al adenocarcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically diseased lung samples.
	R3:	80th percentile of Al squamous cell carcinoma lung tumor samples divided by the 90th percentile of Al for normal and chronically diseased lung samples.
	R4:	80th percentile of Al adenocarcinoma lung tumor samples divided by the 80th percentile of Al for squamous cell carcinoma lung tumor samples.
	R5:	70th percentile of Al for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of Al for all normal lung, chronically
15		diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all
		normal lung, chronically diseased lung and tumor samples

20	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2	R3	R4	R5
20	100035			AFFX control: GAPDH					6.76
	100036			AFFX control: GAPDH					5.77
	100037	•		AFFX control: GAPDH					5.75
	100071	A28102		Human GABAa receptor alpha-3 subunit		8.00			
25	100114	X02308	Hs.82962	thymidylate synthetase					5.71
	100154	H60720	Hs.81892	KIAA0101 gene product	3.84				
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,					5.67
	100269	NM_001949	Hs.1189	E2F transcription factor 3	2.55				
	100287	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e					5.66
	100297	AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
25	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.	- 07				4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				4 00
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82 3.79
	100372	NM_014791	Hs.184339	KIAA0175 gene product			-	15.65	3.79
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic				15.05	5.49
40	100486	T19006	Hs.10842	RAN, member RAS oncogene family					4.17
40	100491 100516	D56165 D90278	Hs.275163	non-metastatic cells 2, protein (NM238) carcinoembryonic antigen-related cell ad		7.20			7.17
	100516		Hs.11 Hs.99949	prolactin-induced protein		7.20		14.20	
	100522	X51501 NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10			17.20	
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	3.10			9.30	
45	100629	AA015693	Hs.21291	mitogen-activated protein kinase kinase				20.60	
73	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1	0.20	8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k		0.00		10.00	
	100709	N26539	Hs.100469	myelold/lymphoid or mixed-lineage leukem			24.80		
50	100761	BE208491	Hs.295112	KIAA0618 gene product		7.60			
	100830	AC004770	Hs.4756	flap structure-specific endonuclease 1					7.99
	100867	U14622		gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogena (multiple endocrine n		8.00			
	100906	AU076916	Hs.5398	guanine monphosphate synthetase					5.16
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				
	101045	J05614		gb:Human proliferating cell nuclear anti					4.69
	101061	NM_000175	Hs.180532	glucose phosphate isomerase					4.19
	101071.		Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
60	101124	L10343	Hs,112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				r co
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (400				5.69
	101204	L24203	Hs.82237	ataxia-telangiactasia group D-associated	4.08		6.40		
	101210	L29301	Hs.2353	opioid receptor, mu 1	2.53		0.40		
65	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	233				7.90
05	101228 101233	AA333387 AL135173	Hs.82916 Hs.878	chaperonin containing TCP1, subunit 6A (sorbitol dehydrogenase					4.45
	101233	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				1.10
	101342	U52112	Hs.182018	interleukin-1 receptor-associated kinase	4.00				4.17
	101346	AJ738616	Hs.77348	hydroxyprostagiandin dehydrogenase 15-(N				21.89	
70	101369	NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
, ,	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (comilin)					7.90
	101448	NM 000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31				
	101482	AL035668	Hs.73853	bone morphogenetic protein 2				38.80	
75	101466	BE262660	Hs.170197	glutamic-oxaloacetic transaminase 2, mit					4.01
	101484	AA053486	Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958		gb::Human parathyroid hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
00	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				
80	101535	X57152	Hs.99853	fibrillarin					4.65
	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h				9.09	
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	54.00				
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
85	101664	AA436989	Hs.121017	H2A histone family, member A	7.00	7 00			
93	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

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	101695	M69136	Hs.135626	chymase 1, mast cell	4.79				
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21				
	101748	NIM_001944 M80244	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	55.50				4.10
5	101759 101771	NM_002432	Hs.184601 Hs.153837	solute carrier family 7 (cationic amino myeloid cell nuclear differentiation ant				18.57	4.10
	101804	M86699	Hs.169840	TTK protein kinase	4.50				
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kO (conn	140.00				
	101833 101842	AU076442 M93221	Hs.117938 Hs.75182	collagen, type XVII, atpha 1 mannose receptor, C type 1	2.56			12.80	
10	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor				12.00	5.88
	102002	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min		7.80			
	102039	AL134223	Hs.306098	aldo-keto reductase family 1, member C1			7.40		4.35
	102072 102083	U09410 T35901	Hs.78743 Hs.75117	zinc finger protein 131 (clone pHZ-10) Interleukin enhancer binding Tactor 2, 4			7.40		5.12
15	102101	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,				12.00	3.12
-•	102123	NM_001809	Hs.1594	centromere protein A (17kD)	6.20				
	102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.62				
	102193 102217	AL035335 AA829978	Hs.313 Hs.301613	secreted phosphoprotein 1 (asteopontin, JTV1 gene	5.85				6.18
20	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu					4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1					5.80
	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.50				C 4 P
	102305 102330	AL043202 BE298063	Hs.90073 Hs.77254	chromosome segregation 1 (yeast homolog) chromobox homolog 1 (Drosophila HP1 beta					5.15 4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro				9.33	4.11
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	8.87				
	102368	U39817	Hs.36820	Bloom syndrome	15.91		40.00		
	102394 102404	NM_003816 NM_005429	Hs.2442 Hs.79141	a disintegrin and metalloproteinase doma vascular endothelial growth factor C			19.20	14.00	
30	102537	U57094	Hs.50477	RAB27A, member RAS oncogene family				12.00	
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2					4.57
	102605	Al435128	Hs.181369	ubiquitin fusion degradation 1-like	77.50				3.98
	102610 102623	U65011 AW249285	Hs.30743 Hs.37110	preferentially expressed antigen in mela melanoma antigen, family A, 9	77.50 12.50				
35	102642	AA205847	Hs.23016	G protein-coupled receptor	12.00		22.00		
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00			
	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	6.50			12.80	
	102669 102672	U71207 U72066	Hs.29279 Hs.29287	eyes absent (Drosophila) homolog 2 retinoblastoma-binding protein 8	6.50 8.50				
40	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	0.00				9.24
	102696	BE540274	Hs.239	forkhead box M1					5.54
	102768	U82321	Lb. 400000	gb:Homo sapiens clone 14.98 mRNA sequenc		6.60			3.78
	102781 102784	BE258778 U85658	Hs.108809 Hs.61796	chaperonin containing TCP1, subunit 7 (e transcription factor AP-2 gamma (activat					4.26
45	102824	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H			14.40		
	102829	NM_006183	Hs.80962	neurotensin	8.00				
	102888 102892	AJ346201 BE440042	Hs.76118 Hs.83326	ubiquifin carboxyl-terminal esterase L1 matrix metalloproteinase 3 (stromelysin			6.70		5.50
	102913	NM_002275	Hs.80342	keratin 15	4.64		0.70		
50	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	2.93				
	102951	X15218	Hs.2969	v-sid avian sarcoma viral oncogene homol				11.40	7.00
	102983 103023	BE387202 AW500470	Hs.118638 Hs.117950	non-metastatic cells 1, protein (NM23A) multifunctional polypeptide similar to S	3.01				7.26
	103036	M13509	Hs.83169	matrix metafloproteinase 1 (Interstitial	27.90				
55	103038	AA926960	Hs.334883	CDC28 protein kinase 1					8.79
	103060	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin		9.80			4.27
	103099 103119	Al693251 X63629	Hs.8248 Hs.2877	NADH dehydrogenase (ubiquinone) Fe-S pro cadherin 3, type 1, P-cadherin (placenta	4.05	5.00			
	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07				
60	103185	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmi		7.40			5.62
	103192 103223	M22440 BE275607	Hs.170009 Hs.1708	transforming growth factor, alpha chaperonin containing TCP1, subunit 3 (g		7.40			4.70
	103242	X76342	Hs.389	elcohol dahydrogenase 7 (class IV), mu o			100.00		4.70
	103316	XB3301	Hs.324728	SMA5				9.80	
65	103375	NM_005982 AL036166	Hs.54416	sine oculis homeobox (Drosophila) homolo coated vesicle membrane protein	9.71 14.00				
	103376 103385	NIM_007069	Hs.323378 Hs.37189	similar to rat HREV107	14.00			11.00	
	103391	X94453	Hs.114366	pyrrolina-5-carboxytate synthetase (glut	2.93				
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,					5.15
70	103430 103445	BE564090 X98834	Hs.20716 Hs.79971	translocase of inner mitochondrial membr sal (Drosophila)-like 2				21.40	3.98
	103476	Y07701	Hs.293007	aminopeptidase puromycin sensitive		13.00			
	103477	AJ011812	Hs.119018	transcription factor NRF			6.40		
75	103478	BE514982	Hs.38991	S100 calcium-binding protein A2	5.02				
13	103515 103558	Y10275 BE616547	Hs.56407 Hs.2785	phosphoserine phosphatase keratin 17	10.50 6.41				
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp					3.84
	103587	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	78.50				
80	103594 103636	Al368680 NIM_006235	Hs.816 Hs.2407	SRY (sex determining region Y)-box 2 POU domain, class 2, associating factor	6.51 3.50				
Q.	103768	AF086009	113.2401	gb:Homo saplens full length insert cDNA	3.30				4.48
	103841	AA314821	Hs.38178	hypothetical protein FLJ23468		8.00			
	103847	AF219946	Hs.102237	tubby super-family protein		10.40		15.00	
85	103913 104094	AW967500 AA418187	Hs.133543 Hs.330515	ESTs ESTs			6.60	15.60	
		- 4 17 101	, 10,000,10						

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	104150	AL122044	Hs.331633	hypothetical protein DKFZp566N034				26.00	1 C 1/030	2/124/0
	104257	BE560621	Hs.9222	estrogen receptor binding site associate		6.80				
	104261	AW248364	Hs.5409	RNA polymerase I subunit					3.98	
5	104331 104415	AB040450 BE410992	Hs.279862 Hs.258730	cdk inhibitor p21 binding protein hemo-regulated initiation factor 2-alpha		6.80 10.29				
	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21	10.23				
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m				15.79		
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fis, clone H	0.40			17.40		
10	104660 104689	BE298565 AA420450	Hs.14846 Hs.292911	Homo saptens mRNA; cDNA DKFZp564D016 (tr ESTs, Highly similar to S60712 band-6-pr	6.40				6.55	
10	104754	Al206234	Hs.155924	cAMP responsive element modulator				10.00	0.55	
	104758	BE560269	Hs.7010	NPD002 protein					4.47	
	104971	BE311926	Hs.15830	hypothetical protein FLJ12691	2.87					
15	105011 105012	BE091926 AF098158	Hs.16244 Hs.9329	mitotic spindle coiled-coil related prot chromosome 20 open reading frame 1	3.83 2.86					
15	105026	AA809485	Hs.124219	hypothetical protein FLJ12934	2.00	11.00				
	105076	Al598252	Hs.37810	hypothetical protein MGC14833					5.01	
	105132		Hs.247280	HBV associated factor					3.99	
20	105143 105158	A1368836 AW976357	Hs.24608 Hs.234545	ESTs, Weakly similar to 138022 hypotheti hypothetical protein NUF2R		16.00	11.00			
20	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32	10.00				
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	3.00					
	105264	AA227934	H- 00000	gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi				10.00		
25	105298 105409	BE387790 AW505076	Hs.26369 Hs.301855	hypothetical protein FLJ20287 DiGeorge syndrome critical region gene 8	3.69			9.20		
20	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,			7.80	3.20		
	105667	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	4.12					
	105743	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	3.82					
30	105782 105848	H09748 AW954064	Hs.57987 Hs.24951	B-cell CLL/lymphorna 11B (zinc finger pro ESTs			27.00			
50	105891	U55984	Hs.289088	heat shock 90kD protein 1, alpha			7.60		4.14	
	106019	AF221993	Hs.46743	McKusick-Kaufman syndrome			16.80			
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip			23.40			
35	106073 106126		Hs.17834 Hs.22972	downstream neighbor of SON	9.50					
23	106159	AK001301	Hs.3487	hypothetical protein FLJ13352 hypothetical protein FLJ10439	6.00				3.95	
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36					6.04	
	106260	A)097144	Hs.5250	ESTs, Wealdy similar to ALU1_HUMAN ALU S			13.20			
40	106300 106307	Y10043 AA436174	Hs.19114 Hs.37751	high-mobility group (nonhistone chromoso		6.60			5.02	
40	106307	AA025610	Hs.9605	ESTs, Weakly similar to putative p150 [cleavage and polyadenylation specific ta		6.60			5.04	
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced					7.25	
	106440	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub			13.80			
45	106481 106586	D61594 AA243837	Hs.17279 Hs.57787	tyrosylprotein sulfotransferase 1 ESTs	4.75			10.84		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr				45.60		
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	28.00					
	106785	Y15227	Hs.20149	deleted in lymphocytic laukemia, 1	3.00		44.40			
50	106813 106895	C05766 AK001826	Hs.181022 Hs.25245	CGI-07 protein hypothetical protein FLJ11269			11.40 6.00			•
	106913	Al219346	Hs.86178	M-phase phosphoprotein 9		6.56	0.00			
	106919	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU S					4.27	
	107054	AJ076459	Hs.15978	KIAA1272 protein	474			34.80		
55	107059 107098	BE614410 AI823593	Hs.23044 Hs.27688	RAD51 (S. cerevisiae) homolog (E coli Re ESTs	4.71			24.80		
	107104	AU076640	Hs.15243	nucleolar protein 1 (120kD)				24.00	7.05	
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60		•			
	107198	AV657225	Hs.9846	KIAA1040 protein programmed cell death 2		19.20				
60	107203 107217	D20426 AL080235	Hs.41639 Hs.35861	DKFZP586E1621 protein	9.50	7.60				
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71					
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence			8.71			•
	107516 107529		Hs.99853 Hs.296585	fibrillarin nucleolar protein (KKE/D repeat)					4.33 4.00	
65		AA019551	Hs.294151	Homo sapiens, clone IMAGE:3603838, mRNA,		10.80			4.00 3	
	107851	AA022953	Hs.61172	EST			8.00			
	107901		Hs.335952	keratin 6B	3.40					
		BE153855 AW392555	Hs.61460 Hs.18878	lg superfamily receptor LNIR hypothetical protein FLJ21620	2.88 7.50					
70	108015	AW298357	Hs.49927	protein kinase NYD-SP15	7.50			23.40		
	108056	AA043675	Hs.62633	ESTs				12.80		
		A1867370 BE245374	Hs.139709	hypothetical protein FLJ12572		7.00		12.80		
	108187 108296		Hs.27842 Hs.161623	hypothetical protein FLJ11210 ESTs		7.00 6.60				
75	108305	AA071391		gb:zm61e06.r1 Strategene fibroblast (937				11.80		
	108393	AA075211		gb:zm86a08.r1 Stratagene ovarian cancer				11.80		
		AL133092	Hs.68055	hypothetical protein DKFZp434I0428		C 40		20.80		
		AA084948 AA086005		gb:zn13b09.s1 Stratagene hNT neuron (937 gb:zi84c04.s1 Stratagene colon (937204)		6.40		25.40		
80	108584	AA088326	Hs.120905	Horno sapiens cDNA FLJ11448 fis, done HE		9.60				
	108597	AK000292	Hs.278732	hypothetical protein FLJ20285				14.60		
		AB029000 AA121514	Hs.70823 Hs.70832	KIAA1077 protein ESTs	3.00			10.00	•	
	108700	AA121514 AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c			11.00	10.00		
85		AU076442	Hs.117938	collagen, type XVII, atpha 1	11.21					

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	108810		Hs.71331	hypothetical protein MGC5350	8.50				
	108816		Hs.270501	ESTs, Moderately similar to ALU2_HUMAN	4.00	7.40			
	108857 108860		Hs.62180 Hs.129911	anilin (Drosophila Scraps homolog), act ESTs	4.00 6.09				
5	108937		Hs.24341	transcriptional co-activator with PDZ-bi	3.00				
	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69				
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro	40.50				4.53
	109166 109227		Hs.73625 Hs.85874	RAB6 interacting, kinesin-like (rabkines Human DNA sequence from clone RP11-16L21	10.58	9.00			
10	109415		Hs.110826	trinucleotide repeat containing 9		51.40			
	109418	AI866946	Hs.161707	ESTs				11.00	
	109454		Hs.295232	ESTs, Moderately similar to A46010 X-II			17.60		
	109502	AW967069 AA564994	Hs.211556 Hs.222851	hypothetical protein MGC5487 ESTs		12.67	9.49		
15	109648	H17800	Hs.7154	ESTs				10.40	
	109680	AB037734	Hs.4993	KIAA1313 protein			33.20		
	109700 109704	F09609 A1743880	Un 40070	gb:HSC33H092 normalized infant brain cDN			11.00	16.00	
	109792		Hs.12876	ESTs gb:yg61f03.s1 Soares Infant brain 1NIB H			11.00	12.60	
20	109981	BE546208	Hs.26090	hypothetical protein FLJ20272	4.00				
	109998	AL042201	Hs.21273	transcription factor NYD-sp10		7.80			
	110039 110156	H11938 AA581322	Hs.21907 Hs.4213	histone acetyltransferase hypothetical protein MGC16207		7.00			4.24
		AA907723	Hs.36962	ESTs	4.50				7.27
25	110551	AW450381	Hs.14529	ESTs		8.60			
	110561 110854	AA379597 BE612992	Hs.5199	HSPC150 protein similar to ubiquilin-con hypothetical protein FLJ10607 similar to	3.06	6 00			
		AW274992	Hs.27931 Hs.72249	three-PDZ containing protein similar to		6.80	8.80		
••		BE178102	Hs.24349	ESTs		6.80			
30		N52980	Hs.83765	dihydrofolale reductase				16.80	
	111337 111434	AA837396 R01608	Hs.263925 Hs.142736	LIS1-interacting protein NUDE1, rat homo ESTs	2.54			9.80	
	111439	Al476429	Hs.19238	ESTs				10.40	
25	111540	U82670	Hs.9786	zinc finger protein 275			15.40		
35	111597	R11499	Hs.189716	ESTS		6.00		9.20	
	111895 111929	T80581 AF027208	Hs.12723 Hs.112360	Homo sapiens clone 25153 mRNA sequence prominin (mouse)-like 1		6.80		14.67	
	112054	R43590		gb.yc85g02.s1 Soares infant brain 1NIB H		10.80			
40	112210	R49645	Hs.7004	ESTs	2.00			10.20	
40	112244 112382	AB029000 R59904	Hs.70823	KIAA1077 protein gb:yh07g12.s1 Soares infant brain 1NIB H	2.99	6.60			
	112392	R60763	Hs.193274	ESTs, Moderately similar to 157588 HSrel		0.00	7.10		
	112442		Hs.285581	Williams-Beuren syndrome chromosome regi	3.00			07.00	
45	112539 112772	R70318 Al992283	Hs.339730 Hs.35437	ESTs ESTs, Moderately similar to 138026 MLN 6				37.20 14.60	
	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin					4.83
	112935	R71449	Hs.268760	ESTs	2.73			40.00	
	112970 112973	AA694010 AB033023	Hs.6932 Hs.318127	Homo sapiens clone 23809 mRNA sequence hypothetical protein FLJ10201	11.50			12.00	
50	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f			10.89		
	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr microtubule-associated protein 1B	15.00		45.04		
	113073 113078	N39342 T40444	Hs.103042 Hs.118354	CAT56 protein		7.00	15.31		
	113238	R45467	Hs.189813	ESTs				41.20	•
55	113591	T91881	Hs.200597	KIAA0563 gene product	05.00			9.40	
	113702 113844	T97307 Al369275	Hs.243010	gb:ye53h05.s1 Soares fetal liver spleen Homo sapiens cDNA FLJ14445 fis, clone HE	25.00			13.91	
	113984	R96696	Hs.35598	ESTs		7.80			
60	114073	R44953	Hs.22908	Homo saplens mRNA; cDNA DKFZp434J1027 (f		7.20			
60	114162	AF155661 AL049468	Hs.22265 Hs.7859	pyruvate dehydrogenase phosphatase ESTs	3,42		6.74		
	114251	H15261	Hs.21948	ESTs			0.74	33.20	
	114285	R44338	Hs.22974	ESTs				13.20	
65	114313	H18456	Hs.27946	ESTS		7.00		10.00	
05	114339 114407	AA782845 BE539976	Hs.22790 Hs.103305	ESTs Homo sapiens mRNA; cDNA DKFZp434B0425 (f		7.80			4.14
	114560	AJ452469	Hs.165221	ESTs				9.80	
	114699 114767	AA127386 AI859865	Hs.154443	gb:zn90d09.r1 Stratagene lung carcinoma minichromosome maintenance deficient (S	2.04	7.60			
70	114793	AA158245	113.13 444 3	gb:zo76c03.s1 Stratagene pancreas (93720	3.21		6.00		
• -	114833	AJ417215	Hs.87159	hypothetical protein FLJ12577				11.40	
	115047	BE270930	Hs.82916	chaperonin containing TCP1, subunit 6A (4.31
	115060 115097	AF052693 AA256213	Hs.198249 Hs.72010	gap junction protein, beta 5 (connexin 3 ESTs				35.40	4.03
75	115113		12010	gbzzr81a04.s1 Soares_NhHMPu_S1 Homo sapi				15.20	
	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m					4.19
	115134 115291	AW968073 BE545072	Hs.194331 Hs.122579	ESTs, Highly similar to A55713 inositol	25 00			12.40	
		AA356792	Hs.334824	hypothetical protein FLJ10461 hypothetical protein FLJ14825	25.00	7.00			
80	115414	AA662240	Hs.283099	AF15q14 protein	3.25				
	115522		Hs.333893	o-Myc target JPO1	3.68				
	115536 115566	AK001468 Al142336	Hs.62180 Hs.43977	anillin (Drosophila Scraps homolog), act Human DNA sequence from clone RP11-196N1	10.50			24.40	
0.5	115645	Al207410	Hs.69280	Homo saplens, clone IMAGE:3636299, mRNA,	4.17				
85	115648	AW016811	Hs.234478	Homo saplens cDNA: FLJ22648 fis, clone H			6.00		

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			Hs.38178	hypothetical protein FLJ23468	3.81	•			1 € 1/0502/124/0
	115652 115697	BE093589 D31382	Hs.63325	transmembrane protease, serine 4	62.14				
	115793		Hs.70333	hypothetical protein MGC10753				11.80	
-	115816		Hs.287588	Homo sapiens cDNA FLJ13675 fis, clone PL				9.71	
5	115892		Hs.50831	ESTs	0.52		27.40		
	115906 115909	AI767756 AW872527	Hs.82302 Hs.59761	Homo sapiens cDNA FLJ14814 fis, clone NT ESTs, Wealdy similar to DAP1_HUMAN DEATH	2.53 11.82				
	115965		Hs.173233	hypothetical protein FLJ10970				34.29	
	115978		Hs.69517	cDNA for differentially expressed CO16 g					8.23
10	115985		Hs.268115	ESTs, Wealty similar to T08599 probable	3.00				
	116090	AJ591147	Hs.61232	ESTs	5.17		8.20		•
	116096 116127		Hs.59982 Hs.279884	ESTs DNAJ domain-containing		10.60	0.20		
	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17		10.00			5.82
15	116190		Hs.67776	ESTs, Weakly similar to T22341 hypotheti					4.08
	116278		Hs.47504	exonuclease 1	9.50				
	116335		Hs.41690	desmocolin 3	3.67	7.00			
	116496 116503	AW450694 AI925316	Hs.21433 Hs.212617	hypothetical protein DKFZp547J036 ESTs		7.00		12.60	
20	116674	AI768015	Hs.92127	ESTs			32.00		
	116929	AA586922	Hs.80475	polymerase (RNA) II (DNA directed) polyp		7.60			
	116973	AJ702054	Hs.1669B2	phosphatidylinositol glycan, class F	•	9.80		40.00	
	116993	AM17023	Hs.40478	ESTS share 8600 c1 Searce rating M2b/LIP Home				10.20 15.20	
25	117079 117317	H92325 Al263517	Hs.43322	gb:ys85f05.s1 Soares relina N2b4HR Homo ESTs				13.40	
	117326	N23629	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60	
	117396	W20128	Hs.296039	ESTs				10.60	
	117412		Hs.42645	ESTs				16.00	
30	117519	N32528	Hs.146286 Hs.112110	kinesin family member 13A mitochondrial ribosomal protein L42				9.11	4.01
50	117693 117721	AW179019 N46100	Hs.93939	EST				19.80	4.01
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	271				
	117903		Hs.47111	ESTs				17.80	4.47
35	117992		Hs.172089	Homo saplens mRNA; cDNA DKFZp586l2022 (f ESTs				10.60	4.17
33	118013 118017	A!674126 Al813444	Hs.94031 Hs.42197	ESTS			8.82	10.00	
	118186	N22886	Hs.42380	ESTs		7.00			
	118325	AI868065	Hs.166184	Intersectin 2			0.44	13.80	
40	118367	N64269 N64339	Hs.48946 Hs.48956	EST gap junction protein, beta 6 (connextn 3	3.14		6.14		
TU	118358 118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	0.14		12.40		
	118709	AA232970	Hs.293774	ESTs				12.20	
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50				
45	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22	9.60			
43	119052 119164	R10889 AF221993	Hs.46743	gb:yf38d02.s1 Soares fatal liver spleen McKusick-Kaufman syndrome		5.00	6.60		
	119186	Al979147	Hs.101265	hypothetical protein FLJ22593				10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon Il Homo sa				9.44	
50	119490	AA195276	Hs.263858	ESTs, Moderately similar to 834087 hypot ESTs			14.80	11.80	
30	119499 119599	Al918906 W45552	Hs.55080	gb:zc26d03.s1 Soares_senescent_fibroblas		12.60	14.00		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00				
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50				
55	119941	AA699485	Hs.58896	ESTS	7.73	8.00			
55	119994 120102	AA642402 W67353	Hs.59142 Hs.170218	ESTs KIAA0251 protein	7.10		39.60		•
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91				•
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par			8.20		
60	120486	AW368377	Hs.137569	turnor protein 63 kDa with strong homolog	8.73	7.00			
OU	120599 120699	AA804448 AI683243	Hs.104463 Hs.97258	ESTs ESTs, Moderately similar to S29539 ribos		7.00		10.00	
	120715	AA292700	115.37 2.00	gbzs59a06.s1 NCI_CGAP_GCB1 Homo saplens		9.40			
	120821	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein				13.80	
65	120859	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol		9.00			
03	120880 120983	AA360240 AA398209	Hs.97019 . Hs.97587	EST EST		15.60	27.66		
	121034		Hs.271623	nucleoporin 50kO			20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like		22,80			
70	121313		Hs.97872	ESTs	25.74			10.00	
70	121369 121376		Hs.128791 Hs.187958	CGI-09 protein solute carrier family 6 (neurotransmitte	25.71				5.42
	121476		Hs.97903	ESTs		8.30			
	121509	AA868939	Hs.97888	ESTs		8.59			
75	121553		Hs.48820	TATA box binding protein (TBP)-essociat	18.50 7.00				
, ,	121753 121838		Hs.323518 Hs.98441	WD repeat domain 5 ESTs				10.40	
	121857		Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00				
	121991	AA430058	Hs.98649	EST				12.20	
80	122089		Hs.98682	hypothetical protein FKSG32			8.60 6.14		
OU	122105 122163		Hs.98699 Hs.98829	ESTs EST			6.14	10.40	
	122318			gb:zv60b05.rl Soares_testis_NHT Homo sap				18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam	13.50				
85	122338 122414	AA443311 Al313473	Hs.98998 Hs.99087	ESTs ESTs, Wealthy similar to S47073 finger pr	4.80	8.00			
	146414		110.00001	me to a steer of a state of the					

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	122512	AF053305	Hs.98658	budding uninhibited by benzimidazoles 1			8.80		
		AA449352	Hs.99217	ESTs				9.40	
	122702 122852	A1220089	Hs.99439	ESTS		9.20		10.40	
5	122925	A1580056 AW268962	Hs.98992 Hs.111335	ESTs ESTs		6.80		10.40	
	123005	AW369771	Hs.52620	integrin, beta 8			12.60		
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro					5.35
	123160 123315	AA488687 AA496369	Hs.284235	ESTs, Weakly similar to 138022 hypotheti gb:zv37d10.s1 Soares ovary tumor NbHOT H			6.06 12.40		
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po			11.80		
- •	123497	AA765256	Hs.135191	ESTs, Wealty similar to unnamed protein		12.00			
	123518	AL035414	Hs.21068	hypothetical protein		40.00	13.00		
	123519 123614	AW015887 AK000492	Hs.112574 Hs.98806	ESTs hypothetical protein		12.20	7.80		
15	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L				10.60	
	123573	BE550112	Hs.158549	ESTs, Weakly similar to T203_HUMAN TRANS	23.00				
	123727	AI083986	Hs.282977	hypothetical protein FLJ13490		7.00	9.80		
	123731 123752	AA509839 AA227714	Hs.179703	gb:ae62f01.s1 Stratagene lung carcinoma KIAA0129 gene product	3.50		5.00		
20	123900	AA521223	Hs.112953	EST				12.80	
	124006	Al147155	Hs.270016	ESTs	97.00				
	124059 124069	BE387335 AF134160	Hs.283713 Hs.7327	ESTs, Wealthy similar to S64054 hypotheti claudin 1	3.02		27.80		
	124191	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha			21.00	35.80	
25	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma		7.20			
	124297 124305	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f gb:EST375294 MAGE resequences, MAGH Homo				11.00 16.00	
	124505	AW963221 Al360119.com	mHs.181013	phosphoglycerate mutase 1 (brain)				10.00	6.08
••	124874	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog				21.00	
30	124904	AK000483	Hs.93872	KIAA1682 protein		9.40		10.00	•
	124969 125000	Al650360 T58615	Hs.100256 Hs.110640	ESTs ESTs				10:80 9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotheti		7.60		0.00	
25	125266	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO		6.59			
35	125299	T32982 Al057052	Hs.102720	ESTS				9.57 14.00	
	125356 125370	AA256743	Hs.133554 Hs.134158	ESTs, Weakly similar to Z195_HUMAN ZINC Homo saplens, Similar to KIAA0092 gene p			8.20	. 14.00	
	125418	AA777690	Hs.188501	ESTs				13.20	•
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096		21.40			
40	125437 125446	Al609449 BE219987	Hs.140197 Hs.166982	ESTs phosphatidylinositol glycan, class F		6.96 8.80			
	125711	AA305800	Hs.5672	hypothetical protein AF140225				11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5				15.00	4.31
45	125757 125769	Al274906 BE270266	Hs.166835 Hs.82128	ESTs, Highly similar to 1814460A p53-ass 5T4 oncofetal trophobiast glycoprotein	3.20			15.60	
	125839	AW836261	Hs.337717	ESTs		8.20			
	125850 125875	W85858	Hs.99804	ESTs	2.65	7.40			•
	125924	H14480 BE272506	Hs.82109	gb:ym18b09.r1 Soares infant brain 1NIB H syndecan 1		7.40			4.23
50	125972	Al927475	Hs.35406	ESTs, Highly similar to unnamed protein				40.00	3.98
	126034 126327	H60340 AA432266	Hs.44648	gb:yr39b04.r1 Soares fetal liver spieen ESTs		11.60		10.60	
	126345	N49713	15.77070	gb:yv23f06.s1 Soares fetal liver spleen		6.67			
55	126435	AW614529	Hs.285847	CGI-19 protein				10.60	4.38
55	126487 126521	AA283809 AJ475110	Hs.184601 Hs.203933	solute carrier family 7 (cationic amino ESTs		6.60			4.30
	126522	W31912	15.20000	gb::c76d03.s1 Pancreatic Islet Homo sapi		0.00		14.80	
	126543	AL035B64	Hs.69517	cDNA for differentially expressed CO16 g			7.00		4.01
60	126567 126605	AA058394 AA676910	Hs.57887	ESTs, Wealty similar to KIAA0758 protein gb:zi65h07.s1 Soares_fetal_liver_spleen_			7.80	11.60	
00	126627	AA497044	Hs.20887	hypothetical protein FLJ10392				14.60	
	126628	N49776	Hs.170994	hypothetical protein MGC10946	8.00				
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C nuclear phosphoprotein similar to S. cer	2.92 7.50				
65	126795 126802	AW975076 AW805510	Hs.172589 Hs.97056	hypothetical protein FLJ21634	1.50	11.60			
	126892	AF121856	Hs.284291	sorting nextin 6	3.50				
	126928	AA480902	Hs.137401	ESTs gb:zq89h10.r1 Stratagene hNT neuron (937				22.83 11.80	
	126979 126986	AA210954 Al279892	Hs.46801	sorting needs 14				11.60	
70	126992	AI809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s				20.80	
	127066 127099	R25066 AA347668		gb:yg42c07.r1 Soares Infant brain 1NIB H				27.60 21.60	
	127139	AA830233	Hs.293585	gb:EST54026 Fetal heart II Homo sapiens ESTs				11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famili	3.10				
75	127221	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.76			16.80	
	127225 127313	AA315933 AK002014	Hs.120879 Hs.47546	ESTs Homo sapiens cDNA FLJ11458 fis, clone HE	14.00			10.00	
	127444	AW978474	Hs.7560	Homo sapiens mRNA for KIAA1729 protein,				13.60	
90	127500	AW971353	Hs.162115	ESTS TO TO THE PROPERTY OF THE		11.20	7.00		
80	127524 127540	AI243596 N45572	Hs.94830 Hs.105362	ESTs, Moderately similar to T03094 A-kin Homo saplens, clone MGC:18257, mRNA, com	3.53		7.80		
	127599	AA613204	Hs.150399	ESTs				13.80	
	127609	XB0031	Hs.530	collagen, type IV, alpha 3 (Goodpasture				28.00	
85	127662 127668	W80755 Al343257	Hs.8294 Hs.139993	KIAA0196 gene product ESTs	•			19.80 11.20	
	,000		100000						

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		Al239495	Hs. 120189	ESTs				. 14.18	
	127812 127817	AA741368 AA836641	Hs.291434 Hs.163085	ESTs ESTs	4.50			24.60	
_	127959	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L				9.20	
5	127960	A1613226	Hs.41569	phosphatidic acid phosphatase type 2A				16.83	
	127969 128015	F06498 Z21169	Hs.93748 Hs.334659	Homo sapiens cDNA FLJ14676 fis, clone NT		13.60 7.00			
	128027	AJ433721	Hs.164153	hypothetical protein MGC14139 ESTs		7.00		37.40	
10	128077	Al310330	Hs.128720	ESTs				9.60	
10	128166 128226	NM_006147	Hs.11801	interferon regulatory factor 6	19.00			9.24	
	128305	AI284940 AI954968	Hs.289082 Hs.279009	GM2 ganglioside activator protein matrix Gla protein	13.00			10.40	
	128341	AA191420	Hs.185030	ESTs		9.00			•
15	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul		10.00			4.30
13	128539 128568	R46163 H12912	Hs.258618 Hs.274691	ESTs adenylate kinase 3		12.60			4.56
	128572	AA933022	Hs.256583	Interleukin enhancer binding factor 3, 9				10.00	
	128777	AJ878918	Hs.10526	cysteine and glycine-rich protein 2			16.80		A 40
20	128781 128796	N71826 AJ000152	Hs.105465 Hs.105924	small nuclear ribonucleoprotein polypept defensin, beta 2		8.12			4.48
	128920	AA622037	Hs.166468	programmed cell death 5		•			4.62
	128924	BE279383	Hs.26557	plakophilin 3		12.00			4.04
	128971 129008	H05132 AL079648	Hs.107510 Hs.301088	ESTs ESTs		12.60 8.80			
25	129041	BE382756	Hs.169902	solute carrier family 2 (facilitated glu					6.05
	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59	٠			
	129105 129189	Al769160 AB023179	Hs.108681 Hs.9059	Homo sapiens brain tumor associated prot KIAA0962 protein		8.00	6.67		
	129229	AF013758	Hs.109543	polyadanylate binding protein-interactin	4.00	0.00			
30	129241	A1878857	Hs.109706	hematological and neurological expressed					4.06
	129300 129404	W94197 AL267700	Hs.110165 Hs.317584	ribosomal protein L26 homolog ESTs	2.55 18.00				
	129457	X61959	Hs.207776	aspartytglucosaminidase	6.50				•
25	129466	L42583	Hs.334309	keratin 6A	12.94				
35	129494 129605	AI148976	Hs.112062 Hs.115947	ESTs keratin 16 (focal non-epidermolytic palm				11.00	4.46
	129641	AF061812 Al911527	Hs.11805	ESTs				12.00	4.40
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic					4.70
40	129703 129720	BE388665 AA156214	Hs.179999 Hs.12152	Homo sapiens, clone IMAGE:3457003, mRNA APMCF1 protein					4.02 5.71
70	129748	M16707	Hs.123053	H4 histone, family 2	3.50				U.7 1
	129890	Al868872	Hs.282804	hypothetical protein FLJ22704					4.21
	129896 129945	BE295568 BE514376	Hs.13225 Hs.165998	UDP-GaltbetaGlcNAc beta 1,4- galactosyli	2.56				4.03
45	130010	AA301116	Hs.142838	PAI-1 mRNA-binding protein nucleolar phosphoprotein Nopp34			7.00		4.00
	130026	T40480	Hs.332112	EST		6.40			
	130080 130149	X14850	Hs.147097	H2A histone family, member X	2.74				4.65
	130285	AW067805 AA063546	Hs.172665 Hs.75981	methylenetetrahydrofolate defrydrogenase ublquitin specific protease 14 (tRNA-gua	2.14		7.40		
50	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic					3.91
	130482 130500	AW409701 AB007913	Hs.1578 Hs.158291	baculoviral IAP repeat-containing 5 (sur KIAA0444 protein	4.87			9.60	•
	130524	U89995	Hs.159234	forkhead box E1 (thyroid transcription f			13.40	3.00	
E E	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)			8.20		
55	130553 130567	AF062649 AA383092	Hs.252587 Hs.1608	pituitary tumor-transforming 1			7.00		6.06
	130577	M69241	Hs.162	replication protein A3 (14kD) Insulin-like growth factor binding prote	3.04		7.00		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87				
60	130648	AI458165 L29472	Hs.17296 Hs.1602	hypothetical protein MGC2376				16.20 17.80	
00	130697 130744	H59696	Hs.18747	major histocompatibility complex, class POP7 (processing of precursor, S. cerevi				17.00	5.28
	130800	A)187292	Hs.19574	hypothetical protein MGC5469					4.43
	130867 130869	NM_001072	Hs.284239 Hs.2057	UDP glycosyltransferase 1 family, polype uridine monophosphate synthetase (orotat	16.84				4.92
65	130925	J03626 ÅF093419	Hs.169378	multiple PDZ domain protein				9.60	4.52
	130994	W17044	Hs.327337	ESTs		12.40			
	131028	AI879165	Hs.2227 Hs.288650	CCAAT/enhancer binding protein (C/EBP),	10.21			9.80	
	131031 131041	NM_001650 T15767	Hs.22452	aquaporin 4 Homo sapiens mRNA for KIAA1737 protein,				9.60	,
70	131058	W28545	Hs.101514	hypothetical protein FLJ10342				17.00	
	131090 131112		Hs.2288 Hs.168950	visinin-like 1 Homo sapiens mRNA; cDNA DKFZp566A1046 (f	2.74		8.80		
	131148	AW953575	Hs.303125	p63-induced protein PIGPC1	3.12		0.00		
75	131185	BE280074	Hs.23960	cyclin B1	3.07				
75	131200 131219	BE540516 W25005	Hs.293732 Hs.24395	hypothetical protein MGC3195	3.07 2.87				
	131257	AW339037	Hs.24395	small inducible cytokine subfamily B (Cy ESTs	201			14.67	
	131375	AW293165	Hs.143134	ESTs			19.20		
80	131460	NM_003729	Hs.27076	RNA 3-terminal phosphate cyclase	3.50				
οU	131476 131510	AI521663 BE245374	Hs.334644 Hs.27842	hypothetical protein FLJ14568 hypothetical protein FLJ11210	15.00		7.80		
	131646	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magneshim hom			7.00		
	131786	BE000971	Hs.306083	Novel human gene mapping to chomosome 22	2.65			or an	
85	131839 131843	AB014533 AA192315	Hs.33010 Hs.184062	KIAA0633 protein putative Rab5-interacting protein				35.20	4.11
	.5.510			E					

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	131877 131885	J04088 BE502341	Hs.156346 Hs.3402	topoisomerase (DNA) II alpha (170kD) ESTs	19.00 6.48				
	131921 131945	AA456093 NM_002916	Hs.34720 Hs.35120	ESTs replication factor C (activator 1) 4 (37	56.00		8.40		
5	131958		Hs.3566	ART-4 protein	30.00				3.82
	131965 132000		Hs.35962 Hs.36978	ESTs melanoma antigen, family A, 3	3.03	9.80			
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30	3.00			
10	132109 132114	AW190902 NM_006152	Hs.40098 Hs.40202	cysteine knot superfamily 1, BMP antagon lymphold-restricted membrane protein	21.00	8.40			
	132162	AA315805	Hs.94560	desmoglein 2		0.40			12.25
	132164 132180	A1752235 NM_004460	Hs.41270 Hs.418	procollagen-lysine, 2-oxogiutarate 5-dio fibroblast activation protein, alpha	2.70 2.71				
	132181		Hs.16773	Homo sapiens clone TCCCIA00427 mRNA sequ	3.83				
15	132182 132231		Hs.70499 Hs.42635	ecotropic viral integration site 2A hypothetical protein DKFZp434K2435	9.50			13.20	
	132277	AK001745	Hs.184628	hypothetical protein FLJ 10883	4.50				•
	132328 132394	NM_014787 AK001680	Hs.44896 Hs.30488	DnaJ (Hsp40) homolog, subfamily B, membe DKFZP434F091 protein				9.20 19.80	
20	132424		Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A			8.60	13.00	
	132528 132543	T78736 BE568452	Hs.50758 Hs.5101	SMC4 (structural maintenance of chromoso protein regulator of cytokinesis 1	4.38		27.40		
	132544	L19778	Hs.51011	H2A histone family, member P		7.00			
25	132550 132552	AW969253 BE621985	Hs.170195 Hs.296922	bone morphogenetic protein 7 (osteogenic thiopurine S-methyltransferase	2.64			15.83	
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624			6.60	10.00	
	132617 132638	AF037335 AI796870	Hs.5338 Hs.54277	carbonic anhydrase XII DNA segment on chromosome X (unique) 992	4.95	8.20			
20	132653	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.38	0.24			
30	132669 132710	W38586 W74001	Hs.293981 Hs.55279	guanine nucleotide binding protein (G pr serine (or cysteine) proteinase inhibito	4.60				4.36
	132771		Hs.56407	phosphoserine phosphatase	4.60 3.71				
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2, eukaryotic translation initiation factor				9.48	£ 02
35	132833 132892		Hs.57783 Hs.9973	tensin				12.00	5.83
	132906	BE613337 AW014195	Hs.234896	geminin	3.09				2.07
	132959 132962		Hs.61472 Hs.6153	ESTs, Wealthy stratlar to YAE6_YEAST HYPOT CGI-48 protein	3.50				3.87
40	132990 132994	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18 3.19				
70	133000	AA112748 AL042444	Hs.279905 Hs.62402	cione HQ0310 PRO0310p1 p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96				
	133050 133083	X73424 BE244588	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55				4.00
	133086	L17131	Hs.6456 Hs.139800	chaperonin containing TCP1, subunit 2 (b high-mobility group (nonhistone chromoso					8.96
45	133134 133155	AF198620	Hs.65648	RNA binding motif protein 8A			•	10.80	4.28
	133181	M58583 X91662	Hs.662 Hs.66744	cerebellin 1 precursor twist (Drosophila) homolog (acrocephalos	3.00			10.00	
	133204	BE267696	Hs.254105	enolase 1, (alpha)		12.50			4.63
50	133412 133421	U41493 AF134160	Hs.73112 Hs.7327	guanine nucleotide binding protein (G pr claudin 1	2.85	12.30			
	133451 133453	AW970026 Al659306	Hs.73818	ubiquinol-cytochrome c reductase hinge p		6.80			4.66
	133504	NM_004415	Hs.73826 Hs.74316	protein tyrosine phosphatase, non-recept desmoptakin (DPI, DPII)	6.14	0.00			
55	133506 133615	BE562958 M62843	Hs.74346 Hs.75236	hypothetical protein MGC14353 ELAV (embryonic lethal, abnormal vision,				17.80	4.55
55	133527	NM_002047	Hs.75280	glycyl-IRNA synthetase				17.00	4.85
	133649 133669	U25849 NM_006925	Hs.75393 Hs.166975	acid phosphatase 1, soluble splicing factor, arginine/serine-rich 5				14.00	6.34
CO	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran			6.11	17.00	
60	133776 133865	BE268649 AB011155	Hs.177766 Hs.170290	ADP-ribosyltransferase (NAD+; poly (ADP- discs, large (Drosophila) homolog 5	3.07				4.91
	133946	AJ001258	Hs.173878	NIPSNAP, C. elegans, homolog 1	Ų.U)				4.60
	133973 134047	N55540 BE262529	Hs.78026 Hs.78771	ESTs, Weakly similar to similar to ankyr phosphoglycerate kinase 1				13.00	3.85
65	134098	BE513171	Hs.79086	mitochondrial riposomal protein L3	2.56				5.55
	134107 134112	NM_005629 AW449809	Hs.187958 Hs.79150	solute carrier family 6 (neurotransmitte chaperonin containing TCP1, subunit 4 (d			8.20		4.08
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	31.00				4.00
70	134160 134168	T98152 AA398908	Hs.79432 Hs.181634	fibrillin 2 (congenital contractural ara Homo saplens cDNA: FLJ23602 fis, clone L			24.60		6.71
, ,	134185	AA285136	Hs.301914	neuronal specific transcription factor D				14.74	,
	134201 134272		Hs.79886 Hs.278614	ribose 5-phosphate Isomerase A (ribose 5 protease, sertine, 15	4.50	8.40			
75	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod		9.00			
75	134353 134367	AL138201 AA339449	Hs.82120 Hs.82285	nuclear receptor subfamily 4, group A, m phosphoribosylglychnamide formyltransfer	2.80			16.40	
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.68				
	134423 134469	H53497 AA279661	Hs.83006 Hs.83753	CGI-139 protein small nuclear ribonucteoprotein polypept					3.84 5.81
80	134470	X54942	Hs.83758	CDC28 protein kinase 2					4.21
		AW246273 BE148534	Hs.84131 Hs.84168	threonyl-IRNA synthetase UV-B repressed sequence, HUR 7		13.60		•	7.30
	134510	NM_002757	Hs.250870	mitogen-activated protein kinase kinase				9.70	
85	134548 134654	N95406 AK001741	Hs.333495 Hs.8739	Deleted in split-hand/split-foot 1 regio hypothetical protein FLJ 10879	6.00		•		4.63
				**					

	W	O 02/086	443					PCT/US02/1247		
	134724	AF045239	Hs.321576	ring finger protein 22				12.00		
	134743	AAD44163	Hs.89463	potassium large conductance calcium-acti	4.00					
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone			25.20			
-	134806	AD001528	Hs.89718	spermine synthase					4.58	
3	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucte					4.79	
	134859	D26488	Hs.90315	KIAA0007 protein			6.20			
	134891	R51083	Hs.90787	ESTs			7.40			
	134950	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00					
10	134993	BE409809	Hs.301005	purine-rich etement binding protein B					4.48	
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50					
	135080	A1761180	Hs.94211	rcd1 (required for cell differentiation,	5.00					
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00				
	135145	AW014729	Hs.95262	nuclear factor related to kappa B bindin					4.01	
1.5	135184	U13222	Hs.96028	forkhead box D1			7.00			
15	135242	AL583187	Hs.9700	cyclin E1	13.50					
	135286	AW023482	Hs.97849	ESTs	6.46					
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		6.80				
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00					
20	135371	NM_006025	Hs.997	protease, serine, 22	8.00					
20	135393	L11244	Hs.99886	complement component 4-binding protein,				14.60		

TABLE 58 shows the accession numbers for those primekeys lacking unigenelD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oaldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Diama	lletens Con an	about 12 miles south
	Pkøy:	ber: Gene cluster n	obeset Identifier number
30	Accession		unider Ssion numbers
-	noocssio	L GCIDAIR COC	Salar Humbers
	Pkey	CAT number	Accessions
			· ·
35	117079	1621717_1	H92325 T97125
33	124305	242183_1	AW963221 AA344870 AA344871 H93331
	101502	182026	M26958 .
	109792	754958_1	R49625 F10674
	126034	1598157_1	H60340 N91637
40	102768	44641_1	U82321 H66077
40	126345	1653833_1	N49713 N49819 W03810
	127066	1703458_1	R25066 R20144 R20145 X43845
	1270 9 9 119243	244301_1 1774795_1	AA347668 AW956810 Z44271 F07065 F07064 R13506 T12603 T12604
	125875	1566433_1	H14480 N98295
45	112054	1538292_1	R43590 F10439
.5	126979	171411_1	AA210954 AA211007
	126992	880655_1	AJB09521 112174 Z42556
	122318	292419 1	AA429743 AA442754
	114699	135322 1	AA127386 R15644 AA127404
50	114793	150742_1	AA158245 AA158235
	108305	111550_1	AA071391 AA069892 AA069891
	108393	113411_1	AA075211 AA075245 AA075126 AA074946
	100867	tigr_HT4586	U14622
E E	123731	genbank_AA609	
55	109700	genbank_F09609	
	120715	genbank AA292	
	113702	genbank_T97307	
	115113	genbank_AA256	
60	101045 108554	entrez_J05614	J05614
00	108573	genbank_AA0849 genbank_AA0866	
	119052	149538_1	R10889 R10888
	126522	416020 1	W31912 A1167491
	126605	439280 1	AA576910 AA778853 AA778865 W66800
65	103768	46922_1	W42667 A1580740 A1690440 A1661350 AW467906 AW151450 A1825927 AL041716 A1885600 A1742213 AW248624 A1955498 AA033947
			AAB45593 AI623711 NG85B3 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195
			AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107
			A)199673 A)811766 A)275832 A)422233 A)191852 A)096682 A)580124 A)683612 AA582453 AA927559 AA486415 T32414 A)084978 H44849
70			H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881
70			AW362477 AA089997 Al350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 Al858420 AA600214
			AI970774 AI857712 AI683081 AI885584 AW131150 AI567981 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375
			AL566663 AW512676 AL570580 AL023690 AA448216 AL079853 AL422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332
			AW192394 Al167350 Al217879 Al129152 AA719509 Al350480 AA663418 Al003634 AW118546 AA180261 AA442833 Al268625 AA888881
75			AI038759 AA846723 AI248770 AA993694 AI280335 AI885107 AW518649 AA641563 AA995835 AA582521 AI276744 AA436478 AI017360
, ,			AI620763 AI859887 N73926 AI076327 AI741615 A160617 AW172819 A492005 AA677429 AA996334 AI693771 AI950039 AI245629 AI288515 AI866186 T93293 AA173262 AA599779 AI680092 AW439316 AI084555 AI272672 AI583507 AW473219 AA738132 AW473283 AI367492
			AA995410 A1689624 AA206353 A1033095 A1040382 AA873630 A1221074 A1934840 A1418680 AA844306 R94503 AA773520 AA843169
	•		AA219425 AA629658 AI811719 AW411275 AI590981 W37907 AI591178 AI684051 AA983238 AA669347 AA976239 AA704570 AI628339
			A1884391 A1241580 A1003539 AW176687 AA009650 N34566 A1333493 A1186070 AA070827 AA411683 A1280884 AA872023 AA207255
80			AA021576 N71953 AI885888 AW076039 T15777 AI537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788
			AI859431 H20478 AA218882 AA757465 AA100995 AI864135 AI934209 AA070503 H47008 AA219846 W61039 W93907 AW385050 W37967
			W78028 AA189007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009649 C03892 AW149464 AA310963 AA219693
			AA069747 R29207 AA094784 AA293615 AA447848 AI984167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409
0.5			AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737
85			W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310

AA36789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281 AA209340 N55174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849 AI286629 AA843996 W15260 AI188286 AW248079 R15836

119599 genbank_W45552 W45552 genbant_R59904 R59904 genbant_R59204 R59904 genbant_AA227934 AA227934 entrez_A28102 A28102 714071_1 A496369 AA496646 5 112382 105264 100071 123315

10

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59580 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the retative level of mRNA expression.

15 Unique Eos probeset identifier number Pkey:

Exemplar Accession number, Genbank accession number UnigenelD: Unigene number

Unigene Title: Unigene gene title
R1: average of AI for samples from non-smokers with edenocarcinoma divided by the 90th percentile of AI for samples from smokers with edenocarcinoma average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell 20

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		carcinom	8			
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
25	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
	101174	L17330	Hs.280	pre-TANK call associated protein	15.00	
	101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	thyrold hormone receptor interactor 8		12.00
	101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias		2.68
30	101972	882472		gb:beta -pol=DNA polymerase beta (exon a		211
	102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
	102832	U92015		gb:Human clone 143789 defective mariner	13.50	
25	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	
35	103439	X98266		gb:H.sapiens mRNA for ligase like protei		2.50
	103563	L02911	Hs.150402	activin A receptor, type I	9.00	
	103857	AJ076795	Hs.45033	lacrimal profine rich protein	40.00	3.94
	104239	AB002367	Hs.21355	doublecorfin and CaM kinase-like 1	13.50	40.00
40	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	40.50	12.66
40	104907	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	247
	106131	BE514788	Hs.295244	SNARE protein	7.00	2.17
	106672	H47233	Hs.30643	ESTs	7.00	•
	106872	T56887	Hs.18282 Hs.32501	KIAA1134 protein	11.50	2.38
45	106960	AA156238 Z43846	Hs.194478	ESTS	9.50	2.30
73	106971 107982	AA035375	Hs.57887	Homo saplens mRNA; cDNA DKFZp43401572 (f ESTs, Weakly similar to KIAA0758 protei	8.30	2.95
	107552	AA100796	ns.37007	gb:zm26c06.s1 Stratagene pancreas (93720	16.50	2.50
	108599	AB018549	Hs.69328	MD-2 protein	13.00	
	108563	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti	13.50	2.40
50	109247	AA314907	Hs.85950	ESTs	7.00	2.40
20	109630	R44607	Hs.22672	ESTs	1.00	5.00
	110193	Al004874	Hs.310764	Homo saplens mRNA; cDNA DKFZp434M082 (fr	12.50	0.00
	110234	H24458	Hs.32085	EST	16.50	
	110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	8.00	
55	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	17.00	
	111057	T79639	Hs.14629	ESTs .	16.50	
	111950	AF071594	Hs.110457	Wolf-Hirschhorn syndrome candidate 1	11.00	
	112291	R53972	Hs.26026	EST8		3.00
	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
60	113009	T23699	Hs.7246	ESTs		4.50
	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32.50	
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
15	113121	T48011	Hs.8764	EST		2.21
65	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
	113757	AA703095	Hs.18631	ESTs		2.65
	113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	
	113884	A1333076	Hs.28529	chromosome 12 open reading frame 2		6.00
70	113936	W17056	Hs.83623	nuclear receptor subfamily 1, group i, m		4.63
70	114875	AA235609	Hs.236443	Homo saplens mRNA; cDNA DKFZp564N1063 (7.00
	114987	AA251016	Hs.87808	EST		6.00
	115460	AW958439	Hs.38613	ESTs ESTs		2.27
	115722	W91892	Hs.59609	ESTs	9.50	9.00
75	116261 116830	AA4B1788 H61037	Hs.190150 Hs.70404	ESTs, Wealthy similar to ALU2_HUMAN ALU	9.50 8.50	
75	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
	117178			ESTs	7.50	2.68
	117757	H98675 AF088019	Hs.269034 Hs.46732	EST	7.50	2.00
	118283	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	16.50	
80	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule	10.30	2.50
00	118657	AJ822106	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sani		3.50
	120404	AB023230	Hs.96427	KIAA 1013 protein	7.00	5.00
	120524	AA261852	Hs.192905	ESTs	6.00	
85	120688	AW207555	Hs.97093	Homo saplens cONA: FLJ23004 fis, clone L	17.92	
				· · · · · · · · · · · · · · · · · · ·		

	W	O 02/086	443				PCT/US02/12476
	121558	AA412497		nbzf95g12.s1 Soares testis_NHT Homo sap		2.95	
	121676	H56037	Hs.108146	ESTs	10.00		
	121936	AI024600	Hs.98612	ESTs	15.00		
	121938	AA428659	Hs.98610	ESTs	14.00		
5	122177	AA435789	Hs.98833	EST	8.93		
_	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fts, clone HE	13.04		
	123551	AA608837		gh;af03h12.s1 Soares_testis_NHT Homo sao	11.50		
	123756	AA609971	Hs.112795	EST	11.00		
	123861	AA620840		gb:af89g01.s1 Soares_testis_NHT Homo sap		2.50	
10	124371	N24924	Hs.188601	ESTs	6.50		
	127477	BE328720	Hs.280651	ESTs		4.33	
	127591	Al190540	Hs.131092	ESTs		3.02	
	128252	AA455924	Hs.192228	ESTs	7.00		
	128426	Al265784	Hs.145197	ESTs		2.08	
15	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ 12900 fis, clone NT		2.11	
	128945	AJ990506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (fr	10.00		
	129105	Al769160	Hs.108681	Homo sapiens brain tumor associated prot	15.50		
	129235	AW977238	Hs.126084	KIAA1055 protein		4.25	
	129506	AB020684	Hs.11217	KIAA0877 protein	6.50		
20	129595	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9		10.00	
	130160	AA305688	Hs.267695	UDP-Gat:betaGlcNAc beta 1,3-galactosyltr	20.00		
	130340	D82326	Hs.239106	solute carrier family 3 (cystine, dibasi	11.50		
	131220	AB023194	Hs.300855	KIAA0977 protein	17.50		
	131430	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10		
25	132114	NM_006152		lymphoid-restricted membrane protein		6.15	
	132458	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C		5.58	
	132647	NM_006927		sialyliransferase 48 (bela-galactosidase	7.50		
	132655	D49372	Hs.54460	small inducible cytokine subfamily A (Cy		2.53	
	132682	A1077500	Hs.54900	serologically defined colon cancer antig		2.50	
30	132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein		2.83	
	132812	R50333	Hs.92186	Leman coiled-coil protein		3.82	
	133337	AF085983	Hs.293676	ESTs		5.00	
	133876	AL134906	Hs.771	phosphorylase, glycogen; liver (Hers dis		3.00	
	134119	AW157837		fasciculation and elongation protein zet		2.06	
35	134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit	•	2.27	
	134542	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi		11.50	
	135002	AA448542	Hs.251677	G antigen 7B	87.00	*****	
	135305	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 fis, clone PL	•••	6.50	
	100000	77 250050	10.00200	Troite displace del d'il de l'idea (lej diol. d'il			
40							
	TABLE 6B	show the acce	ssion numbers	for those primekeys lacking unigenelD's for Table 6A.	For each probeset we ha	we listed the ge	ne cluster number from which the
	olioonucles	ofides were des	sloned. Gene o	fusters were compiled using sequences derived from	Genbank ESTs and mRNA	s. These sequ	ences were clustered based on sequence
	similarity u	sino Clusterino	and Alignmen	Tools (DoubleTwist, Oakland California). The Genba	nk accession numbers for	sequences com	prising each cluster are listed in the
	Accession		,			•	•
45							
	Pkey:	Unique Ecs	probeset iden	lifier number			
		er: Gene clust					
	Accession	Genbank a	ccession numb	ers			
50							

Pkey

CAT number Accessions

WO 02/086443

Table 7A shows 93 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Afrymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average tritensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Pkey: ExAcon:

Unique Eos probeset identifier number Examplar Accession number, Genbank accession number

Urigenet Unigene number
Urigene Title:
Urigene Title:
Urigene pene title
Urigene pene title
R1:
90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with adenocarcinoma.
R2:
90th percentile of AI for samples from smokers with squamous cell cardinoma divided by the average of AI for samples from non-smokers with squamous cell 10

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	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3		164.10
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein		77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971 101046	BE379727 K01160	Hs.83213	fatty acid binding protein 4, adipocyte	463.80	
20	101056	AW970254	Hs.889	(NONE) Charot-Leyden crystal protein	672.00 66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2	00.00	77.20
	101497		Hs.37034	hameo bax A5	62.80	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	
25	101677	NM_000715	Hs.1012	complement component 4-binding protein,	186.20	
25	101745 101941	M88700 S77583	Hs.150403	dopa decarboxylase (aromatic L-amino aci gb:HERVK10/HUMMTV reverse transcriptase	80.08 99.20	
	102125	NM_006456	Hs.288215	sialyltransferase	33.20	103.10
	102242	U27185	Hs.82547	relinoic acid receptor responder (tazaro	67.00	
20	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha		69.70
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	153.00	05.70
	102669 102796	U71207 AL079646	Hs.29279 Hs.107019	eyes absent (Drosophila) homolog 2 symplekin; Huntingtin interacting protei		65.70 58.80
	102829	NM_006183	Hs.80962	neurolensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	
	103242	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o		212.10
	103260	X78416	Hs.3155	caseln, alpha		130.70
	103351 104212	X89211 AB002298	Hs.173035	gb:H.sapiens DNA for endogenous retrovir	64.60 66.80	
40	104252	AF002246	Hs.210863	KIAA0300 protein cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	94.40	
	105024	AA126311	Hs.9879	ESTs	68.20	
	106260	Al097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S		74.60
45	106440	AA449563	Hs.151393	glutamate-cystelne ligase, catalytic sub	77.00	71.10
73	106566 106605	BE298210 AW772298	Hs.21103	gb:601118016F1 NIH_MGC_17 Homo saplens c Homo saplens mRNA; cDNA DKFZp5648076 (fr	73.20 83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222	۵۵.۵۵	62.30
	106654	AW075485	Hs.286049	phosphoserine aminotransferase		202.40
50	106999	H93281	Hs.10710	hypothetical protein FLJ20417		89.60
50	108700	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
	108810 108857	AW295647 AK001468	Hs.71331 Hs.62180	hypothetical protein MGC5350 anillin (Drosophila Scraps homolog), act		95.50 C3.40
	109597	AA989362	Hs.293780	ESTs	85.00	63.40
	109691	T65568	Hs.12860	ESTs	55.55	58.70
55	109704	AI743880	Hs.12876	ESTs		60.60
	110942	R63503	Hs.28419	ESTs	76.40	
	111722 112891	R23924 T03927	Hs.23596 Hs.293147	EST ESTs, Moderately similar to A46010 X-li	74.60 64.80	
	112992	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	04.00	76.70
60	113073	N39342	Hs.103042	microtubule-associated protein 1B		120.20
	114251	H15261	Hs.21948	ESTs	127.20	
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291 115815	BE545072 AW905328	Hs.122579 Hs.180842	hypothetical protein FLJ10461 ribosomal protein L13	66.40	91.00
65	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	00.40	226.60
••	115965	AA001732	Hs.173233	hypothetical protein FLJ10970	82.80	
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093		361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	
70	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	C2 50
70	118466 120484	N66741 AA253170	Hs.96473	gb:yz33g08.s1 Morton Fetal Cochlea Homo EST	81.60	63.50
	120983	AA398209	Hs.97587	EST	01.00	81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
75	121423	AW973352	Hs.290585	ESTs	64.40	
75	122553	AA451884	Hs.190121	ESTs		60.40
	122946	A1718702	Hs.308026	major histocompatibility complex, class	188.60	00.00
	123130 124472	AA487200 N52517	Hs.102670	gb:ab19f02.s1 Stratagene tung (937210) H EST	71.00	80.20
0.0	124526	N62096	Hs.293185	ESTs, Wealty similar to JC7328 amino aci	, 1.00	104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs	***	69.90
	- 125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	CO 10
	126020 126547	H79863 U47732	Hs.114243 Hs.84072	ESTs transmembrane 4 superfamily member 3		62.40 62.80
85	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra		60.10
						-

	W	O 02/086	443				PCT/US02/12476
	127472	AA761378	Hs.192013	ESTs	70.20		
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00		
	127742	AW293496	Hs.180138	ESTs	85.20		
		AI022103	Hs.124511		96.60		
5		AW889132	Hs.11916	riboldnase	*****	78.90	
		AA650274	Hs.41296	fibronectin leucine rich trensmembrane p		106.90	
		AW160432	Hs.296460	craniofacial development protein 1	66.80		
		AW935187	Hs.170162	KIAA1357 protein	00.00	58.53	
		AB040930	Hs.126085	KIAA1497 protein	64.20	55.55	
10		H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80		
10		AW067800	Hs.155223	stanniocalcin 2	05.00	139.60	
		AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60	
					64,40	04.00	
		AB040900	Hs.6189	KIAA1467 protein			
1.5		BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20		
15		AB014548	Hs.31921	KIAA0648 protein	97.80		
		AB018324	Hs.42676	KIAA0781 protein		71.00	
	132856	NM_001448		glypican 4		88.40	
	132977	AA093322	Hs.301404	RNA binding motif protein 3 .	133.20		
	133749		Hs.10018	solute carrier family 20 (phosphate tran		59.30	
20		Al110684	Hs.7645	fibrinogen, B beta polypeptide	341.00		
	134264	AF149297	Hs.8087	NAG-5 protein		64.30	
	134265	M83772	Hs.80876	flavin containing monocxygenase 3		232.53	
	134346		Hs.82037	TATA box binding protein (TBP)-essociate	66.00		
		AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80	
25		AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30	
~~		N75765	Hs.93765	liporna HMGIC fusion partner	71.40		
		AL564123	Hs.42500	ADP-ribosylation factor-like 5	70.40		
	155555	70007120	113.72000	ADI AIDOS JEDONI INCON-IND S	10.40		
20							
30	TABLE 7	B shows the acc	cession number	ers for those primekeys lacking unigenelD's for Ta	ble 7A. For each p	robeset we have listed t	he gene cluster number from which the
	oligonuch	ectides were de	signed. Gena	clusters were compiled using sequences derived	from Genbank EST	is and mRNAs. These s	sequences were clustered based on sequen
			and Alignmer	nt Tools (DoubleTwist, Oakland California). The C	Senbank accession	numbers for sequences	comprising each cluster are listed in the
	*Accessio	m" column.					•
35	Pkev:	Holono Ec	s probeset ide	ntifier mumber			
55		ber: Gene clust		INTER INTIME			
	Accession		er number accession numi	ham			
	ACCESSIO	ii. Gendank e	ocession mum	Ders			
	Pkey	CAT number	Accessions	3			
40	-						
	103207	306354	X72790				
	106566	120358_1	BE298210	Al672315 AW086489 BE298417 AA455921 AA9	02537 BE327124 R	14963 AA085210 AW21	74273 Al333584 Al369742 Al039658
			A1885095	A1476470 A1287650 A1885299 A1985381 AW5926	24 AW340136 AI26	6556 AA456390 AI3108	B15 AA484951
	116571	genbank D4		D45652			
45	118466	genbank_N6		N66741			
40	101046	entrez_K011		INVITI			
	101941	entrez_S775					
	103351	entrez_X892		A A 407000			
50	123130	genbank_AA	440/2UU	AA487200			
J U							

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Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body lissues. Chronically diseased lung samples represent chronic normalignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5

Pkey: Unique Eos probeset identifier number
ExAcor: Exemplar Accession number, Genbank accession number
Unigene ID: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for lung turnors divided by 90th percentile of AI for normal lung
R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung 10

	R2:	R2: 70th percentile of Al for chronically diseased tung divided by 90th percentile of Al for normal tung								
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2				
15	300097	Al916973	Hs.213603	ESTs	5.46	4.69				
	300117	AW189787	Hs.147474	ESTs	0.5B	0.56				
	300197	A1686661	Hs.218286	ESTs	4.26	5.44				
	300201	Al308300	Un 107505	gb:ta90c06.x1 NCI_CGAP_Bm20 Homo sapten	0.62 1.68	0.83 1.75				
20	300225 300247	Al989963 AWZ74682	Hs.197505 Hs.161394	ESTs ESTs	1.08	2.28				
20	300256	Al469095	Hs.298241	Transmembrane protease, serine 3	0.86	1.00				
	300337	AJ707881	Hs.202090	ESTs	5.80	9.09				
	300362	Z42308		gb:HSC0FB121 normalized infant brain cDN	4.1B	12.78				
25	300374	A1859947	Hs.314158	ESTs	2.99	4.38				
25	300387 300440	AW270150	Hs.254516 Hs.146164	ESTs ESTs	1.50 3.98	2.53 5.25				
	300441	AJ421541 R10367	Hs.307921	EST, Wealty similar to Z232_HUMAN ZINC F	3.18	6.80				
	300449	Al362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62				
••	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83				
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75				
	300627	W27363	LL 420757	gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60	12.60				
	300630 300716	AW118822 AI216113	Hs.128757 Hs.126280	ESTs hypothetical protein FLJ23393	2.91 1.00	5.86 0.92				
	300738	Al623332	Hs.130541	KIAA1542 protein	1.82	1.71				
35	300777	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22				
	300790	AM92471	Hs.188270	ESTs	1.29	1.18				
	300832	AI68B147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56				
	300838 300838	Z44942 A1582897	Hs.22958 Hs.192570	calcium channel alpha2-delta3 subunit hypothelical protein FLJ22028	4.90 1.70	6.34 2.81				
40	300878	AW449802	Hs.285901	Homo sapiens cDNA FLJ20428 fis, clone KA	4.56	7,91				
	300897	AI890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23	1.58				
	300926	AA504860		gb:ab03a10.s1 Stratagene fetal refina 93	2.13	3.50				
	300960	A1041019	Hs.152454	ESTs	2.74	4.45				
45	300961	AW204069 AA593373	Hs.312716	ESTs, Wealthy similar to unnamed protein	1.00 1.46	1.00 1.51				
73	300962 300967	AA565209	Hs.293744 Hs.269439	ESTs	0.39	1.30				
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208845 1 BM-00	1.49	1.08				
	300988	Al927208	Hs.208952	ESTs	0.16	0.37				
50	301050	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen I	3.23	1.94				
50	301098	AA577570	Hs.185918	ESTS	6.76 3.16	14.28 8.85				
	301157 301162	AA729905 Al142118	Hs.231916 Hs.129004	ESTs	1.68	7.18				
	301170	AA737594	Hs.247606	ESTs	4.40	6.42				
	301192	AI808751	Hs.121188	ESTs	6.38	11.59				
55	301193	AA758115	Hs.128350	ESTs, Wealdy similar to JC5423 2-hydroxy	4.35	7.78				
	301267 301281	AW297762	Hs.255690 Hs.190586	ESTs	1.56 2.19	1.61 1.78				
	301341	AA843986 Al819198	Hs.208229	ESTs	0.76	0.76				
	301382	AA912839	Hs. 163369	EST8	1.00	1.81				
60	301407	AW450466	Hs.126830	ESTs	1.48	1.51				
	301452	AA975688	Hs.159955	ESTs	0.51	1.46				
	301483	AW272467	Hs.254655	Untitled	2.40 2.79	5.02 3.41				
	301494 301521	A1678034 A1733621	Hs.131099 Hs.133011	ESTs zinc finger protein 117 (HPF9)	0.67	0.67				
65	301531	AI077462	Hs.134084	ESTs	2.52	3.76				
	301580	Al878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92				
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70				
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70 4.20	4.22 8.78				
70	301718 301799	F07744 AA384252	Hs.7987 Hs.286132	DKFZP434F162 protein D15F37 (pseudogene)	5.93	7.04				
, 0	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76				
	301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.58	1.36				
	301846	R20002	Hs.6823	hypothetical protein FLJ10430	1.00	1.00				
75	301868	T71508	Hs.13861	ESTs, Weakly similar to pH sensitive max	2.88 2.28	5.49 3.80				
, ,	301882 301905	178054 A)991127	Hs.117202	gb:yc97g09_r1 Soares infant brein 1NIB H ESTs	1.00	1.00				
	301948	AA344647	Hs.116724	aldo-kato reductase family 1, member B11	5.28	2.28				
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48				
90	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42				
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25				
	302041 302072	NM_001501 AJ238381	Hs.129/15 Hs.132576	gonadotropin-releasing hormone 2 paired box gene 9	0.71 1.60	0.99 1.71				
	302094	A1286176	Hs.6786	ESTs	0.52	1.20				
0.5	302095	AW044300	Hs.137506	Homo sapiens BAC clone RP11-120J2 from 7	2.75	4.93				
85	302148	AW269618	Hs.23244	ESTs	3.04	3.87				

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	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-GatthetaGlcNAc beta 1,4- galactosyll	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinosilide-specific phospholipase	2.76	3.65
3	302209 302235	AF047445 AL049987	Hs.159297 Hs.166351	killer cell lectin-like receptur subfami Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.00 1.68	1.00 1.50
	302233	AL117607	Hs.175563	Homo saplens mRNA; cDNA DKFZp564N0763 (f	1.00	211
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
10	302350	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U85751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63 5.82	2.67 9.34
	302409 302423	AF155156 AB028977	Hs.218028 Hs.225974	adaptor-related protein complex 4, epsil KIAA1054 protein	3.68	3.18
15	302432	AL080068	Hs.272534	Homo saptens mRNA; cDNA DKFZp564J062 (fr	244	6.77
	302435	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302437	AB024730	Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
20	302472	AA317451	Hs.6335 ·	SWI/SNF related, matrix associated, acti	2.04	2.13
20	302476 302489	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44 0.51	1.89 1.10
	302409	T80660 AA885502	Hs.230424 Hs.187032	Homo sapiens cDNA FLJ13540 fis, clone PL ESTs	2.64	4.87
	302552	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
25	302630	AB029488	Hs.272100	SMS3 protein	0.52	1.24
	302634	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1.00	1.00
	302638	AA463798	Hs.102696	MCT-1 protein	1.58	1.02
	302647 302655	X57723 AJ227892	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72 1.00	6.85 4.32
30	302656	AW293005	Hs.146274 Hs.70704	ESTs Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
50	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.r1 Weizmann Offactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
25	302697	AJ001408		gb:Homo sapiens mRNA for immunoglobulin	4.25	8.13
35	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91	8.68
	302711 302719	L08442 W69724	Hs.288959	gb:Human autonomousty replicating sequen hypothetical protein FLJ20920	2.20 0.54	2.73 1.02
	302742	L12069	ns.200333	gb:Homo sapiens (clone WR4.10VH) anti-th	4.28	11.57
	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
40	302771	H98476	Hs.42522	ESTs	2.94	4.58
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	274
	302802 302803	Y08250 AA442824	Hs.293961	gb:H.saplens mRNA for variable region of ESTs, Moderately similar to putative DNA	1.13 3.14	0.77 10.68
45	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04	8.24
	302847	X98940	110.102001	gb:H.saplens rearranged lg heavy chain (1.80	1.92
	302885	AL137763	Hs.132127	hypothetical protein LOC57822	1.00	1.00
	302943	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
50	302977	AW263124	Hs.315111	hypothetical protein FLJ 12894	2.45	2.62
20	303006 303011	AF078950 AF090405	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L gb:Homo sapiens clone 2A1 scFV aniibody	4.88 1.41	8.61 1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-i	0.72	0.76
	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
55	303090	AA443259	Hs.146288	kinesin family member 13A	4.08	6.46
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50	4.37
	303094 303095	AF195513 AF202051	Hs.278953 Hs.134079	Pur-gamma NM23-H8	5.38 3.26	8.38 4.08
	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
60	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
65	303234	AA132255	Hs.143951	ESTs	2.28	3.17
05	303251 303295	AW340037 AA205625	Hs.115897 Hs.208067	protocadherin 12 ESTs	0.38 2.30	1.02 1.00
	303297	T80072	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.86	4.48
	. 303316	AF033122	Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
	303467	AA398801	Hs.323397	ESTs	4.54	9.65
70	303506	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598 303637	AA382814 AF056083	Hs.24879	gb:EST96097 Testis I Homo sapiens cDNA 5	4.96 2.06	9.14 2.02
	303655	AA504702	Hs.258802	phosphatidic acid phosphatase type 2C ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
75	303756	AJ738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (Importin) beta 3	2.30	2.57
	303907	AW457774	Hs.171880	polymerase (RNA) II (DNA directed) polyp	3.10	5.79
80	303946	AW474196	Hs.306637	Homo sapiens cDNA FLJ12363 fis, clone MA	5.06	11.86
30	303978 303981	AW513315 AW513804	Hs.278834	gbxxx43c12.x1 NCL_CGAP_Ut1 Homo sepiens ESTs, Weakly similar to ALU1_HUMAN ALU 8	5.14 2.83	7.31 4.06
	303990	AW515465	1971004	gboxu71a11.x1 NCI_CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		gb:x168f05.x1 NCI_CGAP_U12 Homo sapiens	2.20	9.35
0.5	303999	AW516611		gb:xp70b11.x1 NCI_OGAP_Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gb:xt66h02_x1 NCI_CGAP_Ut2 Homo sapiens	3.21	4.07

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	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs. 181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
_	304026.			gb:FB26F2 Fetal brain, Stratagene Homo s	5.88	11.80
5	304028	T03266	11- 044004	gb:FB7C1 Fetal brain, Stratagene Homo sa	5.59	13.46
	304036 304046	T16855 T54803	Hs.244621	ribosomal protein S14 gb:yb42d06.s1 Stratagene fetal spleen (9	6.55 6.18	14.43 12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
10	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90	4.18
	304122	H28966		gb:ym31a06.s1 Soares Infant brain 1NIB H	1.00 0.79	2.76 1.18
	304155 304203	H68696 N56929		gb:yr78b06.s1 Soares fetal liver spleen gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
15	304234	W81608	_	gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, PO	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78466	proteasome (prosome, macropain) 26S sub	2.93	4.42
20	304348	AA179868	11- 400470	gb:zp38g12.s1 Stratagene muscle 937209 H	3.98	10.96
20	304415 304430	AA290747 AA347682	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase gb:EST54044 Fetal heart II Homo sapiens	3.32 1.00	5.99 1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
~ -	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
25	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8.23
	304546	AA485074	Hs.297681	serine (or cysteine) proteinase inhibito	0.55	1.20
	304607 304640	AA513322 AA524440	Hs.111334	gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien ferritin, light polypaptide	1.95 2.10	2.10 2.83
	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
30	304735	AA576453	110.0100	gb:nm75h11,s1 NCI_CGAP_Co9 Homo saplens	1.33	0.88
	304760	AA580401		gb:nn13g09.s1 NCI_CGAP_Co12 Homo saplens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein	7.16	11.01
35	304921 304966	AA603092 AA613893	Hs.297753 Hs.282435	vimentin ESTs	2.47 6.78	4.24 11.66
55	304987	AA618044	Hs.300697	Immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876	. 2.00000	gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stratagene lung (937210) H	1.00	1.00
40	305072	AA641012		gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68	11.59
40	305111	AA644187	Hs.303405	ESTS	1.48	1.37
	305148 305159	AA654070 AA659166	Hs.275668	gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens EST, Wealdy similar to EF1D_HUMAN ELONG	1.76 1.00	4.61 2.15
	305190	AA665955	15.213000	gb:ag57d12.s1 Gesster Wilms turnor Homo s	5.31	8.14
	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
45	305235	AA670480		gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11	8.66
	305245	AA676695	Hs.81328	nuclear factor of kappa light polypeptid	4.38	7.53
	305312	AA700201	Hs.163019	gb:zj44f07.s1 Soares_fetal_liver_spleen_ EST	2.13 1.20	2.66 1.40
	305322 305394	AA701597 AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
50	305413	AA724659	110.000001	gb:al10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856		gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens	2.21	2.86
	305476	AA745664	Hs.287445	hypothetical protein FLJ11726	3.36	6.54
	305483	AA748030	Hs.303512	EST	1.00	2.02
55	305528 305612	AA769156 AA782347	Hs.272572	gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens hemoglobin, alpha 2	6.44 0.19	9.10 0.79
33	305614	AA782866	NS.212312	gb:aj09h02.s1 Soares_parathyroid_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57	10.20
	305637	AA806124		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo saplens	4.78	12.42
C 0	305639	AA806138		gb::oe29c12.s1 NCI_CGAP_Pr25 Homo saplens	0.89	0.70
60	305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GC80 Homo sapiens4		8.71
	305690 305726	AA813477 AA828156	Hs.73742	gb:ai67a05.s1 Soares_testis_NHT Homo sap ribosomal protein, targe, P0	4.91 0.19	9.40 0.81
	305728	AA828209	115.75742	gb:of34a02.s1 NCI_CGAP_Kid6 Homo sapiens	5.12	9.29
	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom	1.66	4.11
65	305792	AA845256		gb:ek84a08.s1 Barstead spleen HPLRB2 Hom	2.34	4.25
	305864	AA864374	Hs.73742	ribosomal protein, large, P0	0.30	1.40
	305901	AA872968		gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910 305015	AA875981 AA897116		gb:nx21h02.s1 NCI_CGAP_GC3 Homo sapiens gb:am08b07.s1 Soares_NFI_T_GBC_S1 Homo s1	0.32 56	1.01 1.12
70	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21	7.90
	306020	AA897630	Hs.130027	EST	1.96	6.59
	306063	AA906316		gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	305065	AA906725		gb:ok78g02.s1 NCL_CGAP_GC4 Homo sapiens	7.19	13.48
75	306104	AA910956 AA911861		gbrok85h11.s1 NCL_CGAP_Kid3 Homo septens	6.50 4.21	9.13 5.25
, ,	306109 306148	AA917409	Hs.288036	gb:og21e07.s1 NCI_CGAP_PNS1 Horno saplens tRNA isopentenytoyrophosphate transferes	2.20	5.25 2.70
	305242	AA932805	. 22.0000	gb:oo60g04.s1 NCI_CGAP_Lu5 Homo sapiens	2.84	5.35
	306288	AA936900		gb:oi53h05.s1 NCI_CGAP_HN3 Homo sapiens	1.60	1.12
00	305325	AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
80	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650 AA970222	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30 0.95	5.74 2.45
	306396 306428	AA970223 AA975110	Hs.191228	gb:op09d05.s1 NCI_CGAP_Kid5 Homo saptens hypothetical protein FLJ20284	3.19	2.45 4.10
	306442	AA976899	113.131220	gb:og35e09.s1 NOI_CGAP_GC4 Homo sapiens	4.67	7.44
85	306446	AA977348		gb:oq72e12.s1 NCI_CGAP_Kid6 Homo saplens	3.92	6.27

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	306458	AA978186	11. 400000	gbxxp33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467 306510	AA983508 AA988546	Hs.163593	ribosomal protein L18a gb:or84d07.s1 NCL_CGAP_tu5 Horno saptens	3.72 1.00	5.37 1.00
	306555	AA994304	Hs.276083	EST, Wealty similar to RL23_HUMAN 60S R	6.61	10.91
5	306557	AA994530	12270000	gbcou57e08.s1 NCI_CGAP_Br2 Homo saplans	16.20	31.83
	306572	AA995686		gb:os25c12.s1 NCI_CGAP_Kid5 Homo saplens	2.51	6.52
	306582	AA996248		gbos18c10.s1 NCL_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	AI000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
10	306605 306656	A1000497 A1004024	Hs.119500	ribosomal protein, large P2	1.96 0.11	8.60 0.45
10	306676	AI005603	Hs.284136	gb:ou11b07x1 Soares_NFL_T_GBC_S1 Homo s PRO2047 protein	9.56	17.28
	306686	AI015615	113204130	gb:ov29f10.x1 Soares_testis_NHT Homo sap	1.86	3.60
	305702	AI022565	Hs.307670	EST	1.47	1.19
	305728	AI027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
15	306751	AI032589		gb:ow70h12s1 Soares_fetal_liver_spleen_	3.91	5.21
	305767	A1038963	Hs.249118	ESTS	3.33	6.06
	306892 306897	A1092465 A1093967		gb:qa75h12x1 Soares_fetal_heart_NbHH19W gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	3.77 2.12	7.45 2.85
	306956	Al125111		gb:am66f03.s1 Barstead splean HPLRB2 Hom	6.10	10.52
20	306958	AJ125152		gb:am55e09.x1 Johnston frontal cortex Ho	1.72	1.56
	307035	Al142774	Hs.119122	ribosomal protein L13a	2.00	4.70
	307041	AJ144243		gbxqb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	Al167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapl	4.88	8.52
25	307181	Al189251	Un 111224	gbqc99g06.x1 Soares_pregnant_uterus_NbH	3.55 2.46	6.44 4.65
23	307297 307317	AI205798 AI208303	Hs.111334 Hs.147333	ferrifin, light polypeptide EST	5.64	10.13
	307327	Al214142	Hs.246381	CD68 antigen	3.18	5.15
	307382	AJ223158	Hs.147885	ESTs	2.02	3.73
20	307410	AJ241715	Hs.77039	ribosomal protein S3A	0.72	0.48
30	307415	AJ242118		gb:qh92b02x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
	307423	A1243206	Hs.179573	collagen, type I, alpha 2	2.60 3.18	5.44 7.67
	307426 307517	A1243364 A1275055		gbxqh30g11.x1 Soares_NFL_T_GBC_S1 Homo s gbxql72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00	1.00
	307551	Al281556		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens	3.40	11.20
35	307561	Al282207		gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
	307608	Al290295		gb:qm01f02.x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AJ306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	AJ318285	U- 270070	gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59 1.90	1.31 2.13
40	307701 307718	Al318583 Al333406	Hs.276672 Hs.83753	EST, Wealdy similar to RL6_HUMAN 60S RI small nuclear ribonucleoprotein polypept	0.45	0.99
70	307730	Al336092	113.00133	gb:qt43b07.x1 Soares_fetal_tung_NbHL19W	1.51	0.99
	307760	AJ342387		gb:qt27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	AJ342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo sapiens	4.52	12.58
45	307783	Al347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo saplens	1.42	1.00
45	307796	Al350556		gbxt18f09.x1 NCL_CGAP_GC4 Homo sapiens	6.57	9.61
	307807 307808	Al351799 Al351826		gb:qt09d02.xt NCI_CGAP_GC4 Homo saplens gb:qt09g03.xt NCI_CGAP_GC4 Homo saplens	3.38 0.33	7.68 0.86
	307820	Al355761		gbxtt94a11.x1 NCI_CGAP_Co14 Homo sapiens	7.94	21.57
	307830	Al358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
50	307852	Al365541		gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
	307902	AI380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo septens	3.13	4.99
	307997	AI434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002 308011	A1435240 A1439473	Hs.283442	ESTs gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien	5.86 3.79	12.64 5.83
55	308023	A1452732	Hs.251577	hemoglobin, alpha 1	0.38	0.88
	308041	AJ458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	AM68938	Hs.276877	EST, Wealty similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AJ474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
60	308101	AJ475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87
00	308106 308122	AI476803 AI480123	Hs.309411	gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2 EST	2.70	8.72 3.86
	308154	Al500600	114600.611	gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sapiens	0.66	1.33
	308171	Al523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
CE	308211	Al557029	Hs.278572	anaplastic lymphoma klnase (Ki-1)	2.43	2.14
65	308213	AI557041		gb:PT2.1_12_E04.r tumor2 Homo sapiens cD	3.34	3.79
	308216 308219	AI557135 AI557246		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61 4.87	4.78 7.94
	308271	AL567844	Hs.252259	gb:PT2.1_15_D07.r tumor2 Homo saptens cD ribosomal protein S3	2.40	6.35
	308319	AL583983	Hs.181165	eukaryotic translation elongation factor	2.45	3.33
70	308362	AI613519	Hs.105749	KIAA0553 protein	1.24	1.41
	308413	Al636253	Hs.196511	ESTs	3.16	4.82
	308450	A1650860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464 308588	AI672425 AI718299	Hs.277117	EST, Moderately similar to 138055 myosi ob:as51g12.x1 Barstead aorta HPLRB5 Homo	4.87 3.90	8.27 5.64
75	308599	AI719893		gb:as47d07.x1 Barstead aorta HPLR86 Homo	3.32	5.12
	308615	AI738593	Hs.101774	hypothetical protein FLJ23045	3.11	2.36
	308643	AI745040		gb:tr19a12x1 NCI_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	A1760864		gbtwi09c10x1 NOI_CGAP_CLL1 Homo sapiens	0.82	0.99
90	308697	AI767143	Un pro con	gb:wi97a07.x1 NCL_CGAP_Kid12 Homo saplen	2.76	5.59
80	308762 308778	A1807405 A1811109	Hs.259408	ESTS obt@doi1 v1 NCL CGAP Ov23 Home serious	3.17	6.30 1.00
	308778 308782	AI811767	Hs.2186	gb:tr04c11.x1 NCI_CGAP_Ov23 Homo saplens eukaryotic translation elongation factor	1.00 2.94	5.15
	308808	AI818289		gb:wk52c01.x1 NCL_CGAP_Pr22 Homo saptens	4.41	8.34
05	308823	AI824118	Hs.217493	annexin A2	1.85	1.92
85	308875	A1832332		gh:at48g03.x1 Barstead colon HPLR87 Homo	2.52	3.80

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		O 02/086		Illumorin hote A V ehromoroma	3.38	7.96
	308879 308886	AIB32763 AIB33240	Hs.75968	thymosin, beta 4, X chromosome gb:at76d10.x1 Barstead colon HPLRB7 Homo	3.06	2.65
	308898	AI858845		gb:wi32d10.x1 NCI_CGAP_Ut1 Homo sapiens	2.45	3.44
_	308934	AI865023	Hs.177	phosphalidylinositol glycan, class H	4.14	6.76
5	308966	A1870704		gb.wl47h01.x1 NCI_CGAP_Ut1 Homo saptens	1.00	1.00
	308979	AJ873111		gb:w/52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tq39/01.x1 NCI_CGAP_Ut1 Homo saptens	0.61	0.59 4.42
	309051 309069	AI911975	Hs.78202	gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens SWI/SNF related, matrix associated, act	1.78 3.27	5.88
10	309083	AI917355 AI922426	Hs.119598	ribosomal protein L3	2.39	3.34
10	309105	AI925503	Hs.265884	ESTs	5.54	17.78
	309122	AI928178		gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00	2.92
	309128	Al928816	Hs.180842	ribosomal protein L13	1.38	5.55
1.5	309164	AJ937761		gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
15	309177	A395111B	11- 900 400	gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97 7.46
	309288 309299	AJ991525 AW003478	Hs.299426	ESTs gb;wq66c06.x1 NCI_CGAP_GC6 Homo saptens	4.86 4.36	9.43
	309303	AW004823		gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens	2.88	7.54
	309411	AW085201	Hs.244144	EST	4.30	7.14
20	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60
	309499	AW136325	Hs.279771	Homo sapiens clone PP1596 unknown mRNA	2.82	3.55 3.95
25	309529 309532	AW150807 AW151119	Hs.181357	taminin receptor 1 (67kD, ribosomal pro gbxg33e10.x1 NCL_CGAP_Ut1 Homo sapiens	4.78 1.18	4.40
23	309526	AW192004	Hs.2976B1	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHHU Ig garmin	1.47	1.39
	309675	AW205681	Hs.253506	EST, Moderately similar to ATPN_HUMAN A	5.68	15,20
20	309693	AW237221	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.00	1.00
30	309695	AW238011	Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25 8.35
	309747	AW264889		gb:xq36h02x1 NCI_CGAP_Lu28 Homo sapkens gb:xs13c10x1 NCI_CGAP_Kid11 Homo sapien	5.00 5.76	11.90
	309769 309782	AW272346 AW275156	Hs.156110	immunoglobulin kappa constant	0.42	0.69
35	309783	AW275401	Hs.254798	EST	1.00	4.11
	309799	AW276964		gb:xp58h01.x1 NOI_CGAP_Ov39 Homo sapiens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.05	1.18
40	309923	AW340684		gb:hd05g08.x1 Soares_NFL_T_GBC_S1 Home s	2.30 7.41	3.67 13.71
40	309928 309931	AW341418 AW341683		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1,20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_Ut2 Homo sapisns	4.90	18.29
	309964	AW449111	Hs.257111	hypothetical protein MGC3265	1.99	3.07
4 -	310002	AJ439095	Hs.323079	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	0.20	0.47
45	310096	AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76 5.83
	310109	Al203094 AW197233	Hs.148633 Hs.147253	ESTs ESTs	2.06 2.92	3.55
	310112 310115	AW197233 AJ611317	Hs.223796	ESTs	1.25	0.84
50	310121	AW195642	Hs.148901	ESTs	1.00	2.71
	310146	AJ206614	Hs.197422	ESTS	9.50	15.31
	310193	AJ627653	Hs.147562	ESTs	2.85	4.18
	310255	AW450439	Hs.153378	ESTs	4.26	10.63
55	310261	AI240483	Hs.201217.	ESTs metallothionein 1E (functional)	3.28 0.26	4.40 0.86
33	310264 310275	AI915771 AI242102	Hs.74170 Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15	8.06
	310290	AW013815	Hs.149103	ESTs	2.19	3.12
C C	310333	AI253200	Hs.145402	ESTs	1.17	1.91
60	310346	AI261340	Hs.145517	ESTs	4.81	9.95
	310385	AJ263392	Hs.156151	ESTs	5.96 2.90	7.79 4.63
	310443 310444	AW119018 AW195632	Hs.164231 Hs.252956	ESTs ESTs	0.85	1.01
	310446	AI275715	Hs.145926	ESTs	2.18	3.85
65	310468	AI984074	Hs.198398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3.87	8.12
	310514	AI681145	Hs.160724	ESTS	3.30	7.33
70	310524	AW082270	Hs.12496 Hs.208024	ESTs, Highly similar to AC004836 1 simil	0.72 3.26	1.44 3.46
70	310547 310584	A1302654 A1653007	Hs.156304	ESTS ESTS	2.39	4.08
	310608	AI962234	Hs.196102	ESTs	5.60	6.49
	310624	Al341594		gb:Human endogenous retrovirus H proteas	4.91	9.09
75	310636	AI814373	Hs.164175	ESTs	1.85	1.71
75	310648	AJ347863	Hs.156672	ESTs	0.17	0.69
	310694	A1654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40 4.82	13.22 6.27
	310695 310714	A)472124 A)418446	Hs.157757 Hs.157882	ESTs ESTs	1.76	3.51
	310722	AI989803	Hs.157289	ESTs	1.14	6.85
80	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	A1376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554	Hs.161286	ESTs	2.84	1.96
	310851	AW291714	Hs.221703	ESTs	1.00	2.32
85	310854	AJ421677 AJ871000	Hs.161332	ESTs ESTs	6.37 6.07	7.94 9.84
95	310858	MO1 1000	Hs.161330	ESTs	201	3.04

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	310864	Al924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTs	1.00	3.63
	310896	AW157731	Hs.270982	ESTs, Moderately similar to ALU7_HUMAN A	7.07	16.68
_	310922	AW195634	Hs.170401	ESTs	1.00	1.00
5	310955	AJ560210	Hs.263912	ESTs	10.08	17.66
_	310957	AW190974	Hs.196918	ESTs	2.18	3.18
	311000	AI521830	Hs.171050	ESTs	3.06	6.64
	311012	AW298070	Hs.241097	ESTs	1.23	3.77
	311034	Al564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
10	311074	AW290922	Hs.199848	ESTs	6.04	14.19
10	311134	A1990849	Hs.196971	ESTs	3.54	6.96
	311174	AW450552	Hs.205457	periaxin	0.65	0.95
	311187	A1638374	Hs.224189	ESTs	2,46	2.78
		A1656040			1.10	2.52
15	311220		Hs. 196532	ESTs	1,41	1.75
IJ	311230	A1989808	Hs.197663	ESTs		
	311236	A1653378	Hs.197674	ESTs	218	211
	311242	AW016812	Hs.200266	ESTs	0.63	5.11
	311258	AJ571221	Hs.199887	ESTs	1.00	1,41
20	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
20	311294	AA826425	Hs.291829	ESTs	1.04	2.69
	311308	F12664	Hs.49000	ESTs	1.98	6.70
	311351	AI682303	Hs.201274	ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
0.5	311405	AW290961	Hs.201815	ESTs	3.80	11.66
25	311409	A1698839		gb:nwd31f02_x1 Soares_NFL_T_GBC_S1 Homo s	3.84	6.94
	311420	Al936291	Hs.209867	ESTs	5.30	12.56
	311443	Al791521	Hs.192205	ESTs	4.39	6.09
	311467	AI934909	Hs.175377	ESTs	1.00	1.04
	311479	AI933672	Hs.211399	ESTs	2.76	5.61
30	311488	R57390	Hs.301064	arfaptin 1	2.50	5.73
	311495	AW300077	Hs.221358	ESTs .	3.63	6.09
	311511	AW444568	Hs.210303	ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
	311537	AI805121	Hs.211828	ESTs	3.69	5.85
35	311543	AJ681360	Hs.201259	ESTs	1.73	1.34
55	311551	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.31	6.12
	311557	AI819230	Hs.211238	interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128		2.25	3.41
	311559			KIAA1292 protein	2.68	5.90
40		AW008271	Hs.265848	similar to rat myomegalin	2.39	3.32
40	311563	AI922143	Hs.211334	ESTs		
	311588	AI827834	Hs.211227	ESTs	2.47	3.85
	311616	AW450675	Hs.212709	ESTs	1.00	1.00
	311621	Al924307	Hs.213464	ESTs	4.16	6.74
15	311635	AJ928456	Hs.213081	ESTs	2.17	3.76
45	311668	AW193674	Hs.240044	ESTs	2.60	3.12
	311672	R11807	Hs.20914	hypothetical protein FLJ23056	2.79	5.18
	311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA	5.00	8.17
50	311735	AW294416	Hs.144587	Homo sapiens cDNA FLJ12981 fis, clone NT	0.96	0.72
	311743	T99079	Hs.191194	ESTs	1.00	1.95
	311783	AJ682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
~ ~	311799	AA780791	Hs.14014	ESTs, Wealdy similar to KIAA0973 protein	8.52	13.32
55	311819	AW265275	Hs.254325	ESTs	3.58	3.91
	311823	AI089422	Hs.131297	ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTs	0.88	0.87
	311896	AW206447		gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su	1.66	1.13
60	311910	N28365	Hs.22579	Homo sapiens clone CDABP0036 mRNA sequen	1.66	2.30
	311923	T60843	Hs.189679	ESTs	0.42	2.63
	311933	Al597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02	2.33
	311960	AW440133	Hs.189690	ESTs	3.87	6.62
65	311967	AJ382726	Hs.182434	ESTs	5.80	8.14
	311975	AA804374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	178886	Hs.284450	ESTs	3.78	4.92
	312046	AJ580018	Hs.268591	ESTs	4.11	7.32
70	312056	T83748	Hs.268594	ESTs	2.36	3.08
, ,	312064	AA676713	Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093	T91809	Hs.121296	ESTS	0.68	0.85
	312094	Z78390	. 13. 12 1230	gb:HSZ78390 Human fetal brain S. Maier-E	3.05	4.48
75	312097	Al352096	Un 112100	zinc finger protein 148 (pHZ-52)	4.52	9.70
, ,			Hs.112180			
	312118	T85332	Hs.178294	ESTS	2.40	2.60
	312128	Al052609	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67	1.03
80	312175	AA953383	Hs.127554	ESTs	5.85	10.60
οV	312179	A1052572	Hs.269864	EST6	241	3.32
	312201	Al928365	Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207	H90213	Hs.191330	ESTs	2.20	4.55
	312220	N74613		gb:za55a07.s1 Soares fetal liver spieen	4.28	11.13
05	312252	AI128388	Hs.143655	ESTs	1.64	1.57
85	312304	AA491949	Hs.269392	ESTs	0.12	2.47

	W	U 02/08				
	312318	AW235092	Hs.143981	ESTs	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R65210	Hs.186937	EST ₈	0.44	1.74
_	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96
5	312339	AA524394	Hs.165544	ESTs	3.07	0.95
	312353	A1675558	Hs.181867	ESTs	10.08	16.73
	312375	Al375096	Hs.172405	cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
	312389	Al863140	•	gb:tz43h12x1 NCI_CGAP_Bm52 Homo sapten	2.37	3.98
10	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
10	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	Al167637	Hs.146924	ESTs	1.11	1.00
		Al168177		ESTs	5.89	8.24
15	312507		Hs.143653			8.92
15	312520	Al742591	Hs.205392	ESTs	3.30	
	312548	A1566228	Hs.159426	hypothetical protein PRO2121	1.38	1.65
	312564	H21520	Hs.35088	ESTs	0.40	0.77
	312583	Al193122	Hs.124141	ESTs	0.13	0.94
20	312599	AI865073	Hs.125720	ESTs	3.75	5.29
20	312602	AA046451	Hs.165200	ESTs	6.78	12.93
	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	Al240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	B.93	13.78
	312873	AI690071	Hs.283552	ESTs, Wealthy similar to unnamed protein	4.20	6.23
	312893	AI016204	Hs.172922	ESTs	2.67	3.15
	312902	AW292797	Hs.130316	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.19	0.71
	312925	N90868	Hs.271695	ESTs	2.50	4.25
30	312936	Al681581	Hs.121525	ESTs	1.00	1.17
50	312975	A1640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.60	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
				ESTs	2.03	2.13
35	312984	N25871	Hs.177337		5.52	8.42
33	313000	Al147412	Hs.146657	ESTs		1.39
	313029	AA731520	Hs.170504	ESTs	0.96	
	313039	Al419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.48	13.20
	313049	AW293055	Hs.119357	ESTs	6.44	10.73
40	313056	Al651930	Hs.135684	ESTs	1.51	2.04
40	313058	D81015	Hs.125382	ESTs	0.25	1.50
	313070	Al422023	Hs.161338	ESTs	B.56	11.60
	313097	AI676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
	313136	N592B4	Hs.288010	EST ₈	0.49	1.36
45	313153	A1240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTs .	0.30	0.66
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.16	8.76
	313239	W19632	Hs.124170	ESTs	1.00	3.87
	313265	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	0.74	2.06
50	313267	Al770008	Hs.129583	ESTs	0.23	1.30
• •	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	Al362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
	313325	Al420511	Hs.127832	ESTs	1.20	2.27
55	313357	AW074848	Hs.201501	ESTs	4.02	5.33
J J	313393	AJ674685	Hs.200141	ESTs	1.36	2.84
	313399	AW376889	Hs.194097	ESTs	2.58	5.26
	313414	Al241540	Hs.132933	ESTs	6.57	15.07
	313417	AA741151	Hs.137323	ESTs	0.63	3.01
60			Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
00	313457 313499	AA576052 Al261390	Hs.146085	KIAA1345 protein	0.91	2.37
				ESTs	3.41	7.08
	313516 313556	AA029058 AA628517	Hs.135145 Hs.118502	ESTs	0.23	0.70
65	313569	AJ273419	Hs.135146	hypothetical protein FLJ13984	1.88 0.73	1.00 2.27
UJ	313570	AAD41455	Hs.209312	ESTs		
	313638	AJ753075	Hs.104627	Homo sapiens cDNA FLJ10158 fis, clone HE	1.00	1.72
	313662	AA740151	Hs.130425	ESTs	0.20	1.42
	313671	W49823	Hs.104613	RP42 homolog	1.00	1.00
70	313672	AW468891	Hs.122948	ESTs	3.46	5.80
70	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	0.51	0.97
	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	A1744687	Hs.257806	ESTs	2.13	2.99
76	313774	AW136836	Hs.144583	ESTs	1.38	1.19
75	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022	Hs.133294	ESTs	1.15	0.91
	313834	AW418779	Hs.114889	ESTs	0.68	3.14
	313835	A1538438	Hs.159087	ESTs	5.74	8.88
80.	313852	H18633	Hs.123641	protein tyrosine phosphatase, receptor t	0.16	1.14
	313854	AW470806	Hs.275002	ESTs	2.09	4.05
	313865	AA731470	Hs.163839	ESTs	3.41	4.09
	313871	AW471088	Hs.145950	EST ₈	5.28	6.83
	313883	A1949384	10.170000	gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens	290	10.91
85	313915	AI969390	Hs.163443	Homo saptens cDNA FLJ11576 fis, clone HE	1.00	1.00
J <i>J</i>	010010	. 2003000	10.100440	LIMITED SECTION OF LATE AND ADDRESS OF THE PERSON OF THE P		

	W	O 02/08	6443			
	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957 Hs.226780	ESTs	0.46 4.10	0.75
5	313983 314035	AI829133 AA164199	Hs.270152	ESTs ESTs	5.88	6.40 7.90
•	314037	AW300048	Hs.275272	ESTs	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86 2.90	1.21
10	314103 314107	AI028477 AA806113	Hs.132775 Hs.189025	ESTs ESTs	2.00	5.29 1.66
10	314113	AA218986	Hs.118854	ESTs	0.91	4.17
	314124	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.53	3.32
	314126	AA226431	11- 404000	gb:nc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
15	314128 314151	AA935633 AA236163	Hs.194628 Hs.202430	ESTs ESTs	2.90 4.15	6.35 6.45
15	314184	AW081795	Hs.233465	ESTS	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253 314262	AA278679 AW086215	Hs.189510 Hs.246096	ESTs	4.98 0.38	7.16 1.94
20	314320	AA811598	Hs.275809	ESTs	3.34	5.66
	314332	AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo sapiens clone 24629 mRNA sequence	4.35	4.78
25	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
23	314351 314376	AA292275 AJ628633	Hs.193746 Hs.324679	ESTs ESTs	3.07 4.10	3.77 6.11
	314443	AA827125	Hs.192043	EST8	6.20	13.67
	314458	A1217440	Hs.143873	ESTs	0.58	2.49
30	314466	AA767818	Hs.122707	ESTs	2.53	2.62
30	314478 314482	AI521173 AL043807	Hs.125507 Hs.134182	DEAD-box protein ESTs	3.94 1.30	5.65 1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210852	T-box, brain, 1	3.12	6.16
25	314529	AL046412	Hs.202151	ESTs	3.43	6.87
35	314546 314562	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38 2.29	1.00 5.27
	314579	Al564127 AW197442	Hs.143493 Hs.116998	ESTs ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
40	314585	AA918474	Hs.216363	ESTs	1.08	1.40
40	314589 314592	AW384790 AA435761	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00 0.90	1.00 2.60
	314603	AA418024	Hs.192148 Hs.270670	ESTs ESTs	4.56	6.29
	314604	AA946582	Hs.8700	deleted in liver cancer 1	3.42	3.92
4.5	314606	AA418241	Hs.188767	ESTs	2.97	4.55
45	314648 314699	AA878419 Al038719	Hs.132801	gb:EST391378 MAGE resequences, MAGP Homo1 ESTs	3.66	1.36 4.97
	314701	Al754634	Hs.131987	ESTS	0.03	0.90
	314710	AJ669131	Hs.290989	EST	3.40	7.52
50	314750	AI095005	Hs.135174	ESTs	2.80	6.54
50	314767 314801	AW135412 AA481027	Hs.164002 Hs.109045	ESTs hypothetical protein FLJ10498	3.20 1.00	4,26 1,00
	314817	Al694139	Hs.192855	ESTs	0.91	0.99
	314835	Al281370	Hs.76064	ribosomal protein L27a	5.75	7.44
55	314852	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapten	1.68	4.34
55	314853 314940	AA729232 AW452768	Hs.153279	ESTs .	0.60 10.10	1.85 16.20
	314941	AA515902	Hs.162045 Hs.130650	ESTs	0.31	1.02
	314943	Al476797	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.18	0.37
60	314955	AA521382	Hs.192534	ESTs	2.59	3.90
60	314973 315004	AW273128 AA527941	Hs.300268 Hs.325351	ESTs	1.05	1.25
	315004	Al538613	Hs.298241	EST Transmembrane protease, serine 3	5.64 0.52	13.63 1.78
	315033	A1493046	Hs.146133	ESTs	2.46	1.00
CE	315035	AI569476	Hs.177135	ESTs	0.34	1.33
65	315056	Al202703	Hs.152414	ESTs	2.10	2.64
	315069 315071	AI821517 AA552690	Hs.105866 Hs.152423	ESTs Homo sapiens cDNA: FLJ21274 fis, clone C	1.00 1.78	1.30 1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
70	315078	AA568548	Hs.190616	ESTs .	3.00	3.79
70	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120 315175	AA564991 Al025842	Hs.269477 Hs.152530	ESTs ESTs	0.64 0.61	1.44 1.91
	315193	AI241331	Hs.131765	ESTs	1.06	0.97
75	315196	AA972756	Hs.44898	Homo saptens clone TCCCTA00151 mRNA sequ	0.48	1.96
75	315200	AI808235	Hs.307686	EST	3.76	9.40
	315254 315353	Al474433 AW452508	Hs.179556 Hs.279610	ESTs hypothetical protein FLJ 10493	5.37 1.00	9.36 1.30
	315397	AA218940	Hs.137516	fidgefin-like 1	3.38	2.24
00	315403	AW362980	Hs.163924	EŠTs	2.04	5.23
80	315431	AA622104	Hs.184838	ESTs	2.36	8.04
	315454 315455	Al239473 AW393391	Hs.156919	gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s ESTs	3.46 3.78	7.64 5.76
	315455	A1681671	Hs.312671	ESTs, Moderately similar to OVCA1	0.89	2.15
0.5	315483	AW512763	Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	Al193048	Hs.128685	ESTs	1.67	1.78

	W	O 02/08	6443			
	315530	At200852	Hs.127780	ESTs	1.05	1.01
	315541	Al168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552	AW445034	Hs.256578	ESTs	1.00	2.22
5	315562 315577	AA737415 AW513545	Hs.152826 Hs.17283	ESTs hypothetical protein FLJ10890	2.66 2.20	2.48 2.25
9	315587	Al268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo saplens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05
	315623	AA364078	Hs.258189	ESTs	7,44	12.56
10	315634 315658	AAB37085 AA912347	Hs.220585 Hs.136585	ESTs ESTs	0.50 0.43	1.40 1.22
10	315677	Al932662	Hs.164073	ESTs	0.60	1.39
	315708	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	AJ418055	Hs.161160	ESTs	2.88	263
15	315730 315745	H25899 Al821759	Hs.201591	ESTs ESTs	0.11 3.50	0.60 7.25
13	315791	AA678177	Hs.191856	gbzi15a05.s1 Soares_fetat_liver_spleen_	1.78	2.63
	315801	AAB27752	Hs.266134	ESTs	4.31	6.23
	315820	Al652022	Hs.258785	ESTs	2.35	3.01
20	315878	AA683335 Al821911	Hs.189046	ESTs	2.12 1.03	2.64 1.97
20	315905 315923	Al052789	Hs.209452 Hs.133263	ESTs ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21	0.85
	315978	AA830893	Hs.119769	ESTs	3.09	3.41
25	316001	A1248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82 1.63
25	316011 316012	AW516953 AA764950	Hs.201372 Hs.119898	ESTs ESTs	0.35 6.56	8.13
	316040	Al983409	Hs.189226	ESTs	5.69	10.69
	316048	AI720759	Hs.224971	ESTs	2.84	10.45
30	316076	AW297895	Hs.116424	ESTs	0.30	1.05 1.43
30	316124 316151	Al308862 Al806016	Hs.167028 Hs.156520	ESTs ESTs	1.00 5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20	3.96
	316204	AA731509	Hs.120257	ESTs	4.92	6.94
35	316232	AW297853	Hs.251203	ESTS	1.48	1.60
33	316275 316291	Al671041 AW375974	Hs.292611 Hs.156704	ESTs, Moderately similar to ALU1_HUMAN A ESTs	5.86 2.73	12.14 2.69
	316303	AA740994	Hs.209609	ESTs	1.53	1.26
	316344	AA744518	Hs.120610	ESTs	3.66	8.34
40	316346	Al028478	Hs.157447	ESTs	3.51	6.69
40	316365 316380	A1627845 A1393378	Hs.210776 Hs.164496	ESTs ESTs	2.50 1.16	4.33 2.16
	316470	AA809902	Hs.243813	ESTs	5.40	10.34
	316509	AA767310	Hs.291766	ESTs	2.46	2.89
45	316514	AA768037	Hs.291571	ESTs .	4.70	6.04
40	316519 316609	A1929097 AW292520	Hs.122082	gb:od10c11.s1 NCI_CGAP_GCB1 Homo saplens ESTs	4.41 1.00	9.70 2.89
	316633	Al125586	Hs.127955	ESTs	2.61	3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
50	316711 316713	Al743721 Al090671	Hs.285316 Hs.134807	ESTs, Moderately similar to ALU7_HUMAN A hypothetical protein FLJ12057	4.45 0.30	6.95 2.40
50	316715	Al440266	Hs.170673	ESTs, Weakly similar to AF126780 1 retin	0.20	1.45
	316787	AW369770	Hs.130351	ESTs	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
55	316811 316812	AA922060 AW135045	Hs.132471 Hs.232001	ESTs ESTs	1.00 3.28	1.32 4.70
55	316818	AA827176	Hs.124316	ESTs	0.67	1.81
	316824	AA837416	Hs.124299	ESTs	3.53	6.00
	316827	A1380429	Hs.172445	ESTs .	0.72	1.56
60	316891 316951	AW298119 AA134365	Hs.202536 Hs.57548	ESTs ·	1.64 1.45	2.97 1.08
00	316970	AA860172	Hs.132406	ESTs	1.00	1.53
	316971	AA860212	Hs.170991	ESTs	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001 317008	AI627917 AW051597	Hs.233694 Hs.143707	hypothetical protein FLJ11350 ESTs	3.56 0.69	4.37 1.37
05	317051	AA873253	Hs.126233	ESTs	6.18	12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137 317196	AW341567 Al348258	Hs.125710 Hs.153412	ESTS ESTS	2.82 1.98	5.12 2.51
, 0	317212	Al866468	Hs.148294	ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparofosteonectin, owov and kazal-like d	2.74	0.88
75	317266 317282	AA906289 AI807444	Hs.203614 Hs.176101	ESTs ESTs	1.00 2.60	1.00 4.21
	317285	AW370882	Hs.222080	ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320 317413	AA927151 AW341701	Hs.130452 Hs.126622	ESTs ESTs	3.58 2.08	8.13 4.92
	317417	AA918420	Hs.145378	ESTs ·	3.06	4.79
	317452	AA972955	Hs.135568	ESTs	4.22	9.21
	317519	A1859695	Hs.126860	ESTs	1.88	4.15
8 5	317521 317529	AI824338 AI916517	Hs.126891 Hs.126865	ESTs ESTs	3.12 2.73	4.55 3.34

	W	O 02/080	5443			
	317570	AJ733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20	11.95
	317598	AW206035	Hs.192123	ESTs	0.33	1.56
_	317627	AI346110	Hs.132553	ESTs	1.50	1.39
5	317650	AI733310	Hs.127346	ESTs	0.48	1.46
	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686	AA969051	Hs.187319	ESTs	1.00	1.01
10	317692	Al307659	Hs.174794	ESTs	5.33	9.59
10	317701	AJ674774	Hs.128014	ESTs	1.00	1.00
	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	A1733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59	1.30
15	317777	Al143525	Hs.47313	KIAA0258 gene product	1.00	2.48
13	317799	AM98273	Hs.128808	ESTs	1.78	211
	317803	AA983251	Hs.128899	ESTS	0.80	1.06
	317821 317848	Al368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17 5.30	0.68 8.16
		AJ820575	Hs.129086 Hs.152982	Homo sapiens cDNA FLJ12007 fis, clone HE hypothetical protein FLJ13117	1.30	2.28
20	317850 317861	N29974 AW341064	Hs.132362	ESTs	2.18	5.93
40	317865	A1298794	Hs.129130	ESTS	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	A1827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
	317890	Al915599	Hs.129225	ESTs	4.68	7.48
25	317899	A1952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.14	3.37
25	317986	A1005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
	318023	AW243058	Hs.131155	ESTs	2.92	5.22
30	318054	AW449270	Hs.232140	ESTs	3.92	6.37
-	318068	AJ024540	Hs.131574	ESTs	1.21	1.27
	318117	Al208304	Hs.250114	ESTs	0.86	1.17
	318187	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
	318223	Al077540	Hs.134090	ESTs	1.05	0.90
35	318240	AJ085377	Hs.143610	ESTs	3.10	2.40
	318255	Al082692	Hs.134662	ESTs	0.02	1.05
	318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	Al093840	Hs.143758	ESTs	4.98	7.90
	318369	Al493501	Hs.170974	ESTs	2.46	5.62
40	318428	Al949409	Hs.194591	ESTs	0.77	0.45
	318458	Al149783	Hs.158438	ESTs	3.54	4.92
	318467	Al151395	Hs.144834	ESTs	4.56	5.62
	318473	Al939339	Hs.146883	ESTs	2.08	4.05
'	318476	AI693927	Hs.265165	ESTs	4.22	8.07
45	318487	AJ167877	Hs.143716	ESTs	1.47	1.05
	318488	Al217431	Hs.144709	ESTs	1.40	4.14
	318491	· T26477	Hs.22883	ESTs, Weakty similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5/3	2.58	5.20
	318537	AA377908	Hs.13254	ESTs	3.26	4.18
50	318538	N28625	Hs.74034	Homo sapiens clone 24651 mRNA sequence	0.35	1.07
	318547	R20578	Hs.90431	ESTs	3.22	4.60
	318552	R18364	Hs.90363	ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Weakly similar to unnamed protein	1.91	1.98
	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6,22
55	318587	AA779704	Hs.168830	Homo sapians cDNA FL/12136 fis, clone MA	0.85	2.46
	318596	A)470235	Hs.172698	EST	4.88	4.93
	318622	T48325	Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
60	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
60	318548	177141	Hs.184411	albumin	6.27	9.91
	318650	AA393302	Hs.176626	hypothetical protein EDAG-1	3.96	8.84
	318671	AA188823	Hs.299254	Homo sapiens cDNA: FLJ23597 fls, clone L	1.53	0.81
	318579	T58115	Hs.10336	ESTS	1.00	2.19
65	318711	Al936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
UJ	318725	AI962487	Hs.242990	ESTS	1.08	2.46 1.33
	318728	Z30201	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	1.49
	318740	NM_002543		oxidised low density lipoprotein (lectin	0.25 1.00	3.01
	318776	R24963	Hs.23766 Hs.5181	ESTs	2.70	3.86
70	318784 318816	H00148 F07873		proliferation-associated 2G4, 38kO ESTs	3.90	7.13
, 0	318865	H10818	Hs.21273		2.25	3.56
	318879	R56332	Hs.18268	gb:ym04f10.r1 Soares infant brain 1NIB H adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs. 124952	ESTs	4.79	14.13
	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
75	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03	0.91
	318925	Z43577	Hs.21470	ESTs	2.23	3.80
	318936	Al219221	Hs.308298	ESTs	1.86	7.16
	318982	Z44140	Hs.269622	ESTs	5.84	9.79
	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
80	319041	Z44720	Hs.98365	ESTs, Wealdy similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein	1.00	1.07
	319170	R13578	Hs.285306	putative setenocysteine lyase	3.79	5.03
	319196	F07953	Hs.16085	putative G-protein coupled receptor	1.00	2.98
_	319199	F07361	Hs.13306	ESTs	3.53	5.66
85	319242	F11472	Hs.12839	ESTs	5.87	7.26

	W	O 02/08	6443			
	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270	R13474	Hs.290263	ESTs COLAGO	4.80	10.40
5	319279 319282	T65094 AA461358	Hs.12677 Hs.12876	OGI-147 protein ESTs	1.50 1.00	2.11 1.00
•	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481	II. oorooo	gbdHSC2QE041 normalized infant brain cDN	1.10	1.00
10	319370 319391	H54254 R06304	Hs.325823 Hs.13911	ESTs, Moderately similar to ALU5_HUMAN A	0.16 1.26	0.73 2.43
	319398	H67130	Hs.301743	ESTs ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
	319407	R05329		gb:ye91b04_r1 Soares fetal liver spleen	2.00	3.54
15	319425	T82930		gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433	R05050	Hs.191198	ESTs	6.15	14.13
	319437	AA282420	Hs.111991	ESTs, Wealthy similar to Y48A5A.1 (Celeg	3.26 1.76	5.68
	319466 319471	Al809937 R06546	Hs.116417 Hs.19717	ESTs ESTs	4.29	5.65 4.84
20	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	A1382429	Hs.250799	ESTs	2.08	2.82
	319508	T99898	Hs.270104	ESTs, Moderately similar to ALU8_HUMAN A	2.80	4.39
25	319523	T69499	Hs.191184	ESTS	1.55 1.65	3.25 1.19
23	319545 319546	R83716 R09692	Hs.14355	Homo saptens cDNA FLJ13207 fis, clone NT gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
20	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
30	319604	R11679	Hs.297753	vimentin	1.68	3.41
	319609 319611	AW247514 H14957	Hs.12293	hypothetical protein FLJ21103	3.06 2.76	4.24 4.24
	319653	AA770183	Hs.173515	gb:ym19c10.r1 Soares infant brain 1NIB H uncharacterized hypothalamus protein HT0	251	3.55
	319657	R19897	Hs.106604	ESTs	5.32	7.68
35	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chatn A, H	5.18	12.55
	319662	H06382	Hs.21400	ESTs	1.58	1.56
	319708 319742	R15372 177668	Hs.22664 Hs.21162	ESTs ESTs	1.00 2.48	1.22 3.13
40	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11.61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63	6.56
45	319812	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.63	1.32
43	319834 319878	AA071267 T78517	Hs.13941	gb:zm61g01.r1 Stratagene fibroblast (937 ESTs	0.30 3.99	0.94 6.44
	319882	AA258981	Hs.291392	ESTs ·	5.09	7.36
	319912	177559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40	9.42
50	319944	T79248	Hs.133510	ESTs	3.31	5.39
	319947 319962	AA160967 H06350	Hs.14479 Hs.135056	Homo sapiens cDNA FLJ14199 fis, clone NT Human DNA sequence from clone RP5-850E9	2.90 1.81	4.95 1,57
	320007	AA336314	ns. 133030	gb:EST40943 Endometrial tumor Homo sapie	3.42	6.29
	320018	T83263		gb:yd40h09.r1 Soares fetal liver spicen	277	5.14
55	320030	H63789	Hs.296288	ESTs, Wealty similar to KIAA0638 protein	4.10	6.69
	320032	A1699772	Hs.292664	ESTs, Weakly similar to A45010 X-linked	3.27	3.27
	320040	AA233671	Hs.87164	hypothetical protein FLJ14001	1.81	1.64
	320047	T86564	Hs.302256	EST EOV 12 foddward forlor	3.38 5.00	7.36 16.73
60	320053	H58138	Hs.120844 Hs.117915	FOXU2 forkhead factor ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112	T92107	Hs.188489	ESTs	2.27	2.06
	320140	H94179	Hs.119023	SMC2 (structural maintenance of chromoso	1.00	1.00
65	320188 320193	AW419200 AA831259	Hs.172318	ESTs ESTs	1.26 2.58	1.00 6.23
05	320195	R62203	Hs.17132 Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70 .	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00	1.17
70 '	320220	AF054910	Hs.127111	tektin 2 (testicular)	0.18	1.09
	320225 320231	AF058989 H03139	Hs.128231 Hs.24683	G antigen, family B, 1 (prostate associa ESTs	5.26 1.59	13.75 1.93
	320260	NM_003608		G protein-coupled receptor 65	1.38	4.56
	320267	AL049337	Hs.132571	Homo saplens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
75	320268	H06019	Hs.151293	Homo saptens cDNA FLJ 10664 fis, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41	1.01
	320325	A1167978	Hs.139851	caveolin 2	0.05	0.67
	320330 320339	AF026004 H10807	Hs.141660 Hs.281434	chloride channel 2 Homo sapiens cDNA FLJ14028 fis, clone HE	2.17 1.81	1.26 2.32
80	320388	H16065	·Hs.31286	ESTs	1.00	3.22
	320402	R22291	Hs.23368	Homo sapiens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs	11.25	20.78
85	320436 320438	AA253352 W24548	Hs.293663 Hs.5669	ESTs ESTs	2.22 3.53	3.49 8.14
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		U 02/08				
	320448	Al240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo sapiens mRNA: cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	follistatin-like 1	0.65	1.18
-	320499	R32555	Hs.24321	Horno sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
5	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34572	Hs.324522	EST ₈	3.16	5.63
	320536	AA331732	Hs.137224	ESTB	2.83	5.83
10	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
10	320564	AF056209	Hs.159396	peptidytglycine alpha-amidating monooxyg	1.22	0.81
					1.84	2.44
	320587	Z44524	Hs.167456	Homo saplens mRNA full length insert cDN		
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
1.5	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	A1904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
	320676	AA132650	Hs.300511	ESTs	3.63	5.37
•	320683	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320689	AA334609	Hs.171929	ESTs, Wealthy similar to A54849 collagen	1.27	1.02
	320696	AW135016	Hs.172780	ESTs	3.53	4.60
	320714	AJ445591		gb:yq04a10.r1 Soares fetal liver spleen	1.06	0.85
	320727	U96044	Hs.181125	immunoglobulin lambda locus	1.35	1.49
	320771	AI793266	Hs.117176	poly(A)-binding protein, nuclear 1	0.04	0.82
25					2.96	4.33
23	320794	AA281993	Hs.91226	ESTS		
	320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
20	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
30	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	AJ473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
	320921	R94038 T	Hs.199538	inhibin, bela C	2.20	1.17
	320927	Al205786	Hs.213923	ESTs	0.1B	1.46
35	320957	AI878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544	1002020	gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321045		Hs.269055	ESTs	2.69	4.25
		H27794			2.14	2.56
40	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2		
40	321059	Al092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo sapiens done 24941 mRNA sequence	4.79	7.41
	321102	AA018305		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
	321130	1142750	Un 435404	ESTs .	4 00	
4.5	321130	H43750	Hs.125494	C016	1.00	3.14
45	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
45						
45	321142 321155	AJ817933 AA336635	Hs.298351	ASPL protein hypothetical protein MGC5338	8.73	15.36
45	321142 321155 321158	AJ817933 AA336635 AA700289	Hs.298351 Hs.99598	ASPL protein hypothetical protein MGC5338 gb:yu76f11.r1 Soares fetal liver spleen	8.73 3.04 4.62	15.36 5.03
	321142 321155 321158 321170	AJ817933 AA336635 AA700289 N53742	Hs.298351	ASPL protein hypothetical protein MGC5338 gb:yu76f11.r1 Soares fetal liver spleen ESTs	8.73 3.04	15.36 5.03 8.39
	321142 321155 321158 321170 321199	AJ817933 AA336635 AA700289 N53742 AW385512	Hs.298351 Hs.99598 Hs.172982	ASPL protein hypothetical protein MGC5338 gb:yu76f11.r1 Scares fetal liver spleen ESTs gb:yy56d10.s1 Scares_multiple_sclerosis_	8.73 3.04 4.62 2.21 5.69	15.36 5.03 8.39 4.46 8.01
4550	321142 321155 321158 321170 321199 321206	AJ817933 AA336635 AA700289 N53742 AW385512 H54178	Hs.298351 Hs.99598 Hs.172982 Hs.226469	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_sclerosis_ Homo sapiens cDNA FLJ12417 fis, clone MA	8.73 3.04 4.62 2.21 5.69 4.00	15.36 5.03 8.39 4.46 8.01 7.32
	321142 321155 321158 321170 321199 321206 321225	AJ817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414	ASPL protein hypothetical protein MGC5338 gbyy76f11.r1 Soares fetal liver spleen ESTs gbyy56d10.s1 Soares_multiple_solerosis_ Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp56481462 (f	8.73 3.04 4.62 2.21 5.69 4.00 4.17	15.36 5.03 8.39 4.46 8.01 7.32 4.63
	321142 321155 321158 321170 321199 321206 321225 321238	AJ817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941	Hs.298351 Hs.99598 Hs.172982 Hs.226469	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FL112417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp56481462 (f Sert/Arg-related nuclear matrix protein (8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00	15,36 5.03 8.39 4.46 8.01 7.32 4.63 1.00
	321142 321155 321158 321170 321199 321206 321225 321236 321244	AJ817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414	ASPL protein hypothetical protein MGC5338 gb:yu76f11.r1 Soares fetal liver spleen ESTs gb:yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp56481462 (f SerIArg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 immunoglobu	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18	15,36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13
50	321142 321155 321158 321170 321199 321206 321225 321236 321244 321270	AI817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF2p56481462 (f gb;Homo sapiens in matrix protein (gb;Homo sapiens isolate AN.1 immunoglobu gb;yv76c06.s1 Soares fetal liver spleen	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26
	321142 321155 321158 321170 321199 321206 321225 321238 321244 321270 321317	AI817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AI937060	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF2p56481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 mmunoglobu gb;yy76c06.s1 Soares fetal liver spleen KJAA1151 protein	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65
50	321142 321155 321158 321170 321199 321206 321225 321236 321244 321270 321317 321318	AU817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R33560 AB033041	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp56481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb;yy76c06.s1 Soares fetal liver spleen KAA1151 protein KAA1151 protein KAA1151 protein	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00
50	321142 321155 321158 321170 321199 321206 321225 321238 321244 321270 321317 321318 321325	AI817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AI937060 AB033041 AB033100	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646	ASPL protein hypothetical protein MGC5338 gb:yu76f11.r1 Soares fetal liver spleen ESTs gb:yy56d10.s1 Soares_multiple_solerosis_ Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp56481462 (f SerIArg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb:yv76c06.s1 Soares fetal liver spleen KIAA1151 protein (KIAA1151 protein KIAA1215 protein (KIAA1 protein (similar to mouse paladin)	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93
50	321142 321155 321158 321170 321199 321205 321225 321224 321270 321317 321318 321325 321342	AI817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AB033041 AB033041 AB033100 AA127984	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_sclerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF2p56481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KIAA1151 protein KIAA1215 protein KIAA1215 protein KIAA protein (similar to mouse paladin) transcription factor BMAL2	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44 4.94	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.93
50	321142 321155 321158 321179 3211206 321225 321226 321227 32137 321317 321318 321325 321342 321356	AI817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AB033041 AB033041 AB033100 AA127984 R93443	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF256481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 mmunoglobu gb;yv76c06.s1 Soares fetal liver spleen KAA1151 protein (kMA1215 protein (kmilar to mouse paladin) transcription factor BMAL2 ESTs	8.73 3.04 4.62 2.21 5.69 4.00 2.18 3.80 1.81 1.00 0.44 4.94 3.10	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.66
50	321142 321155 321158 321170 321199 321206 321225 321234 321270 321317 321318 321325 321325 321356 321418	AU817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AU937060 AB033041 AB033100 AA127984 R93443 AJ739161	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770 Hs.161075	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp56681462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KAA1151 protein KIAA1151 protein KIAA151 protein (similar to mouse paladin) transcription factor BMAL2 ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.00 2.18 3.80 1.81 1.00 0.44 4.94 3.10 2.28	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.66 2.54
50	321142 321155 321158 321170 321199 321206 321225 321236 321244 321270 321317 321318 321325 321342 321342 321418 321420	AI817933 AA336635 AA700289 N55742 AW385512 H54178 AL080073 AW371941 AF068654 R33560 AI937060 AB033041 AB033100 AA127984 R93443 AT739161 AI368667	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_sclerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF2p56481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KJAA1151 protein KJAA1215 protein KJAA1215 protein KJAA protein (shriikar to mouse paladin) transcription factor BMAL2 ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44 4.94 4.94 4.94 4.10 2.28 1.13	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.93 4.66 2.54 0.97
50	321142 321155 321158 321170 321199 321206 321225 321234 321270 321317 321318 321325 321325 321356 321418	AU817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AU937060 AB033041 AB033100 AA127984 R93443 AJ739161	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770 Hs.161075 Hs.132743	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF256481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KJAA1215 protein KJAA protein (similar to mouse paladin) transcription factor BMAL2 ESTs ESTs ESTs ESTs ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44 4.94 3.10 2.28 1.13 2.42	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.93 4.66 2.54 0.97 3.35
50	321142 321155 321158 321170 321199 321206 321225 321236 321244 321270 321317 321318 321325 321342 321342 321418 321420	AI817933 AA336635 AA700289 N55742 AW385512 H54178 AL080073 AW371941 AF068654 R33560 AI937060 AB033041 AB033100 AA127984 R93443 AT739161 AI368667	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770 Hs.161075	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_sclerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF2p56481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KJAA1151 protein KJAA1215 protein KJAA1215 protein KJAA protein (shriikar to mouse paladin) transcription factor BMAL2 ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44 4.94 4.94 4.94 4.10 2.28 1.13	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.66 2.54 0.97 3.35 3.11
50 55 60	321142 321155 321159 321170 321296 321225 321224 321270 321317 321317 321317 321315 321325 32142 321356 3214130	AB17933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R33560 AB333041 AB033100 AA127984 R93443 AT39161 AJ368667 U05890	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770 Hs.161075 Hs.132743	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF256481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KJAA1215 protein KJAA protein (similar to mouse paladin) transcription factor BMAL2 ESTs ESTs ESTs ESTs ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44 4.94 3.10 2.28 1.13 2.42	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.93 4.66 2.54 0.97 3.35
50 55 60	321142 321155 321156 321170 321199 321206 321226 3212236 321236 321244 321270 321318 321325 321342 321418 321420 321433 321453 321467	AI817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R33560 AI937060 AB033041 AB033100 AA127984 R33443 AT739161 AI368667 U05890 N50080 X13075	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770 Hs.161075 Hs.132743 Hs.82845	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKFZp564B1462 (f Ser/Arg-related nuclear matrix protein { gb:Homo sapiens isotate AN.1 Immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KJAA1151 protein KJAA1151 protein KJAA151 protein KJAA1515 protein KJAA1515 protein KJAA1515 protein Schaller (similar to mouse paladin) transcription factor BMAL2 ESTs ESTs gb:H.sapiens (DIG3) mRNA for immunoglobu Homo sapiens cDNA: FLJ21930 fis, clone H gb:Human 2a12 mRNA for kappa-immunoglobu	8.73 3.04 4.62 2.21 5.69 4.00 4.17 1.00 2.18 3.80 1.81 1.00 0.44 4.94 4.94 1.13 2.28 1.13 2.42 1.60 0.42	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.93 4.66 2.54 0.97 3.35 3.11
50	321142 321155 321158 321170 321199 321205 321225 321244 321270 321317 321318 321356 321448 321453 321453 321453 321453	AB17933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF06854 R33560 AB33041 AB033041 AB033041 AB033100 AA037984 R33443 AI739161 AI368667 U05890 N50080 X13075 AA514198	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.271770 Hs.161075 Hs.132743 Hs.82845 Hs.38540	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF2p56481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KIAA1151 protein KIAA1215 protein KIAA1215 protein KIAA1215 protein Similar to mouse paladin) transcription factor BMAL2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	8.73 3.04 4.22 5.69 4.00 2.18 1.00 2.18 1.00 0.44 4.94 3.10 2.28 1.28 1.28 2.42 1.60 2.42	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.66 2.54 0.97 3.35 3.11 0.72 6.50
50 55 60	321142 321155 321158 321170 321199 321205 321225 321236 321244 321317 321318 321318 321356 321418 321453 321453 321453 321453 321453	AU817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AU837060 AU837060 AU833001 AU937060 AB033041 AB033041 AB033041 AB033041 AB033061 AX127984 R93443 AT739161 AU368667 U05890 N50080 X13075 AA514198 H70665	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300646 Hs.222024 Hs.271770 Hs.161075 Hs.132743 Hs.82845 Hs.38540 Hs.292549	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ12417 fis, clone MA Homo sapiens mRNA; cDNA DKF256481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 mmunoglobu gb;yv76c06.s1 Soares fetal liver spleen KJAA1215 protein KJAA protein (similar to mouse paladin) transcription factor BMAL2 ESTs ESTs ESTs ESTs gb:H.sapiens (DIG3) mRNA for immunoglobu Homo sapiens cDNA: FLJ21930 fis, clone H gb:Human 2a12 mRNA for kappa-immunoglobu ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.00 2.18 3.80 1.00 0.44 4.17 1.00 0.44 4.10 2.28 1.13 2.42 1.60 0.42 4.10	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.66 2.54 0.97 3.35 3.11 0.72 6.50 1.25
50 55 60	321142 321155 321170 321199 321205 321225 321236 321244 321270 321318 321325 321346 321453 321453 321467 321468 321498	AU817933 AA336635 AA700289 N53742 AW385512 H54178 AL080073 AW371941 AF068654 R83560 AB033041 AB033100 AA127984 R93443 AJ739161 AJ68667 U05890 N50080 X13075 AA514198 H70665 AW295517	Hs.298351 Hs.99598 Hs.172982 Hs.226469 Hs.251414 Hs.18192 Hs.6298 Hs.137507 Hs.300546 Hs.222024 Hs.271770 Hs.161075 Hs.132743 Hs.82845 Hs.38540 Hs.292549 Hs.292549	ASPL protein hypothetical protein MGC5338 gb;yu76f11.r1 Soares fetal liver spleen ESTs gb;yy56d10.s1 Soares_multiple_solerosis_Homo sapiens cDNA FLJ1247 fis, chone MA Homo sapiens mRNA; cDNA DKF256481462 (f Ser/Arg-related nuclear matrix protein (gb:Homo sapiens isolate AN.1 Immunoglobu gb;yv76c06.s1 Soares fetal liver spleen KAA1151 protein KAA1151 protein KAA1215 protein KAA1215 protein KAA1215 protein (similar to mouse paladin) transcription factor BMAL2 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	8.73 3.04 4.62 2.21 5.69 4.07 2.18 3.80 1.00 0.44 4.94 4.94 4.94 4.94 2.28 1.13 2.42 1.60 0.42 2.46 0.42 2.46 0.41 0.42	15.36 5.03 8.39 4.46 8.01 7.32 4.63 1.00 9.13 5.26 1.65 1.00 0.93 4.66 2.54 0.97 3.35 3.11 0.72 6.50 1.25 6.24
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	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	AI694875	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.00	1.00
	321777	Al637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
5	321779	N42729	Hs.163835	ESTs	0.90	0.90
_	321829	D81993	Hs.8966	turnor endothetial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49	9.58
	321883	AA426494	Hs.46901	KIAA1462 protein	0.28	0.95
10	321899	N55158	Hs.29468	ESTs	0.39	0.95
	321911	AF026944	Hs.293797	ESTs	6.20	10.76
	321949	R49202	Hs.181694	EST	4.62	10.51
	321955	AI651866	Hs.195689	ESTs	2.89	5.47
	321956	AL110177	Hs.132882	ESTs	0.32	1.25
15			Hs.272759	KIAA1457 protein	1.00	1.83
13	321987 321991	AL133612	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
		AL133627	Hs.84522	ESTs	2.10	3.48
	322002	AA328801		== · · · · · · · · · · · · · · · · · ·	1.00	1.90
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	3.20	9.67
20	322044	AW340926	11- 454570	gb:xy51b10.x1 NCI_CGAP_Lu34.1 Homo sapis		
20	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	Al341937		gb:qt10e03.x1 NCI_CGAP_GC4 Homo sapiens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
25	322091	AI819863	Hs.105243	ESTs	1.59	1.75
25	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
20	322173	H52567		gb.yt85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
30	322178	H56535		gb:yl88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:yt94c02.s1 Soares_pineal_gtand_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20	5.04
	322212	AF087995	Hs.134877	ESTs	3.42	4.84
35	322221	AJ890619	Hs.179562	nucleosome assembly protein 1-like 1	0.82	2.14
	322277	Al640193	Hs.226389	ESTs	3.62	3.98
	322278	AF086283		gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322284	AI792140	Hs.49265	ESTs	0.66	2.76
	322288	AL037273	Hs.7B86	pellino (Drosophila) homolog 1	0.71	0.70
40	322320	AF086419		gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
. •	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348		gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
	322372	W25624	Hs.153943	ESTs	7.37	12.07
45	322374	Al394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothetical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
50	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
50	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
55	322473	AA744286	Hs. 266935	tRNA selenocysteine associated protein	1.75	2.03
55				ESTs	1.00	2.27
	322509 322523	T52172	Hs.302213		2.75	5.49
		W80398	Hs.193197	ESTS	1.25	1.27
	322527	AF147359	11- 070047	gb:Homo sapiens full length insert cDNA	4.57	8.81
60	322560	AI916847	Hs.270947	ESTS	1.00	1.42
UU	322566	W87285	Hs.269587	ESTs qb:zh69c01.r1 Soares_fetal_liver_spleen_	4.18	6.94
	322585	AA837622			2.40	4.85
	322635	AA679084	11- 000040	gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.94	4.64
	322641	AA007352	Hs.256042	ESTs		
65	322653	A1828854	Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
03	322664	AA011522		gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
	322687	Al110759		gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	Al110872	Hs.279812	PRO0327 protein	1.80	1.72
70	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
70	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo saptens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	AJ608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
75	322810	A1962276	Hs.127444	ESTs	4.09	6.90
75	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	AJ377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo saplens cDNA FLJ14035 fis, done HE	5.26	1.22
00	322887	AI986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
80	322913	A1733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	A1365585	Hs.146246	ESTs	0.30	1.14
	322958	A1905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
0.5	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18	2.00
85	322981	AA493252	Hs.159577	ESTs	2.28	2.61

	W	O 02/08	6443			
	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AJ733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
•	323025	AL157565	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	0.06	1.10
5	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	A1700025	Hs.270471	ESTs	2.31 5.38	4.49
10	323102	AL119913	Hs.163615	ESTs	2.38	11.64
10	323155	AL135041	I I - 02404	gb:DKFZp762K2310_r1 762 (synonym: hmel2)	1.06	5.56 1.41
	323176 323191	AW071648 AA195600	Hs.82101 Hs.301570	pleckstrin hornology-like domain, family	0.73	1.24
	323225	AA205654	Hs.24790	ESTs KIAA1573 protein	5.25	11.95
	323232	AA148722	Hs.224680	ESTs	0.45	1.35
15	323256	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
10	323281	Al697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo saplens cDNA: FLJ21578 fis, clone C	12.68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	Al336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
0.5	323359	AA234172	Hs.137418	ESTs	0.34	1.18
25	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	Al672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	ESTS	2.27	1.92
30	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapien	0.43	0.80
20	323449	AA282865	Hs.284153	Fancori anemia, complementation group A	3.19 2.70	3.85 3.20
	323492 323501	H00978	Hs.20887	hypothetical protein FLJ10392	2.04	3.31
	323505	AA182461 Al652287	Hs.84520	ests gb:EST382593 MAGE resequences, MAGK Homo2		3.08
	323515	AA282274	Hs.256083	ESTs	2.69	3.40
35	323541	Al185116	Hs.104613	RP42 homolog	1.20	1.09
-	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	tumor differentially expressed 1	3.70	5.80
	323678	AL042121	Hs.20880	ESTs	3.33	5.10
40	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323745	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cONA DKFZp586F1322 (f	2.06	3.70
15	323856	AA355264	Hs.267604	hypothetical protein FLJ10450	3.42	8.13
45	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36 2.31	1.00 3.33
	323885 323911	AA344308 AL043212	Hs.128427 Hs.92550	Homo sapiens BAC clone RP11-335J18 from ESTs	4.38	5.41
50	323919	AA862973	Hs.220704	ESTs	5.80	10.20
50	323972	AI869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	AI472078	Hs.303662	ESTs	1.00	5.03
	324055	AA528794	Hs.128644	ESTs	0.86	1.00
55	324063	AW292740	Hs.272813	dual oxidase 1	0.45	0.91
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.82	5.12
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	2.40	2.52
	324095	AW377983	Hs.298140	Homo saplens cDNA: FLJ22502 fis, clone H	1.32	4.30
6 0	324129	AJ381918	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	1.40	1.77
60	324132	AW504860	Hs.288836	hypothetical protein FLJ12673	4.24	6.21
	324214	AA412395	Hs.225740	ESTs	6.96	10.69
	324227	AA295552	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324266	AL047634	Hs.231913	ESTs	2.42	4.05
65	324275	AA429088	Hs.98523	ESTS	3.62 0.14	5.38
05	324281 324290	AL048026	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.71	0.70 4.34
	324303	AA432032 AL118754	Hs.304420	ESTs gb:DKFZp761P1910_r1 761 (synonym: harry2)	0.95	0.91
	324312	Al198841	Hs.128173	ESTs	4.06	5.91
	324325	AL138153	Hs.300410	ESTs	5.88	8.25
70	324338	AL138357	Hs.145078	regulator of differentiation (In S. pomb .	0.87	1.25
. •	324341	AW197734	Hs.99807	ESTs. Weakly similar to unnamed protein	1.28	1.00
	324343	AW452016	Hs.293232	ESTs	2.54	3.46
	324371	AA452305	Hs.270319	ESTs	5.85	8.36
95	324382	AW502749	Hs.24724	MFH-amplified sequences with leucine-ric	0.76	1.64
75	324384	AA453396	Hs.127656	KIAA1349 protein	2.88	5.69
	324385	F28212	Hs.284247	KIAA1491 protein	1.81	1.99
	324388	AI924953	Hs.306206	hypothetical protein FLJ11215	1.00	1.00
	324432	AA464510	Hs.152812	ESTs	2.73	2.17
90	324497	AW152624	Hs.136340	ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324510	AI148353	Hs.287425	Homo sapiens cDNA FLJ11569 fis, clone HE	1.00	1.00
	324580	AA492588	Lie 120000	gb:ng99c08.s1 NCL_CGAP_Thy1 Homo saplens	2.18	3.50
	324582	AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.35
	324633 324640	AA572994 AW295832	Hs.325489 Hs.134798	ESTs Moderately similar to TTL MOUSE TU	2.92 5.48	4.22 11.74
85	324640 324675	AW014734	Hs.157969	ESTS MODERACELY STREET WITH MOUSE TO	5.48 0.39	0.73
	GE 7013		. 10/303		J.00	

WO 02/086443 324699 AW504732 Hs.21275 hypothetical protein FLJ11011 1.81 1.34 6.56 324747 AA603532 Hs.130807 1.57 Hs.292385 **ESTs** 324748 AA657457 155 1.00 sterol O-acyltransferase (acyl-Coenzyme Hs.14553 324801 A1819924 5 gbrwd73f12.x1 NCI_CGAP_Lu24 Homo sapiens 7.53 324804 AI692552 324828 AA843926 Hs.124434 2.00 3.25 2.74 1.07 3.43 0.95 324855 AW152305 Hs.122364 Small proline-rich protein SPRK (human, Horno sapiens cDNA: FLJ22785 fis, clone K AI541214 AW297755 Hs.46320 324866 324871 Hs.271923 1.68 1.21 10 324886 AA806794 Hs.131511 **ESTs** 324889 D31010 gb:HUML12147 Human fetal lung Homo saple 2.20 4.65 324948 AW383618 Hs.265459 ESTs, Moderately similar to ALU2_HUMAN A 5.28 3.37 7.05 Hs.125428 Hs.132892 **ESTs** 5.51 324953 A1264628 protocadherin 20 9.81 AA625076 5.12 324958 hypothetical protein FLJ10549 laminin, alpha 4 15 1.08 324988 T06997 Hs.121028 325024 F13254 Hs.78572 5.24 10.22 Hs.105421 Hs.22380 Hs.315562 1.00 2.14 3.17 325105 H97109 EST₅ 1.00 1.99 2.73 325108 AA401863 **ESTs** 325114 325148 D83901 **ESTs** 20 1.86 3.41 AI064690 Hs.171176 EST₅ 325149 Hs.187646 **ESTs** 0.42 0.93 D61117 6.50 6.18 2.64 325187 Al653682 Hs.197812 **ESTs** 11.31 325228 15.76 4.12 325235 25 2.87 4.42 325328 325340 0.29 0.33 325357 16.56 24.29 1.22 0.63 325373 325389 0.88 1.05 30 5.75 14.14 325436 325471 8.46 17.82 325498 3.32 6.42 8.28 5.51 7.48 325557 21.40 325559 35 4.08 4.20 325560 5.24 1.13 325569 1.10 325585 1.00 1.00 325587 2.98 13.40 325597 40 0.78 0.78 325639 325685 0.46 0.95 0.66 1.55 325686 4.48 9.20 325735 325739 0.59 0.88 45 325740 2.42 6.61 7.88 4.74 325792 9.83 7.18 325819 202 264 325883 15.98 325895 50 325925 2.04 10.60 4.18 3.66 7.36 9.03 325932 325941 325969 0.61 0.80 4.88 7.42 325971 55 0.55 7.21 1.07 326025 326046 326099 14.72 3.60 5.98 1.06 326108 3.27 0.45 0.13 326163 5.70 60 1.11 326165 0.45 326189 326204 5.60 9.00 326230 7.00 1.00 9.86 0.52 1.00 1.24 9.20 2.77 12.01 326274 8.09 65 326360 326393 15.35 0.77 326505 326515 5.84 326589 13.49 70 4.01 326592 201 2.53 326605 326692 1.00 1.00 1.00 0.19 2.34 1.31 0.65 7.20 326693 326720 326742 75 0.25 0.83 326770 326818 3.09 4.56 3.45 1.70 2.08 326936 0.41 326964 80 326983 2.02 3.80 1.09 1.20 326991 327036 1.00 8.04 3.05 3.55 4.22 6.31 327040 327053 85 1.40

	WO 02/086443				PCT/US02/12476
	327085		2.50	12.57	101/0002/121/0
	327130 327156		5.38 3.74	8.04 6.58	
_	327220		1.28	1.54	
5	327224		6.56	12.91	
	327288 327321		2.61 2.42	5.40 3.11	
	327332		6.62	10.58	
10	327351 327377		2.69 2.04	4.41 6.72	
10	327395		261	4.50	
	327414		1.00 5.91 6.58 3.79 4.08	8.01	•
	327442 327457		5.91 6.58	9.65 18.01	
15	327473 327483 327562		3.79	7.48	
	327483 327562		4.08 0.68	8.87 2.86	
	327568 327606		0.68 1.00	8.87 2.86 2.00	
20	327606		2.06 5.90	3.61	
20	327611 327642		4.06	14.26 8.74	
	327642 327654	•	1.05	2.08	
	327734 327775		1.00 1.46	1.00 11.79	
25	327796		3.47 3.26	5.65	
	327796 327840 327940		3.26	6.64	
	327984	_	0.36	15.58 1.50	
20	327984 328004		5.84 0.36 1.87 0.42	1.42 0.59 4.68	
30	328021 328068		0.42 2.83	0.59 4.68	
	328100		3.04	5.39 5.20	
	328101 328113		3.54 0.72	5.20 0.91	
35	328157		5.58	5.16	
	328196		₋ 5.76	11.13	
	328197 328264		5.98 3.11	10.58 4.88	
40	328299		3.11 2.20	4.88 3.06	
40	· 328342 328365		1.49 1.00	1.94 1.00	
	328369		4.40	7.36	
	328381 328451		1.86	7.36 4.93 7.56 0.72	
45	328481		5.51 0.13	0.72	
	328500		2.71	3.97	
	328530 328600		5.41 3.14	7.62 10.68	
50	328608		4.56	8.17	
50	328616 328623		2.24 3.04	11.91 5.46	
	328632		0.70	1.19	
	328664 328668		3.48 10.42	6.80 26.47	•
55	328698		9.68	14.56	
	328700		2.74	10.22	•
	328708 328735		0.15 6.23	0.57 8.91	
60	328743 328806		3.62	6.54	
60	328806 328861		0.22 3.68	0.78 10.54	
	328908		5.42	16.36	
	328933 328934		2.02 1.73	5.29 4.45	
65	328949		3.34	5.41	
	329005 329011		2.88	7.26	
	329033	•	2.52 1.00	3.72 1.03	
70	329037		5.07	8.16 2.41 3.25 11.04	
70	329067 329134		1.98 2.24	2.41 3.25	
	329157		2.30	11.04	
	329178 329192		2.64 6.41	5.02 15.27	
75	329194		0.31	0.79	
	329204		1.60	3.75	
	329224 329228		2.99 0.83	6.11 0.83	
00	329288		0.63	0.83 1.01 1.00 1.68	
80	329337 329541		1.00 0.76	1.00 1.68	
	329560		1.34	2.02	
	329588		1.68	2.22	
85	329643 329703		4.1B 1.00	11.77 1.00	

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	329764				5.78	15.50
	329816			•	2.09	5.44
	329860				3.13	10.77
	329993				7.83	14.21
5	330020				5.58	13.12
•	330036				3.32	5.57
	330052				4.31	7.97
	330085				1.34	1.76
					4.70	12.46
10	330088				0.44	1.06
10	330093					
	330100				3.47	4.83
	330106				2.14	3.61
	330107				3.17	6.87
	330120				5.61	11.89
15	330123				4.50	12.74
	330208				1.55	7.62
	330263				13.10	23.38
	330300				2.81	4.98
	330313				3.00	4.41
20	330366				0.67	0.76
20	330372				4.76	11.82
	330385	A A 440740	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14	2.15
		AA449749			0.40	1.15
	330397	D14659	Hs.154387	KIAA0103 gene product		
25	330468	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia-telangiectasla group D-associated	1.67	1.17
	330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guarrine nucleotide binding protein (G pr	0.97	0.96
••	330506	M61906	Hs.6241	phospholnositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a cellular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244	110.20000	(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
33			Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330601	U90916				1.55
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
40	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
40	330630	X78669	Hs.79088	reficulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Wealdy similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AAD17045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	Integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
	330740	AA297746	Hs.22654	Homo saptens voltage-gated sodium channe	0.27	2.04
50					0.44	0.90
<i>5</i> 0	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying		3.23
	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	
	330751	AA428286	Hs.29643	Homo saplens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
	330763	AA450200	Hs.274337	hypothetical protein FLJ20666	0.37	0.97
55	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Wealdy similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
	330844	AA063037	Hs.66803	ESTs	0.93	1.16
60	330901	AA157818	Hs.267319	endogenous retroviral protease	1.02	1.03
	330931	F01443	Hs.284256	hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
	330968	H16568	Hs.23748	ESTs	0.48	0.96
65	331014	H98597	Hs.30340	hypothetical protein KIAA1165	0.29	0.74
05					0.99	8.56
	331046	N66563	Hs.191358	ESTS		
	331060	N75081	Hs.157148	Homo saplens cDNA FLJ11883 fis, clone HE	1.24	1.00
	331099	R36671	Hs.83937	hypothetical protein	0.75	1.03
70	331108	R41408	Hs.21983	ESTS	1.00	2.75
70	331131	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	6.04	10.68
	331135	R61398	Hs.4197	ESTs .	0.80	0.96
	331170	T23451	Hs.159293	ESTs	2.63	4.29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
	331183	T40769	Hs.8469	ESTs	1.00	3.01
75	331203	T82310		(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
		AA303125		Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
80	331341		Hs.23240		0.09	0.91
OV	331359	AA416979	Hs.46901	KIAA1462 protein		
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) horn	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
0.5	331402	AA505135	Hs.44037	ESTs	1.80	3.93
85	331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

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	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531 331547	N51343 N54811		gb:yz15g04.s1 Soares_mufliple_sclerosis_ gb:od74f04.s1 NCI_CGAP_Ov2 Homo saplens	0.98 3.80	1.68 5.75
	331578	N67960	Hs.249989	ESTs	0.11	0.67
5	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110 Hs.240272	PTD007 protein EST	0.93 0.17	0.76 1.34
	331614 331668	N92293 W69707	Hs.58030	EST	2.24	3.82
	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
10	331676	W79834	Hs.58559	ESTs, Wealthy similar to rhotekin [M.musc	0.08 8.72	1.07 4.27
	331681 331692	W85712 W93592	Hs.119571 Hs.152213	collagen, type III, alpha 1 (Ehlers-Danl wingless-type MMTV integration site fami	0.94	0.54
	331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
1.5	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811 331820	AA404500 AA405970	Hs.301570 Hs.97996	ESTs transcription termination factor, mitoc	1.10 0.73	1.00 0.59
	331831	AA412031	Hs.97901	EST	2.77	4.08
	331852	AA418988	Hs.98314	Homo saplens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
20	331943 331959	AA453418 AA460702	Hs.21275 Hs.82772	hypothetical protein FLJ11011 collagen, type XI, alpha 1	0.36 1.00	1.88 1.00
20	331990	AA478102	Hs.139631	ESTs	3.04	3.87
	332002	AA482009	Hs.105104	ESTs	1.19	0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073 ESTs	1.27 0.30	1.03 1.62
25	332029 332033	AA489697 AA489840	Hs.145053 Hs.251014	EST	2.30	3.70
	332048	AA496019	Hs.201591	ESTs	0.17	0.52
	332071	AA598594	Hs.205293	KIAA1211 protein gb:ae41e11.s1 Gessler Wilms tumor Homo s	1.35 0.19	1.23 2.00
	332074 332083	AA599012 AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.13	1.18
30	332085	AA600353	Hs.173933	nuclear factor I/A	0.30	1.50
	332125	AA609861	Hs.312447	ESTs	0.22 8.21	0.62 18.03
	332177 332180	F10812 H03348	Hs.101433 Hs.7327	ESTs claudin 1	2.27	1.57
	332185	H10356	Hs.101689	ESTs	0.09	1.18
35	332203	H49388	Hs.317769	EST	8.05	5.02
	332232 332240	N48891 N54803	Hs.101915 Hs.324267	Stargardt disease 3 (autosomal dominant) ESTs, Wealdy similar to putative p150 [0.78 0.96	0.85 1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidyl	0.27	0.75
40	332280 332299	R38100 R69250	Hs.146381 Hs.21201	RNA binding motif protein, X chromosome nectin 3; DKFZP566B0846 protein	0.39 5.24	1.88 12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71 0.43	0.88 0.86
45	332434 332445	N75542 T637B1	Hs.289068 Hs.11112	Homo sapiens cDNA FLJ11918 fis, clone HE ESTs	0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	tryptase beta 1	0.51 0.79	1.00 1.24
50	332504 332525	AA053917 M17252	Hs.15106 Hs.278430	chromosome 14 open reading frame 1 cytochrome P450, subfamily XXIA (steroid	0.73	1.70
••	332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22 0.93	1.46 1.49
	332539 332559	AA412528 M13955	Hs.20183 Hs.166189	ESTs, Wealdy similar to AF164793 1 prote cytokeratin 2	0.35	1.13
55	332563	N92924	Hs.274407	protease, serine, 16 (thymus)	1.00	1.00
	332565	AA234896	Hs.25272	E1A binding protein p300	0.36 0.53	1.05 0.59
	332594 332634	AA279313 S38953	Hs.3239 Hs.283750	methyl CpG binding protein 2 (Rett syndr tenascin XA	0.38	1.16
	332638	AA283034	Hs.50640	JAK binding protein	1.00	1.70
60	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	6.15	1.16
	332654 332665	AA001296 AA223335	Hs.288217 Hs.63788	hypothetical protein MGC2941 propionyl Coenzyme A carboxylase, beta p	1.50 1.20	2.73 0.91
•	332692	AA496035	Hs.247926	gap junction protein, alpha 5, 40kD (con	0.17	1.12
65	332716	L00058	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.00	1.44
65	332736 332758	L13773 X93921	Hs.114765 Hs.296938	myeloid/lymphoid or mixed-lineage leukem dual specificity phosphatase 7	1.00 0.53	1.81 0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ10902	1.44	1.56
	332792			•	1.70	1.19
70	332816 332858				1.85 1.04	2.47 1.57
70	332906				3.48	8.04
	332911				1.00	1.00
	332912 332922				1.06 1.00	4.40 1.00
75	332956				0.42	0.88
	332959				1.96	6.34
	332982 332984				0.56 0.30	0.99 0.78
	332984				1.47	2.01
80	333058				0.47	1.38
	333097				2.14 2.76	3.19 3.70
	333121 333122				1.92	1.21
0.5	333123				1.85	1.39
85	333138				0.47	0.52

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2420	188 084	

	WO 02/086443		
	333139	1.88	0.84
	333140	0.21	0.64
	333221	1.51 0.75	1.11 1.01
5	333260 333380	6.68	15.75
,	333387	4.56	12.61
•	333512	5.05	8.01
	333524	2.28	3.98
10	333585	2.31	1.53
10	333503	2.23	1.17
	333504	2.51 0.52	1.58 0.98
	333618	1.44	1.36
	333627 333628	1.90	1.90
15	333650	1.85	2.10
1.5	333678	1.85	2.35
	333750	2.18	5.67
	333763	1.99	2.60
20	333767	1.02	0.96
20	333768	1.78 2.15	1.65 2.13
	333769	1.46	253
	333772 333777	1.00	1.42
	333846	2.99	. 4.50
25	333884	0.47	0.94
	333887	0.50	1.00
	333891	0.43	0.89
	333892	0.51	0.91
20	333904	0.26	1.13
30	333906	0.55 1.70	0.98 2.15
	333948 333954	0.37	1.09
	333966	8.10	14.30
	333958	0.63	1.38
35	334061	4.24	12.30
	334094	1.30	12.03
	334113	4.55	8.63
	334161	0.82	1.59
40	334183	0.47	0.76
40	334187	1.36 0.69	3.70 1.04
	334219 334222	1.88	1.70
	334223	4.72	3.14
	334239	0.79	0.62
45	334255	0.45	1.10
	334333	1.00	3.56
	334378	3.98	5.76
	334382	1.50	1.31
50	334492	3.59 5.94	4.75 15.40
30	334562 334588	8.14	19.53
	334516	1.55	1.56
	334633 .	5.16	8.07
	334648	0.59	2.13
55	334787	3.70	7.15
	3348 66	8.13	10.60
	334891	0.32	1.14
	334933	1.00	3.84
60	334934 334945	4.01 1.04	7.43 2.96
00	***************************************		1.14
	334967 334990	0.29 1.50	1.39
	335015	5.88	18.65
	335093	0.55	1.75
65	335120	4.31	8.01
	335125	0.38	1.97
	335179	1.24	1.98
	335188	0.46 1.61	1.47
70	335211 335288	0.73	1.42 0.97
,,	335289	0.20	0.26
	335361	2.18	1.58
	335379	0.50	0.71
	335414	3.64	14.94
75	335416	2.93	3.98
	335496	0.96	0.91
	335497	1.71	1.92
	335548	1.15	2.40 10.54
80	335551 . 335558	3.22 3.42	4.89
00	335586	5.50	12.75
	335619	2.99	3.07
	335620	3.80	8.29
0.5	335621	0.28	0.57
85	335682	0.46	1.17

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	335686	2.55	3.81
	335755	2.24	1.07
	335784	0.20	0.97
-	335814	1.13	1.48
5	335815	2.45	3.51
	335823	1.00	4.16
	335835	0.49	1.70 1.39
	335851	1.66	1.39
10	335868	2.98	6.43 0.99
10	335896	0.98 12.10	21.93
	335936		1.64
	335948	1.00 1.00	4.21
	335983	0.37	1.17
15	335995	1.04	0.84
13	336021 336034	11.40	23.54
	33603B	1.19	1.21
	336065	0.54	1.63
	336107	0.95	0.70
20	336205	3.13	6.29
20	336275	3.20	6.29 10.10
	336292	2.34	3.09
	336331	1.00	1.00
	336419	0.65	0.79
25	336632	2.33	2.16
	336633	2.55	2.23 2.03
	336634	2.19	2.03
	336635	2.69	2.48
	336638	2.13	1.83 2.24
30	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60	1.31
	336675	0.31	1.18
25	336684	1.50	1.14
35	336694	4.74	7.10
	335716	4.43	6.37
	335721	2.20	0.74
	336798	1.64	2.14 12.73
40	336900	6.14	
40	336948	1.00 1.30	1.00 2.09
	337028	4.01	11.53
	337043	1.67	1.84
	337046	2.78	7.35
45	337054	7.20	16.14
43	337128	3.45	5.34
	337162	5.72	11.41
	337183	3.72	5.90
	337184 337192	1.27	1.06
50	337194	1.88	1.68
50	337229	0.22	1.03 3.31
	337268	1.00	3.31
	337299	3.23	5.14
	337325	2.76	3.72
55	337389	5.80	10.42
	337493	2.06	6.30
	337497	7.88	20.29
	337500	3.80	4.48
	337549	1.66	2.31
60	337603	1.27	8.54
	337605	5.76	7.16
	337671	0.73	0.97
	337755	1.54	0.92
	337786	5.07	9.73
65	337809	6.18	12.87
	337862	3.78	12.97
	337871	2.66	8.16
	337958	0.26	1.34
70	338008	1.48	1.12 14.59
70	338033	2.38	2 16
	338083	0.65 1.00	2.16 1.61
	338110	5.86	8.25
	338112	1.70	1.97
75	338145	8.07	18.19
13	338148	1.30	4.55
	338158 229164	2.58	3.57
	338161 270170	1.00	1.00
	338179 338182	3.32	1.00 4.63
80	338189	1.00	3.34
50	338197	0.99	1.69
	338199	4.58	7.62
	338215	6.01	15.85
_	338279	0.53	0.95
85	338316	20.58	38.66

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	338322	3.23	7.39	
	338357	4.10	11.39	
	338359	10.12	21.59	
	338366	0.69	1.02	
5	338374	0.40	1.18	
•	338414	0.47	1.06	
	338418	6.12	13.86	
	338469	3.09	5.11	
	338501	6.28	10.32	
10	338506	6.97	12.41	
	338523	3.10	5.84	
	338549	1.70	2.70	
	338561	0.79	0.81	
	338662	1.72	1.46	
15	338671	0.17	0.91	
	338676	2.10	15.86	
	338726	1.20	1.09	
	338779	0.12	0.57	
	338604	0.99	1.67	
20	338836	1.00	1.00	
	338871	4.30	9.81	
	338872 ·	5.02	12.81	
	338879	0.23	1.12	
	338937	6.55	12.26	
25	338966	1.76	5.42	
	338993	1.00	2.40	
	339047	5.26	10.81	
	339100	5.10	6.88	
	339114	1.00	1.70	
30	339121	1.00	3.75	
	339170	10.36	19.67	
	339229	4.08	13.48	
	339264	2.64	3.83	
~ ~	339293	1.73	1.94	
35				
	•			

TABLE 8B shows the accession numbers for those Pkeys in Table 8A ladding unigenelD's. For each probeset we have listed the gene cluster number from which the digonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oaldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey:		orcheset identifier number
		Gene cluster	number
4.5	Accession:	Genbank acc	ession numbers
45			
	Pkey	CAT number	Accessions
	322044	187363_1	AW340926 AA249063 N86075
	322060	44320_1	Al341937 AW003063 U34725 AA904742
50	321430	42705_1	X57414 X57415
	321467	43034_1	X13075 X13076
	322125	46779_1	R93901 AF075073 R93902
	322166	46861_1	H69434 AF085958 H69846
	322173	46873_1	H52567 H52557 AF085970 H52164
55	322178	46882_1	H56535 AF085980 H56712
	322179	46885_1	H92891 AF085982 H92777
	321577	1615102_1	H84849 H84252 H84260 H86664 H85320
	321587	1615333_1	H95531 H95521 H84529
	313723	111953_1	AA070412 AA102346 AA081885
60	320997	627492_1	H22544 H46842 Al204929
	322278	47271_1	W69304 AF086283 W69200
	321687	218439_1	AA625149 AA313030 AA313052 H97463
	313883	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765
	322320	47422_1	W79150 AF086419
65	322339	814584_1	AJ668646 AJ734214 W17348
	314648	293660_1	AW979268 AA878419 AA431342 AA431628
	300201	682222_1	Al308300 Al308296
	305897	251962	AJ093967
	323155		AL120701 AL135041 AL121524
70	322527	38927_1	AF147359 T58511 T58560
	322585	473768_2	W88919 W89125
	300362	1574395_1	Z42308 H23514
	322635		AA005129 AA679084 AA694399
	322664	85042_1	AA011522 AA702841 AA011691 AA330797
75	315454	380580_1	A1239464 A1239473 AA625812 A1208703
	322687		AF074666 Al110759 AF090902
	314852	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
	307783	697809_1	AJ347274 AW844024
00	324072		AA381722 AA381829 AW963906 AW963902 AA381242
80	300527		AA488472 W27363 AA317053 BE082689 AW967036 BE079872
	323505		AW970512 AA280251 Al652287 BE466438 Al650725 AA551854 AA281574 AW571481
	315791		AA678177 AA677034
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25	319611	1566863_1	H14957 R56522 R11908 BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131
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	306458	AA978186	
	306510	AA988546	
	306557 306572	AA994530 AA995686	•
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	306686	AI015615	
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	308154	AJ500600	
	306956	AJ125111	
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80	303999	AW516611	
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	305759 305792	AA845256	
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	305901	AA872958	
	305910	AA875981	
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13	307517	A1275055	
	307551	Al281556	
	307561 307608	Al282207 Al290295	
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	307764	Al342731	
25	307796	Al350556	
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	307807	Al351799	
	307808 307820	Al351826 Al355761	
30	307852	Al365541	
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	309164 309177	A)937761 A)951118	
25	307902	AJ380462	
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	309476	AW129368	
	309532	AW151119	
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	309799	AW276964	
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	309931 309933	AW341683 AW341936	
	302705	31765_1 U09060 U	
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	304026 304028	T03160 T03266	
	304046	T54803	
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	304456	AA411240	
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	304526 304607	AA476427 AA513322	
	304735	AA576453	
70	304760 306015	AA580401 AA897116	
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	306065 306104	AA906725	
	306109	AA910956 AA911861	
<i>75</i>	306242	AA932805	
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80	330599 331131	1532312 U90437	R54797
50	331203	genbank_R54797 NOT_FOUND_entrez	T82310
	331531	genbank_N51343	N51343
• -	331547 332074	467396_1 AA828597 genbank_AA599012	N54811 AA599012
85		J	

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TABLE 8C shows the genomic position for those Pikeys in Table 8A lacking uniquene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10	Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication sequence of human chromosome 22." Dunham L et al., Nature (1999) 402-489-495. Indicates DNA strand from which exons were predicted. NL position: Indicates nucleotide positions of predicted exons.						
	Pkey	Ref	•	Strand	Nt_position		
	322702	ο	aham I o	4 ~4	Phye	72391 72703	

10				prosent or pro-	
	Pkey	Ref	Strand	Nt_position	
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15	332906	Dunham,		Plus	1923101-1923205
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20	332959	Dunham,		Plus	2518145-2518213
. – –	333138	Dunham,		Plus	3369205-3369323
	333139	Dunham,	l. et.al.	Plus	3369495-3369571
	333221	Dunham,		Plus	3978070-3978187
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	333524	Dunham,		Plus	5612620-5612780
	333585	Dunham,		.Ptus	6234778-6234894
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	333650	Dunham,		Plus	6796852-6797128
	333678	Dunham,		Plus	7068223-7068288
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	333769	Ounham, i		Ptus	7696825-7696707
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6.7	333891	Dunham,		Plus	8156437-8156709
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	333948	Dunham, I		Plus	8583497-8583627
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	334094	Dunham, I		Plus	9889953-9890105
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	334378	Dunham, I		Plus	13907239-13907370
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5	336632 336633	Dunham, I. et.al. Dunham, I. et.al.	Ptus · Ptus	983890-985529 985591-986221
,	336634	Dunham, I. et.al.	Phis	986296-986670
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23	337755	Dunham, I. et.at.	Phus	3971764-3971900
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	338366	Dunham, I. et.al.	Plus	18252026-18252189
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	339047	Dunham, I. et.al.	Plus	30760793-30760968
	339100	Dunham, I. et.al.	Ptus	31141580-31141765
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	335755 335814	Dunham, Dunham,		Minus Minus	25763808-25763747 26320043-26319845
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	335835	Dunham,		Minus	26393311-26393245
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	335948 336066	Dunham, Dunham,		· Minus Minus	27555924-27555788 29241080-29240842
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25.	336275	Dunham,		Minus	32086675-32086536
25.	336292 336331	Dunham, Dunham,		Minus Minus	32818035-32817927 33594527-33594371
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. •	325340	6017033	Minus	166656-166	
	325373	5866920	Minus	1136686-1	
	325367 325389	5866920 5866921	Minus Ptus	922881-92 239672-23	
75	325436	5866939	Minus	29778-299	
	325498	5866967	Plus	173372-17	
	325471 325557	6017034 6056302	Minus Plus	289268-289 50921-510	
10	325559	6249595	Minus	118590-119	
30	325560	6249595	Minus	133794-133	3981
	325569 325587	6249599 6682462	Plus Plus	79927-8021	
	325585	6682462	Plus	126724-126 73476-7357	
35	325597	5866992	Plus	1065020-10	065089
,,	325639	5857002	Plus	253525-25	8008

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	325739	5867038	Minus	205138-205269
	325740	5867038 6469828	Minus	207533-207690
12	325792 325735	6552447	Minus Minus	1018-1176 269122-269190
5	325685	6682468	Plus	117397-117483
	325686 325819	6682468 6682490	Ptus Minus	118337-118439 130314-130370
	329764	6048195	Minus	109733-109968
10	329703	6065793	Minus	139994-140138
10	329643 329816	6448539 6624888	Ptus Minus	53403-53537 70296-70423
	329860	6687260	Minus	163474-163605
	325883	5867087	Plus	22498-22663
15	325895 325925	5867097 5867124	Ptus Ptus	358317-358476 115749-115962
	325932	5867127	Plus	7369-7441
	325941 325969	5867133 5867153	Minus Pkus	64228-64402 101911-102081
	325971	5867153	Plus	105841-106035
20	329993	4567166	Minus	101307-101434
	330020 326163	6671887 5867168	Plus Minus	172397-172491 7831-8035
	326274	5867171	Minus	410289-410404
25	326025	5867176	Plus	70854-70915
23	326046 326099	5867182 5867186	Minus Minus	62668-62825 661381-661510
	326108	5867187	Minus	23784-23903
	326165	5867208	Minus	62787-62929
30	326189 326204	5867212 5867218	Plus Minus	69288-69413 148088-148200
- •	326230	5867230	Minus	301868-301972
	330052 330036	4567182 6042048	Plus Plus	352560-352963 117120-117216
	326360	5867293	Phis	13527-13844
35	326589	5867320	Ptus	22760-22919
	326393 326505	5867341 5867435	Plus Minus	41702-41841 8818-8949
	326515	5867439	Plus	36683-36809
40	326592	6138928	Plus	23689-23828
70	330107 330106	6015249 6015249	Minus Minus	100091-100282 99443-99778
	330100	6015253	Plus	21166-21301
	330093 330088	6015278 6015293	Plus Plus	1043-1199 37517-37638
45	330085	6015302	Minus	59613-59770
	330120	6671864	Minus	127553-127656
	330123 326742	6671869 5867611	Minus Minus	35311-35406 95187-95248
50	326605	5867637	Plus	24656-24749
50	326818 326720	6117831 6552456	Minus Plus	15199-15309 84525-84677
	326770	6598307	Minus	513603-513668
	326692 326693	6682502 6682502	Plus	117697-117899 335002-335095
55	326983	5867657	Minus Minus	16023-16581
	326991	5867660	Plus	18147-18339
	326938 326964	6004446 6469836	Minus Plus	10217-10357 75340-75456
	327040	6531965	Plus	783670-783817
60	327053	6531965 6531965	Plus	2247267-2247437
	327075 327085	6531965	Plus Plus	4041318-4041431 4734947-4735069
	327036	6531965	Plus	319951-320040
65	327130 327158	6531976 5866841	Plus Minus	20247-22343 2462-2620
05	327288	5867481	Plus	48583-48773
	327332	5867516	Minus	56361-56532
	327220 327224	5867525 5867534	Minus Plus	65701-65781 188468-188544
70	327321	6249562	Minus	99745-99836
	327361 327396	6552412 5867743	Minus Plus	61013-62130 8702-8820
	327414	5867750	Plus	102461-102586
75	327442	5867759	Plus	111483-111618
75	327467 327473	5867772 5867775	Plus Plus	88030-88151 75101-75181
	327483	5867783	Plus	181573-181662
	327377	5867793	Minus	37610-37676
80	327562 327568	5857804 5857811	Minus Minus	343989-344474 46152-46287
	327606	6004463	Plus	200262-200495
	327611 327642	5867868 5867891	Minus Minus	175063-175392 2513-2743
0.5	327654	5867910	Minus	97564-97710
85	327734	5867940	Minus	31003-31583

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	327775	5867964	Minus	130791-130871
	327798	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
~	330208	6013599	Plus	66517-66931
5	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-60491
10	328157	5868064	Ptus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5858081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
15	327984	5868216	Plus	66611-66677
13	328021	5902482	Ptus	713478-714590
	328068 328264	6117819 6381912	Plus Plus	253903-254022
	330300	2905862	Minus	55086-55404 3246-3302
	328608	5868222	Minus	87770-87953
20	328600	5868229	Minus	38889-40010
20	328616	5868239	Pius	293920-294224
	328623	5868246	Minus	120020-120126
	328632	5868247	Phrs	76734-76853
	328666	5868254	Minus	778-901
25	328698	5868264	Minus	625555-625633
	328700	5868264	Plus	764089-764203
	328708	5868271	Minus	68114-68854
	328735	5868289	Plus	89389-89455
	328743	5868289	Plus	274838-274726
30	328806	5868324	Plus	29408-29684
	328299	5868366	Minus	149708-149889
	328342	5868383	Ptus	59955-60094
	328365	5868387	Minus	270724-270798
	328369	5858388	Plus	75371-75583
35	328381	5868392	Plus	662758-662848
	328451	5868425	Minus	217275-217336
	328481	5868449	Minus	8987-9180
	328500	5868464	Plus	59098-59481
40	328530	5868482	Plus	334973-335406
40	328664	6004473	Plus	1193739-1193866
	328861	6381928	Minus	108317-108403
	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
45	328934 328949	5868500 6456765	Plus Minus	846342-846448 43552-43619
7,7	330313	6042030	Minus	33642-33775
	329005	5868542	Pas	85470-85673
	330366	2944106	Plus	151837-151914
	330372	6580495	Minus	317461-317688
50	329033	5868561	Minus	5390-5479
20	329037	5868562	Minus	32468-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
	329157	5868687	Minus	145940-146155
55	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190
	329224	5868728	Plus	27422-27664
60	329228	5868728	Minus	50118-50287
	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

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TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granutomatous and carcinoid tumors) retailive to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's tacking UnigenalD's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucteotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pixey's tacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15 Pikey: ExAccn:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number Unigene Title:

R1:

10

Unigene gene title

Average of lung tumors (Including squamous cell carcinomas, edenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples

20

R2: Average of non-matignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples

		,,,,,,,	,5 6	, , , , , , , , , , , , , , , , , , , ,		
	Picey	ExAcon	UnigenelD	Unigene Title	R1	R2
	400195			NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
25	400205			NM_006265*:Horno sapiens RAD21 (S. pombe)	15.80	398.00
	400220			Eos Control	2.28	2.84
	400277			Eos Control	7.68	9.72
	400285			Eas Control	1.00	1.00
20	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
30	400289	X07820	Hs.2258	matrix metalioproteinase 10 (stromelysin	132.45	4.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
	400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
	400303	AA242758	Hs.79136	UV-1 protein, estrogen regulated	1.75	1.65
35	400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87 156.55	1.80 253.00
33	400419	AF084545		Target NM_030878*:Homo sapiens cytochrome P450,	1.00	200
	400512 400517	AF2423B8		lengsin	3.67	87.00
	400560	AF242356		NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
	400664			NM_002425:Homo saptens matrix metallopro	20.26	45.00
40	400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
70	400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
	400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
	400763			Target Exon	7.63	24.00
	401027			Target Exon	1.00	1.00
45	401093			C12000586*:gij6330167 dbj[BAA86477.1] (A	1.00	155.00
	401203			Target Exon	1.00	86.00
	401212			C12000457*:gi[7512178]pir][T30337 polypr	1.00	400.00
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
	401435			C14000397°:gi]7499898[pirl]T33295 hypoth	1.00	64.00
50	401464	AF039241		histone deacetylase 5	3.82	49.00
	401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
	401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
	401760			Target Exon	1.74	35.00
<i>E E</i>	401780			NM_005557*:Homo saplens keratin 16 (foca	26.47	10.50
55	401781			Target Exon	10.33	4.61
	401785			NM_002275°:Homo saplens keratin 15 (KRT1	4.13	2.70 2.10
	401797 401961			Target Exon	1.44 1.41	1.86
	401985	AF053004		NM_021626:Homo saplens serine carboxypep	1.00	177.00
60	401994	AF-033004		class I cylokine receptor Target Exon	61,84	47.00
00	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.58	1.39
	402265			Target Exon	2.09	35.00
	402297			Target Exon	1.00	92.00
65	402408			NM_030920°:Homo sapiens hypothetical pro	28.87	13.00
	402420			C1000823°:gi]10432400[emb]CAC10290.1] (A	1.00	1.44
	402674			Target Exon	7.44	243.00
	402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
70	402994			NM_002463*:Homo sapiens myxovirus (influ	1.37	1.43
70	403137			NM_005381*:Homo sapiens nucleolin (NCL),	1.00	19.00
	403306	NM_006825		transmembrane protein (63kD), endoplasmi	1.00	43.00
	403329			Target Exon	1.00	61.00
	403381			ENSP00000231844*:Ecotropic virus integra	1.00	119.00
75	403478			NM_022342:Homo sapiens kinesin protein 9	28.13 20.23	136.00 76.00
13	403485 403627			C3001813*:gi 12737279 ref XP_012163.1 k	6.30	29.33
	403027			Target Exon	1.30	35.00
	404044			Target Exon ENSP00000237855":DJ398G3.2 (NOVEL PROTE)	1.00	54.00
	404044			NIM_016020":Homo sapiens CGI-75 protein (14.29	91.00
80	404101			C8000950:gi[423560]pir[]A47318 RNA-bindi	1.00	1.00
-	404140			NM_006510:Homo saptens ret finger protei	1.42	1.44
	404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
	404185			Target Exon	1.00	117.00
	404210			NM_005936:Homo saplens myeloid/lymphoid	5.83	13.77
85	404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00
				· · · · · · · · · · · · · · · · · · ·		

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	404287	0 02/000		C6001909:pij704441)dbijBAA18909.11 (D298	29.71	42.00
	404298			C6001238":pi]121715 sp[P26697]GTA3_CHICK	1.30	1.00
	404347			Target Exon	1.00	1.00
5	404440 404721			NM_021048:Homo saptens melanoma antigen, NM_005596*:Homo saptens nuclear factor I	1.00 1.00	15.00 60.00
,	404721	NIM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
	404854			Target Exon	1.61	2.01
	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
10	404927 404996			Target Exon Target Exon	1.00 1.00	1.00 1.00
10	405449			CY000047::gi[11427234]ref[XP_009399.1] z	1.00	1.00
	405568			NM_031413":Homo sapiens cat eye syndrome	1.00	78.00
	405572			Terget Exon	0.76	1.14
15	405646 405676	BE336714		C12000200;gi[4557225[ref]NP_000005.1] al	1.01 1.13	1.28 2.89
13	405770	DE330/14		cytochrome c-1 NM_002362:Horno saptens metanoma antigen,	45.52	37.00
	405932			C15000305;gi]3806122(gb]AAC69198.1] (AF0	1.99	1.99
	406137			NM_000179 :Homo saptens mutS (E. coli) h	2.77	2.38
20	406360 406399			Target Exon	1.00 1.00	35.00 39.00
20	406467			NM_003122*:Homo sapiens serine protease Target Exon	1.00	1.00
	406621	X57809	Hs.181125	Immunoglobulin lambda locus	1.41	1.74
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
25	406663 406671	U24683 AA129547	Hs.293441	immunoglobulin heavy constant mu	2.07 15.00	2.93 51.00
23	406673	M34996	Hs.285754 Hs.198253	met proto-oncogene (hepatocyte growth fa major histocompatibility complex, class	0.98	3.09
	406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged im,	. 1.30	1.53
	406678	U77534		gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
30	406685	M18728	11- 070000	gb:Human nonspecific crossreacting antig	1.48	2.85 8.50
30	406687 406690	M31126 M29540	Hs.272822 Hs.220529	pregnancy specific beta-1-glycoprotein 9 carcinoembryonic antigen-related cell ad	8.61 226.37	350.00
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.01	2.52
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
35	406851	AA609784		major histocompatibility complex, class	0.75	1,91
33	406964 406967	M21305 M24349		gb:Human atpha satellite and satellite 3 gb:Human parathyroid hormone-like protei	38.15 1.00	1114.00 1.00
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312	Hs.237260	EST	1.00	1.00
70	407137 407168	T97307 R45175	Hs.117183	gb:ye53h05.s1 Soares fetal liver spleen ESTs	142.70 2.16	135.00 18.00
	407239	AA076350	Hs.67846	leukocyte immunoglobutin-like receptor,	1.10	1.57
	407242	M18728		gb:Human nonspecific crossreacting antig	1,12	2.85
45	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24 3.53	15.38
45	407289 407300	AA135159 AA102616	Hs.203349 Hs.120769	Homo sapiens cDNA FLJ12149 fis, clone MA gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	3.68 73.00
	407366	AF026942	Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	1.00	26.00
50	407430 407453	AF169351 AJ132087		gb:Homo sapiens protein tyrosine phospha gb:Homo sapiens mRNA for axonemal dynein	1.00 1.00	25.00 75.00
50	407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgtuc	111,20	228.00
	407710	AW022727	Hs.23616	ESTS	1.00	28.00
55	407720 407746	AB037776 AK001962	Hs.38002	KIAA1355 protein hypothetical protein FLJ11100	1.89 1.00	1.31 1.00
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	4.51	5.00
	407758	D50915	Hs.38365	KIAA0125 gene product	1.00	28.00
	407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
60	407788 407790	BE514982 Al027274	Hs.38991 Hs.288941	S100 catcium-binding protein A2 Homo sapiens cDNA FLJ14866 fis, clone PL	7.88 3.63	3.83 42.00
00	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144	Hs.161566	ESTs	173.91	108.00
	407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
65	408000 408031	L11690 AA081395	Hs.620 Hs.42173	bullous pemphigeld antigen 1 (230/240kD) Homo saniens cDNA FLJ10366 fis, clone NT	151.17 9.91	8.00 93.00
•••	408053	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	195.78	231.00
	408070	AW148852		gb:xf05d05.x1 NCI_CGAP_Bm35 Homo sapien	1.00	1.00
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
70	408122 408212	A1432652 AA297567	Hs.42824 Hs.43728	hypothetical protein FLJ10718 hypothetical protein	0.85 5.88	1.71 7.91
. •	408243	Y00787	Hs.624	interleukin 8	4.27	9.98
	408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
	408353 408354	BE439838 Al382803	Hs.44298	mitochondrial ribosomal protein \$17	1.88	1.65
75	408369	R38438	Hs.159235 Hs.182575	ESTs solute carrier family 15 (H??? transport	1.00 1.41	73.00 16.50
-	408380	AF123050	Hs.44532	diubiquilin	15.19	37.22
	408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24
80	408538 408545	AW381532 AW235405	Hs.135188 Hs.253690	ESTs ESTs	1.55 1.00	1.50 1.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1.00	44.00
	408633	AW963372	Hs.46677	PRO2000 protein	107.16	56.00
	408660	AA525775 AA057264	Hs.238936	ESTs, Moderately similar to PC4259 ferri	1.00	1.00
85	408761 408771	AW732573	Hs.47584	ESTs, Wealthy similar to (defiline not ava polassium voltage-gated channel, delayed	52.24 3.05	141.00 109.00
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	408783	AF192522	Hs.47701	NPC1 (Niemann-Pick disease, type C1, gen	1.02	1.07
	408790	AW580227	Hs.47860	neurotrophic lyrosine kinase, receptor,	41.19	61.00
	408805	H59912	Hs.48269	vaccinia related kinase 1	24.67	45.00
5	408841	AW438865	Hs.256862 Hs.182278	ESTS	1.00 1.00	58.00 89.00
,	408873 408908	AL046017 BE296227	Hs.250822	calmodulin 2 (phosphorylase kinase, dell serine/threonine kinase 15	7.76	1.00
	408992	AA059325	Hs.71642	guanine nucleotide binding protein (G pr	1.00	1.00
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) rumb	3.71	5.50
10	409015 409038	BE389387 T97490	Hs.49767 Hs.50002	NM_004553:Homo sapiens NADH dehydrogenas small inducible cytokine subfamily A (Cy	1.44 4.28	1.24 5.32
10	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	112.42	195.00
	409077	AA401369	Hs.190721	ESTs	1.00	17.00
	409093	BE243834	Hs.50441	CGI-04 protein	2.02	1.93
15	409103	AF251237	Hs.112208 Hs.50758	XAGE-1 protein SMC4 (structural maintenance of chromoso	80.44 14.87	40.00 6.00
13	409142 409187	AL136877 AF154830	Hs.50956	carbamoyi-phosphate synthetase 1, miloch	1.00	1.00
	409228	A1654298	Hs.271695	ESTs, Weakly similar to 2109260A B cell	1.22	1.00
	409234	A1879419	Hs.27206	ESTs	1.00	1.00
20	409268	AA625304	Hs.187579	ESTs	11.90 1.00	23.00 1.00
20	409269 409361	AA576953 NM_005982	Hs.22972 Hs.54416	hypothetical protein FLJ13352 sine oculis homeobox (Drosophila) homolo	168,91	35.00
	409404	BE220053	Hs.129056	ESTs	1.00	1.00
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	79.74	96.00
25	409430 409446	R21945	Hs.346735	splicing factor, arginine/sertne-rich 5	1.45	2.10 4.00
23	409506	AI561173 NM_006153	Hs.67688 Hs.54589	ESTs NCK adaptor protein 1	1.00 3.97	28.00
	409522	AA0753B2	120.00	gb:zm87b03.s1 Stratagene ovarian cancer	15.98	141.00
	409582	AA401369	Hs.190721	ESTs	1.00	17.00
30	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	292.12	79.00 82.00
30	409705 409719	M37762 AI769160	Hs.56023 Hs.108681	brain-derived neurotrophic factor Homo sapiens brain tumor associated prot	1.00 1.00	1.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	0.12	18.12
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	20.75	51.00
35	409757	NM_001898	Hs.123114	cystatin SN	22.46	15.80
33	409866 409893	AW502152 AW247090	Hs.57101	gb:UI-HF-BR0p-ajr-f-11-0-UI.r1 NIH_MGC_5 minichromosome maintenance deficient (S.	1.00 1.50	1.00 1.09
	409902	Al337658	Hs.156351	ESTs	25.92	50.00
	409935	AW511413	Hs.278025	ESTs	2.63	2.11
40	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.17 0.91	4.01 2.07
40	409958 410001	NM_001523 AB041036	Hs.57697 Hs.57771	hyaturonan synthase 1 kalikrein 11	1.04	2.28
	410032	BE065985	1.0.0	gb:RC3-BT0319-120200-014-a09 BT0319 Homo	1.00	58.00
	410037	AB020725	Hs.58009	KIAA0918 protein	1.00	34.00
45	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00 1.03	1.00 1.44
43	410048 410076	W76467 T05387	Hs.58218 Hs.7991	proline oxidase homolog ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo saplens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.00	1.00
50	410166 410193	AK001376 AJ132592	Hs.59346 Hs.59757	hypothetical protein FLJ10514 zinc finger protein 281	1.00 42.01	1.00 51.00
50	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.72	1.32
	410309	BE043077	Hs.278153	ESTs	1.00	2.00
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	32.08	75.00
55	410348 410407	AW182663 X66839	Hs.95469 Hs.63287	ESTs carbonic anhydrase IX	1.00 1.40	1.00 1.11
55	410418	D31382	Hs.63325	transmembrane protesse, serine 4	4.30	2.03
	410438	AB037756	Hs.45207	hypothetical protein KIAA1335	1.00	18.00
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.34	1.04
60	410555 410561	W27235 BE540255	Hs.6994	a disintegrin and metalloproteinase doma Homo sapiens cDNA: FLJ22044 fis, clone H	23.99 10.04	1.41 1.00
00	410681	AW246890	Hs.65425	calbindin 1, (28kD)	10.88	18.92
	410781	Al375672	Hs.165028	ESTs	1.00	57.00
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	1.62	3.78
65	411074 411089	X60435 AA456454	Hs.68137	adenylate cyclase activating polypeptide cell division cycle 2-like 1 (PITSLRE pr	1.00 1.56	1.15 1.58
05	411152	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	1.00	84.00
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.82	1.45
	411252	AB018549	Hs.69328	MD-2 protein	7.32	12.74
70	411263 411365	BE297802 M76477	Hs.69360 Hs.289082	kinesin-like 6 (mitotic centromere-assoc GM2 ganglioside activator protein	3.44 1.35	2.55 2.02
, ,	411402	BE297855	Hs.69855	NRAS-related gene	1.00	46.00
	411573	AB029000	Hs.70823	KIAA1077 protein	11.40	11.35
	411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	1.08	1.90
75	411617 411732	AA247994 AA059325	Hs.90063 Hs.71642	neurocalcin delta guanine nucleotide binding protein (G pr	1.74 1.02	2.57 1.00
	411773	NIM_006799	Hs.72026	protease, serine, 21 (testisin)	1.34	2.19
	411789	AF245505	Hs.72157	Adlican	2.19	2.79
	411800	N39342	Hs.103042	microtubule-associated protein 18	23.34	34.00
80	411945 412115	AL033527 AK001763	Hs.92137 Hs.73239	v-myc avian myelocytomatosis viral oncog hypothetical protein FLJ10901	1.00 2.07	8.00 1.64
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	118,48	92.00
	412276	BE262621	Hs.73798	macrophage migration inhibitory factor (1.98	1.49
	412464 412530	T78141 AA766268	Hs.22826	ESTs, Weathy similar to 155214 salivary hypothetical protein FLJ13346	1.16 41.52	1.34 84.00
85	412537	AL031778	Hs.266273	nuclear transcription factor Y, alpha	17,90	55.00

	W	O 02/086	443			
	412659	AW753865	Hs.74376	offactomedin related ER localized protei	14.65	47.00
	412719	AW015610	Hs.816	ESTs	382.46	128.00
	412723	AA648459	Hs.335951	hypothetical protain AF301222	54.90	1.00
	412811	H06382		ESTs	1.00	11.00
5	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
_	412863	AA121673	Hs.59757	zinc finger protein 281	17.63	56.00
	412924	BE018422	Hs.75258	H2A histone family, member Y	1.00	22.00
	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	2.19	2.05
	413011	AW068115	Hs.821	biglycan	1.22	1.88
10	413048	M93221 ·	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063	AL035737	Hs.75184	chifinase 3-like 1 (cartilage glycoprote	3.43	8.71
	413129	AF292100	Hs.104613	RP42 homolog	4.67	4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
	413223	AI732182 ·	Hs.191866	ESTs	5.73	27.00
15	413248	T64858	Hs.21433	hypothetical protein DKFZp547J036	0.99	1.06
13				stem-loop (histone) binding protein	1.00	18.00
	413273	U75679	Hs.75257			1.09
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10 95.94	
	413281	AA861271	Hs.222024	transcription factor BMAL2		69.00
20	413364	BE536218	Hs.137516	fidgetin-like 1	1.00	1.00
20	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.95	2.09
	413409	AJ638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTS	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08	1.46
25	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	79.15	114.00
25	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTs	1.00	1.00
	413690	BE157489		gb:RC1-HT0375-120200-011-e06 HT0375 Homo	1.00	1.00
20	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	3.16	2.32
30	413719	BE439580	Hs.75498	smail Inducible cytokine subfamily A (Oy	2.88	9.52
	413753	U17760	Hs.75517	taminin, beta 3 (nicein (125kD), kalinin	144.10	108.00
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	1.00	17.00
	413833	Z15005	Hs.75573	centromere protein E (312kD)	1.00	1.00
	413882	AA132973	Hs.184492	ESTs	64.24	148.00
35	413926	AA133338	Hs.54310	ESTs	1.00	67.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	43.42	42.00
	413995	BE048146	Hs.75671	syntaxin 1A (brain)	1.23	1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
40	414180	A1863304	Hs. 120905	Homo sapiens cDNA FLJ11448 fis, clone HE	6.92	77.00
	414245	BE148072	Hs.75850	WAS protein family, member 1	1.00⋅	1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	1.78	1.72
45	414341	D80004	Hs.75909	KIAA0182 protein	33,90	151.00
	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32	1.85
	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	226.15	66.00
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.64	1.98
50	414618	Al204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
-	414675	R79015	Hs.296281	Interleukin enhancer binding factor 1	1.51	1.39
	414583	S78296	Hs.76888	hypothetical protein MGC12702	43.61	64.00
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	28.63	71.00
	414711	A3310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
55	414718	H95348	Hs.107987	ESTs	1.00	5.00
55			Hs.77152		1.64	1.44
	414732	AW410976		minichromosome maintenance deficient (S.	65.01	74.00
	414747	U30872 AU077228	Hs.77204	centromere protein F (350/400kD, mitosin	130.35	121.00
	414761		Hs.77256 Hs.77274	enhancer of zeste (Drosophila) homolog 2	2.24	2.19
60	414774	X02419		plasminogen activator, urokinase	1.63	1.53
UU	414806	D14694	Hs.77329	phosphatidylserine synthase 1	1.97	2.60
	414809 414812	AM34699 X72755	Hs.77356 Hs.77367	transferrin receptor (p90, CD71) monokine induced by gamma interferon	3.48	10.60
					103.22	143.00
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	1.80	1.69
65	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	14.29	10.06
UJ	414883	AA926960	M. 77507	CDC28 protein kinase 1		
	414907	X90725	Hs.77597	poto (Drosophia)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telanglectasia and Rad3 related	3.00	2.90
	414945	BE076358	Hs.77667	tymphocyte antigen 6 complex, locus E	1.02	1.21
70	414972	BE263782	Hs.77695	KIAA0008 gene product	1.00	1.00
70	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	34.72	107.00
	415227	AW821113	Hs.72402	ESTs	1.87	49.00
75	415238	R37780	Hs.21422	ESTs	1.00	1.00
75	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450	Hs.6546	ESTs	1.00	1.00
	415339	NM_015156	Hs.78398	KIAA0071 protein	51.18	166.00
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase Inhibito	30.84	63.00
00	415674	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,	1.48	1.39
80	415709	AA649850	Hs.278558	ESTs	1.00	1.00
	415735	AA704162	Hs.120811	ESTs, Weakly similar to 138022 hypotheti	1.00	72.00
	415799	AA653718	Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78857	protein tyrosine phosphatase, receptor-t	24.30	1.00
0.5	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	32.51	35.00
85	415989	Al267700		ESTs	78.69	1.00

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	416018	AW138239	Hs.78977	proprotein convertase subilisin/kexin t	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (39.03	3.00
5	416177	AA174069	Hs.187607	ESTs	1.00	9.00
)	416178 416208	AI808527 AW291168	Hs.192822 Hs.41295	serologically defined breast cancer anti ESTs, Wealdy similar to MUC2_HUMAN MUCIN	3.83 3.67	3.76 1.00
	416209	AA236776	Hs.79078	MAD2 (miliotic arrest deficient, yeast, h	9.70	1.00
	416239	AL038450	Hs.48948	ESTs	83.87	129.00
10	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
10	416322	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	2.08	1.73
	416423	H54375	Hs.268921	ESTs	1.00	89.00
	416448	L13210	Hs.79339	lectin, galactoside-binding, solubla, 3	1.28	1.54
	416498 416658	U33632 U03272	Hs.79351 Hs.79432	potassium channel, subfamily K, member 1 fibrilin 2 (congenital contractural ara	27.29 53.29	67.00 51.00
15	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.96	5.00
	415722	AA354604	Hs.122546		3.68	33.00
	416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Wealdy similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.60962	neurolensin	1.00	1.00
20	417061 417079	A1675944 U65590	Hs.188691 Hs.81134	Homo sapiens cDNA FLJ12033 fis, clone HE	32.95 3.91	156.00 4.93
	417218	AA129547	Hs.285754	interleukin 1 receptor antagonist met proto-oncogene (hepatocyte growth fa	1.00	4.53 51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily 8 (Cy	3.38	2.05
	417308	H60720	Hs.81892	KIAA0101 gene product	82.94	25.36
25	417315	A1080042	Hs.180450	ribosomal protein S24	106.61	121.00
	417324	AW265494		ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornilin)	8.97 2.59	3.27
	417389 417428	BE260964 N87579	Hs.82045 Hs.278871	miditine (neurite growth-promoting factor gb:LL2030F Human fetal heart, Lambda ZAP	1.00	1.82 52.00
30	417433	8E270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	AI681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512	A1979168	. Hs.344096	glycoprotein (transmembrane) nmb	2.14	5.50
	417515	L24203	Hs.82237	ataxia-telanglectasia group D-associated	2.66	1.68
35	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
22	417576 417715	AA339449 AW969587	Hs.82285 Hs.86366	phosphoribosylglycinamide formyltransfer ESTs	42.76 6.35	51.00 2.75
	417720	AA205625	Hs.208067	ESTs	113.31	58.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	2.61	31.00
40	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.35	2.44
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.52	1.11
	417933 417944	X02308 AU077196	Hs.82962 Hs.82985	thymidylate synthetase	4.74 3.61	2.55 5.21
	417975	AA641836	Hs.30085	collagen, type V, alpha 2 hypothetical protein FLJ23186	12.49	38.00
45	417991	AA731452	Hs.190008	ESTs	1.00	26.00
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354	tysyl oxidase-like 2	2.85	2.63
50	418057 418113	NM_012151 AJ272141	Hs.83363	coagulation factor VIII-associated (intr	1.54	1.69 5.22
50	418140	BE613836 .	Hs.83484 Hs.83551	SRY (sex determining region Y)-box 4 microfibrillar-essociated protein 2	6.82 1.26	1.46
	418203	X54942	Hs.83758	CDC28 protein kinase 2	134.19	144.00
	418207	C14685	Hs.34772	ESTs	1.00	1.00
E E	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
55	418236	AW994005	Hs.337534	ESTS	18.53	147.00
	418249 418281	H89226 U09550	Hs.34892 Hs.1154	KIAA1323 protein oviductal glycoprotein 1, 120kD (mucin 9	30.53 1.00	105.00 3.00
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	3.96	5.16
	418300	A)433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
60	418322	AA284166	Hs.84113	cyclin-dependent kinase Inhibitor 3 (CDK	11.96	6.68
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	9.23	2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379 418397	AA218940 NM_001269	Hs.137516 Hs.84746	fidgetin-like 1 chromosome condensation 1	21.68 1.00	44.00 8.00
65	418403	D86978	Hs.84790	KIAA0225 protein	16.91	18.98
••	418462	BE001596	Hs.85266	Integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.66	2.22
70	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.04	2.21
70	418538 418543	BE244323 NM_005329	Hs.85951 Hs.85962	exportin, tRNA (nuclear export receptor	1.33	37.00 1.22
	418574	N28754	113.00302	hyaluronan synthase 3 M-phase phosphoprotein 9	1.04 48.60	1.23 85.00
	418592	X99226	Hs.284153	Fancorii anemia, complementation group A	18.24	26.00
	418641	BE243136	Hs.86947	a disinlegrin and metalloproteinase doma	1.19	1.41
75	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AX001100	Hs.41690	desmocollin 3	112.17	19.00
	418678	NM_001327	Hs.87225	cancerftestis antigen	1.18	1.10
	418686 418689	Z36830 Al360883	Hs.87268 Hs.274448	annexin A8 hypothetical protein FLJ11029	1.54 1.19	1.98 1.04
80	418712	Z42183	. ~~	gbcHSC0BF041 normalized infant brain cDN	1.00	12.00
	418727	AA227609	Hs.94834	ESTs	1.00	49.00
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	49.85	1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
85	418830 418882	BE513731 NM_004996	Hs.88959	hypothetical protein MGC4816 ATP-binding cassette, sub-family C (CFTR	20.97 57.00	23.00
-	71000K		Hs.89433	With Journal Contactor conversel of for 117	57.09	35.00

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	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973	AA233056	Hs.191518	ESTs	4.89	28.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	10.00
_	419079	AW014836	Hs.18844	ESTs	1.09	1.98
5	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06	1.68
_	419088	AI538323	Hs.52620	integrin, beta 8	15.60	51.00
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.11	1.83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10	1.14
10	419183	U60669	Hs.89663		1.00	1.00
10				cytochrome P450, subfamily XXIV (vitamin		
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW950146	Hs.284137	hypothetical protein FLJ12888	1.00	8.00
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	22.63	54.00
15	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703		gb:HUM316G10B Clontech human aorta polyA	1.00	12.00
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.64	1.84
	419474	AW968619	Hs.155849	ESTs	13.63	62.00
20	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
20	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.66	3.63
	419502	AU076704	110.00031		13.05	115.00
			Un nonco	fibrinogen, A alpha polypeptide		
	419539	AF070590	Hs.90869	Homo sapiens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
25	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	1.00	4.00
	419594	AA013051	Hs.91417	topolsomerase (DNA) Il binding protein	94.30	94.00
•	419703	AI793257	Hs.128151	ESTs ·	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00	191.00
	419729	AA586442	Hs.21411	gb:no53a03.s1 NCI_CGAP_SS1 Homo sapiens	1.00	59.00
30	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.02	1.08
- •	419745	AF042001	Hs.93005	stug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	29.87	77.00
	419839	U24577	Hs.93304	phosphotipase A2, group VII (platelet-ac	50.99	214.00
	419936	AI792788	. 10.0004	gb:of91d05.y5 NCI_CGAP_Kd5 Homo sapians	1.00	1.00
35			Hs.93836		1.64	2.47
55	419937	AB040959		DKFZP434N014 protein	15.72	94.00
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f		
	420005	AW271108	Hs.133294	ESTs	3.15	1.43
	420047	A1478658	Hs.94631	brefeldin A-Inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo saplens cDNA FLJ10561 fis, clone NT	1.00	117.00
40	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	1.43	1.21
	420251	AW374968	Hs.348112	Human DNA sequence from clone RP5-1103G7	2.35	3.23
	420259	AF004884	Hs.96253	catclum channel, voltage-dependent, P/Q	0.77	1.15
	420281	AI623693	Hs.323494	ESTs	45.04	54.00
	420309	AW043637	Hs.21766	ESTs, Wealthy similar to ALU5_HUMAN ALU S	49.22	31.00
45	420332	NM_001756	Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00	1.00
	420520	AK001978	Hs.98510	similar to rab11-binding protein	49.74	133.00
					94.65	88.00
50	420552	AK000492	Hs.98806	hypothetical protein		17.00
50	420560	AW207748	Hs.59115	ESTs	1.00	
	420610	AI683183	Hs.99348	distal-less homeo box 5	1.00	13.00
	420689	H 79 979	Hs.88578	ESTB	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
~ ~	420759	T11832	Hs,127797	Homo sapiens cDNA FLJ11381 fis, clone HE	1.00	48.00
55	420783	A1659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25
	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421002	AF116030	Hs.100932	transcription factor 17	1.00	27.00
	421027	AA761198	Hs.55254	ESTs	2.87	38.00
60	421037	AI684808	Hs.197653	ESTs	1.00	46.00
••	421041	N36914	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.00	98.00
	421073	NM_004689	Hs.101448	metastasis associated 1	1.34	1.46
	421110	AJ250717	Hs.1355	cathensin E	119.47	427.00
					1.10	17.00
65	421133	AA401369	Hs.190721	ESTs		
U.	421150	AI913562	Hs.189902	ESTs	1.45	1.63
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00
~~	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.92	3.94
70	421451	AA291377	Hs.50831	ESTs	5.89	14.00
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56	1.08
	421508	NM_004833	Hs.105115	absent in melanoma 2	5.11	5.23
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyttransferase I, I	1.00	3.00
75	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP56400823 protein	1.46	1.88
	421552	AF026692	Hs.105700	secreted fritzled-related protein 4	30.21	50.32
					1.67	1.74
	421574	AJ000152	Hs.105924	defensin, beta 2		
80	421582	AI910275	LL 400000	trefoli factor 1 (breast cancer, estroge	1.23	1.00
OU	421633	AF121860	Hs.106260	sorting nexts 10	1.00	116.00
	421659	NM_014459	Hs.106511	protocadherin 17	0.05	6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	8E314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41	1.20
0.5	421773	W69233	Hs.112457	ESTs	1.12	1.14
85	421777	BE562088	Hs.108196	HSPC037 protein	1.97	1.29
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	421800	AA298151	Hs.222969	ESTs	1.03	1.30
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (OFTR	1.88	1.59
	421896	N62293	Hs.45107	ESTs	11.84	22.80
5	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	45.89	90.00
5	421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	1.13	1.49
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421975 422026	AW961017	Hs.6459	hypothetical protein FLJ11856	1.17 1.00	1.15 52.00
	422020	U80736 AF129535	Hs.110826 Hs.272027	trinucleofide repeat containing 9 F-box only protein 5	67.61	62.00
10	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
**	422109	S73265	Hs.1473	gastrin-releasing peptide	4.18	95.50
	422128	AW881145		gb:QV0-OT0033-010400-182-a07 OT0033 Homo	40.89	71.00
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.13	1.38
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	41.59	96.00
15	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.29	1.68
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.93	5.73
	422282	AF019225	Hs.114309	apolipoprotein L	1.49	1.71
20	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	25.99	10.91
20	422310	AA316622	Hs.98370	cylochrome P450, subfamily IIS, polypept	1.54	1.41
	422311 422330	AF073515 D30783	Hs.114948 Hs.115263	cytokine receptor-like factor 1 epiregulin	1.15 1.00	1.78 112.00
	422354	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	9.39	60.00
	422406	AF025441	Hs.116206	Opa-interacting protein 5	18.33	53.00
25	422424	AI186431	Hs.295638	prostate differentiation factor	1.71	3.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	422487.	AJ010901	Hs.198267	mucin 4, tracheobronchial	73.68	35.54
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	173.97	26.00
20	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.68	2.92
30	422656	AI870435	Hs.1569	LIM homeobox protein 2	1.00	1.00
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Dani	3.89	4.55
•	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	1.05	1.46
	422765 422809	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur hypothetical protein FLJ10549	3.88 99.56	1.53 53.00
35	422867	AK001379 L32137	Hs.121028 Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
55	422938	NM_001809	Hs.1594	centromere protein A (17kD)	70.46	61.00
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	77.74	3.00
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	5.88	8.55
	422963	AA401369	Hs.190721	ESTs	171.41	17.00
40	422976	AU076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	2.12	1.62
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	10.49	35.00
	422986	AA319777	Hs.221974	ESTS	12.40	32.47
	423034 423049	AL119930	U= 400000	gb:DKFZp761A092_r1 761 (synonym: hamy2)	16.41	60.00
45	423049	X59373 AF262992	Hs.188023 Hs.123159	ESTs, Moderately similar to HXDA_HUMAN H sperm associated antigen 4	1.00 1.82	1.00 2.96
	423184	NM_004428	Hs.1624	ephrin-A1	1.14	1.53
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.14	1.69
	423248	AA380177	Hs.125845	ributose-5-phosphate-3-epimerase	7.18	14.00
50	423309	BE006775	Hs.126782	sushi-repeat protein	21.90	64.00
50	423361	AW170055	Hs.47628	EST8	1.00	1.00
	423453 423511	AW450737	Hs.128791	CGI-09 protein	55.52 0.88	66.00
	423518	AF036329 AB007933	Hs.129715 Hs.129729	gonadotropin-releasing hormone 2 ligand of neuronal nitric oxide synthase	1.76	1.17 5.40
	423551	AA327598	Hs.233785	ESTs	3.54	4.33
55	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	38.88	70.00
	423624	AI807408	Hs.166368	EST ₈	1.00	67.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
60	423642	AW452650	Hs.157148	hypothetical protein MGC13204	19.14	58.00
60	423562	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	3.61	13.57
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	240.73	40.00
	423698 423725	AA329796 AJ403108	Hs.1098 Hs.132127	DKFZp434J1813 protein hypothetical protein LOC57822	1.00 4.20	59.00 1.00
	423761	NM_006194	Hs.132576	paired box gene 9	1.00	1.00
65	423787	AJ295745	Hs.236204	nuclear pore complex protein	7.18	6.64
•	423816	AF151064		hypothelical protein	1.00	44.00
	423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	1.00	1.00
	423849	AL157425	Hs.133315	Homo saplens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
70	423887	AL080207	Hs.134585	DKFZP434G232 protein	1.00	1.00
70	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	31.33	31.00
	423954	AW753164	Hs.288604	KIAA1632 protein	5.81	10.87
	423961	D13666	Hs.135348	osteoblast specific factor 2 (fasciclin	3.55 233.42	3.30
	424012 424016	AW368377 AW163729	Hs.137569 Hs.6140	turnor protein 63 kDa with strong homolog hypothetical protein MGC15730	233.42 0.93	68.00 1.01
75	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	21.30	52.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424085	Al351010	Hs.102267	lysyl oxidase	21.91	70.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
00	424120	T80579	Hs.290270	EST8	1.00	1.00
80	424165	AW582904	Hs.142255	islet emyloid polypeptide	1.00	34.00
	424200	AA337221		gb:EST41944 Endometrial tumor Homo saple	13.06	48.00
	424279	L29306	Hs.171814	tryptophan hydroxylase (tryptophan 5-mon	1.00	1.00
	424308 424326	AW975531	Hs.154443	minichromosome maintenance deficient (S.	164.58 53.72	87.00 302.00
85	424320 424340	NM_014479 AA339036	Hs.145296 Hs.7033	disintegrin protease ESTs	53.72 0.88	1.15
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	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364	AW383226	Hs.201189	ESTs, Wealthy similar to G01763 atrophin-	7.02	3.24
	424381	AA285249	Hs.145329	protein kinase Chk2	95.55	92.00
_	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
5	424420	BE614743	Hs.145688	prostaglandin E synthase	1.63	1.33
	424441	X14850	Hs.147097	H2A histone family, member X	1.82	1.29
	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424503	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	milochondrial translational initiation f	1.00	17.00
10	424539	1.02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	32.46	108.00
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.40	2.58
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
15	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
15	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.12	2.23
	424717	AW992292	Hs.152213	wingless-type MMTV integration site fami	1.00	1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.65	1.30
20	424867	AI024860	Hs.153591	Not56 (D. melanogaster)-like protein	1.23	1.05
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Homo	1.24	1.41
	425048	H05468	Hs.164502	ESTs	1.00	11.00
25	425057	AA826434	Hs.1619	achaete-scute complex (Drosophila) homol	7.46	87.00
25	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159	NM_004341	Hs.154868	carbamoyl-phosphale synthetase 2, aspart	3.62	2.73
	425202	AW962282	Hs.152049	ESTs, Wealdy similar to 138022 hypotheti	1.00	53.00
20	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	100.77	44.00
30	425236	AW057800	Hs.155223	stanniocalcin 2	3.30	2.90
	425245	AJ751768	Hs.155314	KIAA0095 gene product	1.91	2.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.41	1.49
	425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
25	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	1.97	1.63
35	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49	123.00
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	1.00	84.00
	425371	D49441	Hs.155981	mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00
40	425424	NM_004954	Hs.157199	ELKL motif kinase	10.58	9.74
	425483	AF231022	Hs.158159	FAT turnor suppressor (Drosophila) homolo	1.74	1.40
	425568	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29	233.00
45	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
45	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	1.00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00	41.00
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	1.00	48.00
50	425810	AI923627	Hs.31903	ESTs	27.39	98.00
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	A1077288	Hs.296323	serum/glucocorticoid regulated kinase	71.16	3.42
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.35	1.34
	426067	AA401369	Hs.190721	EST ₅	1.01	17.00
55	426088	AF038007	Hs.166195	ATPase, Class I, type BB, member 1	26.26	47.00
23	426215	AW067800	Hs.155223	stanniocaicin 2	1.91	2.90
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	22.40	25.00
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp556A1046 (f	1.00	1.00 229.00
	426283	NM_003937 AL389951	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39 4.34	4.08
60	426329	M86699	Hs.271623	nucleoparin 50kD	7.02	1.00
00	426427 426432	AF001601	Hs.169840 Hs.169857	TTK protein kinase paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459	AF151812	Hs.169992	hypothetical 43.2 Kd protein	1.56	1.66
	426471	M22440	Hs.170009	transforming growth factor, alpha	20.60	26.00
65	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
05	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	103.74	41.00
	426536	AI949749	Hs.44441	ESTs	4.65	23.00
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
70	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
. •	426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1	1.51	1.35
	426746	J03626	Hs.2057	undine monophosphate synthetase (orotat	2.13	1.68
	426752	X69490	Hs,172004	tiin	0.02	5.14
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.72	1.71
75 .	425807	AA385315	Hs.156682	ESTs	1.30	1.64
	426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	1.47	1.53
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosylhomocysteine hydrolase	1.51	1.25
	426897	AA401369	Hs.190721	ESTs	141.56	17.00
80	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	32.61	38.00
	426935	880000_MIN	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966	Al493134		sclerostin	1.00	1.00
_	426991	AK001536		Homo saplens cDNA FLJ 10574 fis, clone NT	3.39	2.28
85	427099	AB032953	Hs,173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
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	427239	O 02/086 BE270447	44.5 Hs.174070	ubiquitin carrier protein	1.58	1.05
	427260	AA663848	110.11.10.0	gb:ae70b06.s1 Stratagene schizo brain S1	1.34	1.60
	427281	AA906147	Hs.102869	ESTs .	1.00	66.00
5	427335	AA448542	Hs.251677	G antigen 78	51.83 1.17	4.00 1.95
J	427354 427356	T57896 AVVD23482	Hs.191095 Hs.97849	ESTs ESTs	7.31	41.00
	427376	AA401533	Hs.19440	ESTs	1.00	57.00
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.42	1.32
10	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00 1.00	20.00 1.00
10	427441 427445	AA412605 X80818	Hs.343879 Hs.178078	SPANX family, member C glutamate receptor, metabotropic 4	0.97	1.03
	427505	AA361562	Hs.178761	26S proteasome-associated pad1 homolog	4.60	4.04
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
15	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S. hypothetical protein FLJ23188	97,45 1.50	92.00 3.24
13	427546 427562	AA188763 R56424	Hs.36793 Hs.26534	ESTs	6.81	40.00
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	Al741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666 427668	AI791495	Hs.180142 Hs.180191	calmodulin-like skin protein hypothetical protein FLJ14904	1.37 29.55	1.88 67.00
20	427677	AA298760 NM_007045	Hs.180295	FGFR1 oncogene partner	3.52	2.63
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
25	427719	AI393122	Hs.134726 Hs.180479	ESTs hypothetical protein FLJ20116	7.03 2.92	4.52 1.74
23	427722 427747	AK000123 AW411425	Hs.180655	serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfamil	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97	118.00
30	428004 428023	AA449563 AL038843	Hs.151393	glutamate-cysteine ligase, catalytic sub Homo sapiens cDNA: FLJ23602 fis, clone L	23.82 1,40	1.00 1.33
50	428046	AW812795	Hs.337534	ESTs, Moderately similar to 138022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429	protein disulfide isomerase-related prot	1.86	1.60 42.00
35	428129 428169	Al244311 Al928984	Hs.26912 Hs.182793	ESTs golgi phosphoprotein 2	1.00 2.76	2.11
55	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	85.59	181.00
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	8.57 7.77	21.64 15.90
40	428330 428434	L22524 Al909935	Hs.2256 Hs.65551	matrix metalloproteinase 7 (matrilysin, Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53	204.00
	428471	X57348	Hs.184510	stratifin	6.00	4.60
	428479 428484	Y00272 AF104032	Hs.334562 Hs.184601	cell division cycle 2, G1 to S and G2 to solute carrier family 7 (cationic amino	56.54 3.53	16.00 2.15
45	428505	AL035461	Hs.2281	chromogranin 8 (secretogranin 1)	1.00	1.00
	428532	AF157326	Hs.184786	TBP-interacting protein	1.00	58.00
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00 1.00
	428664 428698	AK001666 AA852773	Hs.189095 Hs.334838	similar to SALL1 (sal (Drosophila)-like KIAA1866 protein	1.00 187.37	255.00
50	428728	NM_016625	Hs.191381	hypothetical protein	47.24	80.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
	428758 428771	AA433988 AB028992	Hs.98502	hypothetical protein FLJ14303 KIAA1069 protein	1.06 1.98	1.13 92.00
	428771	ABUZ0392 AW277121	Hs.193143 Hs.254881	ESTs	1.67	6.15
55	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	1.03	1.27
	428839	A1767756	Hs.82302	Homo sepiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845 428959	AL157579 AF100779	Hs.153610 Hs.194680	KIAA0751 gene product WNT1 inducible signaling pathway protein	1.00 15.16	1.00 27.00
	428989	AF120274	Hs.194689	arternin	1.36	1.24
60	429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065 429164	A1753247 A1688663	Hs.29643 Hs.116586	Homo sapiens cDNA FLJ13103 fis, clone NT ESTs	6.82 19.08	16.47 67.00
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
65	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211 429220	AF052693 AW207206	Hs.198249	gap junction protein, bela 5 (connexin 3 ESTs	1.33 1.00	1.09 7.00
	429228	AI553633	Hs.326447	ESTs	39.47	29.25
70	429259	AA420450	Hs.292911	ESTs, Highty similar to S60712 band-6-pr	2.01	1.18
70	429263 429276	AA019004	Hs.198396 Hs.198612	ATP-binding cassette, sub-family A (ABC1 G protein-coupled receptor 51	1.07 3.70	1.00 142.00
	429359	AF056085 W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
75	429413	NM_014058	Hs.201877	DESC1 protein	41.91	10.00
75	429486 429504	AF155827 X99133	Hs.203963 Hs.204238	hypothetical protein FLJ10339 lipocalin 2 (oncogene 24p3)	12.19 1.61	1.00 1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
80	429551 429563	AW450624 BE619413	Hs.220931 Hs.2437	ESTs eukaryotic translation initiation factor	2.89 1.49	65.00 1.37
50	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.78	1.74
85	429616 429656	A1982722 X05608	Hs.120845 Hs.211584	ESTs neurofilament, light polypeptide (68kD)	1.00 1.00	1.00 4.00
	123000	,	10.611004	more description of all in book backers forces		

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	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfami	1.25	1.21
	429782	NIM_005754	Hs.220689	Ras-GTP ase-activating protein SH3-domain	1.00	7.00
5	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		1.00
3	429918 429978	AW873986 AA249027	Hs.119383	ESTs ribosomal protein S6	1.00 1.98	78.00 3.09
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	1.00	48.00
	430044	AA464510	Hs.152812	ESTs	69.27	59.00
• •	430114	AA847744	Hs.99640	ESTs	1.00	1.00
10	430134	BE380149	Hs.105223	ESTs, Wealty similar to T33188 hypotheti	1.00	51.00
	430147	R60704	Hs.234434	hairylenhancer-of-split related with YRP	1.10	2.22
	430287 430294	AW182459 AI538226	Hs.125759 Hs.32976	ESTs, Wealthy similar to LEU5_HUMAN LEUKE guanine nucleotide binding protein 4	1.00 3.80	127.00 1.47
	430300	U60805	Hs.238648	oncostatin M receptor	1.00	35.00
15	430315	NM_004293	Hs.239147	guarine dearninase	92.31	28.00
	430337	M35707	Hs.239600	calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76	38.00
20	430393 430439	BE185030 AL133561	Hs.241305	estrogen-responsive B box protein DKFZP434B061 protein	1.63 1.00	1.50 1.00
20	430451	AAB36472	Hs.297939	calhepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs	63.35	44.00
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.47	1.91
25	430481	AA479578	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28 4.75	41.00
	430508 430533	Al015435 AA480895	Hs.104637 Hs.57749	ESTs ESTs, Weathy similar to T17288 hypotheti	1.00	7.27 1.00
	430563	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.00	1.59
	430577	Z26317	Hs.94560	desmoglein 2	1.72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686	NM_001942	Hs.2633	desmogtein 1	1.00	1.00
	430788	A1742925	Hs.7179	ESTs, Weakly similar to 2004399A chromos	1.62	1.84
	430890 430935	X54232 AW072916	Hs.2699	glypican 1 zinc finger protein 131 (ctone pHZ-10)	1.58 90.28	1.40 132.00
35	430985	AA490232	Hs.27323	ESTs, Weakly similar to 178885 serine/th	0.94	1.28
-	431009	BE149762	Hs.48956	gap Junction protein, beta 6 (connexin 3	60.25	28.00
	431089	BE041395		ESTs, Wealdy similar to unknown protein	23.32	941.00
	431092	Al332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio	49.43 0.44	62.00 2.20
40	431164 431211	AA493650 M86849	Hs.94367 Hs.323733	Homo sapiens cDNA: FLJ23494 fis, clone L gap lunction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345B24	ESTs	1.00	86.00
45	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	40.55	200.00
45	431342	AW971018	Hs.21659	ESTS	1.00	53.00
	431384	BE158000	Hs.285026 Hs.256311	gb:MR2-HT0377-150200-202-e03 HT0377 Homo granin-like neuroendoorine peptide precu	0.94 1.30	1.14 1.25
	431462 431494	AW583672 AA991355	Hs.298312	hypothetical protein DKFZp434A1315	3.90	26.00
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
50	431548	AI834273	Hs.9711	novel protein	5.66	15.00
	431630	NM_002204	Hs.265829	integrin, aipha 3 (antigen CD49C, aipha	0.99	1.44
	431745	AW972448 BE221880	Hs.163425	ESTs 5-3' exoribonuclease 2	0.99 67.12	3.51 91.00
	431770 431830	Y16645	Hs.268555 Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
55	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.20	3.32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629 Al 137382	Hs.2877 Hs.272320	cadherin 3, type 1, P-cadherin (placenta	51.17 0.94	46.35 1.65
60	432006 432023	R43020	Hs.272320 Hs.236223	Homo saplens mRNA; cDNA DKFZp434L1226 (f EST	0.94	47.00
00	432201	Al538613	Hs.298241	Transmembrane protease, serine 3	1.10	2,24
	432210	Al567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42	1.45
	432226	AW182766	Hs.273558	phosphate cylidylyltransferase 1, cholin	1.00	1.00
65	432239	XB1334	Hs.2936	matrix metalloproteinase 13 (collagenase	18.67	1.00
03	432265	BE382679 AK001239	Hs.285753 Hs.274263	SCG10-like-protein hypothetical protein FLJ10377	1.09 40.98	1.21 58.00
	432281 432365	AK001239 AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	214.00
	432374	W68815	Hs.301885	Homo saplens cDNA FLJ11346 fis, clone PL	157.34	37.00
5 0	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
70	432407	AA221036		gb:zr03f12_r1 Stratagene NT2 neuronal pr	73.71	75.00
	432441	AW292425	Hs.163484	ESTs	56.35	72.00
	432489 432543	A1804855 AA552690	Hs.207530 Hs.152423	ESTs Homo szoiens cDNA; FLJ21274 fis, clone C	1.00 137.72	24.00 98.00
	432552	Al537170	Hs.173725	ESTs, Weakly similar to ALUS_HUMAN ALU S	1.00	31.00
75	432583	AW023524	Hs.162282	potassium channel TASK-4; potassium chan	0.27	35.18
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.87	6.22
	432625	A1243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.53	56.00
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	1.92	5.29 48.00
80	432677 432715	NM_004482 AA247152	Hs.278611 Hs.200483	UDP-N-acetyl-alpha-D-galactosamine:polyp ESTs, Wealdy similar to KIAA1074 protein	1.00 45.13	31.00
	432753	NM_014075	Hs.336938	Homo septens PRO0593 mRNA, complete ods	1.00	68.00
	432788	AA521091	Hs.178499	Homo sapiens cDNA: FLJ23117 fis, clone L	2.69	3.67
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.22	1.34
85	432867	AW016936	Hs.233354	ESTs PRO0327 protein	1.00 10.25	1.00 6.62
33	432917	NM_014125	Hs.241517	· · · · · · · · · · · · · · · · · · ·	14.23	war.

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	432920	U37689	Hs.3128	polymerase (RNA) II (DNA directed) polyp	1.44	1.30
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	154.79	85.64
	433023	AW864793	Hs.87409	thrombospondin 1	20.96	100.00
5	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
3	433091 433159	Y12642 AB035898	Hs.3185 Hs.150587	lymphocyte antigen 6 complex, locus D kinesin-like protein 2	1.20 13.82	1.09 39.00
	433183	AF231338	Hs.222024	transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
10	433409	A1278802	Hs.25661	ESTs	44.81	117.00
10	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	70.39	105.00
	433485	A1493076	Hs.201967	aldo-keto reductase family 1, member C2	11.55	2.00 55.00
	433537 433547	A1733692 W04978	Hs.112488 Hs.303023	ESTs beta tubulin 1, class VI	8.65 25.16	83.00
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	1.00	19.00
15	433647	AA603367	Hs.222294	ESTs	20.30	49.00
	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	tung type-I cell membrane-associated gly	2.29	2.22
	433819	AW511097 D86960	Hs.112765 Hs.3610	ESTs	3.71 62.08	8.00 104.00
20	433862 433980	AA137152	Hs.286049	KIAA0205 gene product phosphoserine aminotransferase	108.91	47.00
	434088	AF116577	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	121.27	87.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.22	1.23
25	434217	AW014795	Hs.23349	ESTs	14.11 2.10	57.00
23	434340 434360	Al193043 AA401369	Hs.128685 Hs.190721	ESTs, Weakly similar to T17226 hypotheti ESTs	40.98	2.56 17.00
	434414	Al798376	113.130121	gb:tr34b07.x1 NCI_CGAP_Ov23 Homo saplens	1,48	1.56
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
20	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	54.91	85.00
30	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.46	2.00
	434627 434699	A1221894 AA643687	Hs.39311 Hs.149425	ESTs Horno sapiens cDNA FLJ11980 fis, clone HE	1.00 1.00	1.00 23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	11.33	1.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1.00	1.00
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	1.25 1.00	1.29 6.00
	434891 434928	AAB14309 AW015595	Hs.123583 Hs.4267	ESTs Homo sapiens clones 24714 and 24715 mRNA	1.00	1.00
40	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69	1.37
	435087	AW975241	Hs.23567	ESTs	1.00	1.00
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.90	1.93
45	435159 435205	AA568879 X54135	Hs.116649 Hs.181125	ESTs immunoglobulin tambda tocus	1.00 1.02	1.00 1.46
73	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	2.04	2.70
	435304	H10709	Hs.269524	ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	interlaukin-1 homolog 1	1.00	38.00
50	435509 435525	AJ458679 AJ831297	Hs.181915 Hs.123310	ESTs ESTs	1.00 1.00	1.00 56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AL224456	Hs.324507	H.sapiens polyA site DNA	3.42	3.92
<i></i>	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	3.95	1.80
55	435766	R11673	Hs.186498	ESTs	1.00	28.00
	435793 436069	AB037734 Al056879	Hs.4993 Hs.263209	KIAA1313 protein ESTs	23.68 1.00	42.00 58.00
	436170	AW450381	Hs.14529	ESTs	1.00	18.00
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.84	22.00
60	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	435217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
	436238 436251	AK002163 BE515065	Hs.301724 Hs.296585	hypothetical protein FLJ11301 nucleolar protein (KKE/O repeat)	2.51 2.33	1.71 1.64
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
65	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	0.75	2.81
	436396	AW992292	Hs.152213	wingless-type MMTV Integration site famil	60.01	1.00
	436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419 436443	Al948626 AW138211	Hs.171356 Hs.128746	ESTs ·	0.95 1.12	1.33 9.26
70	436474	AJ270693	Hs.199887	ESTs	1.00	1.00
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120533	ESTs	1.00	19.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
75	436553 436557	X57809 W15573	Hs.181125 Hs.5027	immunoglobulin lambda locus ESTs, Weakly similar to A47582 B-cell gr	1.08 19.20	1.74 9.75
, ,	436608	AA628980	, 2000	down syndrome critical region protein DS	33.92	25.00
	436667	AW025183	Hs.127680	ESTs	0.89	1.19
	436771	AW975687	Hs.292979	ESTs	1.00	10.00
90	436839	AA401369	Hs.190721	ESTs	1.00	17.00
80	436887 436944	AW953157 AW268614	Hs.193235 Hs.5840	hypothetical protein DKFZp547D155	1.06 1.00	1.15 1.00
	436961	AW375974	Hs.156704	ESTs ESTs	25.13	25.00
	436972	AA284579	Hs.25640	claudin 3	1.59	1.46
05	437016	AU076916	Hs.5398	guanine monphosphate synthetase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

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	437181	Al306615	Hs.125343	ESTs, Wealthy similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to 155214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
_	437259	A1377755	Hs.120695	ESTs	1.00	205.00
5	437270	R18087	Hs.323769 Hs.28846	cisplatin resistance related protein CRR	1.56 113.25	1.54 125.00
	437271 437370	AL137445 AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp5660134 (fr Homo sapiens mRNA; cDNA DKFZp547D023 (fr	1.82	4.57
	437390	Al125859	Hs.112607	ESTs	1.35	1.75
10	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
10	437435	Al306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568 437623	A1954795 D63880	Hs.156135 Hs.5719	ESTs chromosome condensation-related SMC-asso	1.00 1.95	19.00 1.57
	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00	3.00
15	437814	AJ088192	Hs.135474	ESTs, Wealthy similar to DDX9_HUMAN ATP-D	1.00	45.00
	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Wealthy similar to dJ365012.1 [H.sa	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915 437916	AJ637993 BE566249	Hs.202312 Hs.20999	Homo sapiens clone N11 NTera2D1 teratoca hypothetical protein FLJ23142	74.05 23.15	35.00 89.00
20	437937	AI917222	Hs.121655	ESTs	1.00	1.00
	437942	A1888256	Hs.307526	ESTs .	12.28	31.00
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	1.53	10.85
25	438113	AJ467908	Hs.8882	ESTs	1.80	2.39
25	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274 438378	Al918906 AW970529	Hs.55080 Hs.86434	ESTs hypothetical protein FLJ21816	1.00 38.92	1.00 38.00
	438403	AAB06607	Hs.292206	ESTs	1.00	1.00
	438494	AA908578	Hs.130183	ESTs	2.05	80.00
30	438546	AW297204	Hs.125811	ESTs	1.00	131.00
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ESTs	1.00	34.00
	438724 438746	AW612553 Al885815	Hs.114670 Hs.184727	Human DNA sequence from clone RP11-16L21 Human melanoma-associated antigen p97 (m	1.33 2.42	1.10 1.59
35	438779	NM_003787	Hs.6414	nucleolar protein 4	1.00	18.00
J.J.	438821	AA826425	Hs.192375	ESTs	2.03	2.57
	438885	AJ88655B	Hs.184987	ESTs	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22,41	17.00
40	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00 2.20	1.00 1.88
40	438956 439000	W00847 AW979121	Hs.135056	Human DNA sequence from clone RP5-850E9 gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273	ESTs	1.17	1.31
	439024	R95696	Hs.35598	ESTs	1.00	28.00
40	439128	Al949371	Hs.153089	ESTs	1.00	67.00
45	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223 439285	AW238299 AL133916	Hs.250618	UL16 binding protein 2 hypothetical protein FLJ20093	1.93 46.23	1.64 139.00
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	2.00	2.20
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	6.10	7.37
50	439394	AA401369	Hs,190721	ESTs	3.39	17.00
	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451 439452	AF086270	Hs.278554 Hs.57987	heterochromatin-like protein 1	23.28 18.76	52.00 122.00
	439453	AA918317 BE264974	Hs.6566	B-cell CLL/lymphoma 11B (zinc finger pro thyroid hormone receptor interactor 13	2.78	1.58
55	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	1.22	1.44
	439492	AF086310	Hs.103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
60	439606 439670	W79123 AF088076	Hs.58561 Hs.59507	G protein-coupled receptor 87 ESTs, Wealdy similar to AC004858 3 U1 sm	33.61 1.00	1.00 1.00
00	439702	AW085525	Hs.134182	ESTs	4.30	10.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	2.36	1.88
C E	439750	AL359053	Hs.57664	Homo sapiens mRNA full length Insert cDN	2.02	6.08
65	439759	AL359055	Hs.67709	Homo saplens mRNA full length insert cDN	1.00	21.00 25.00
	439780 439840	AL109688 AW449211	Hs.105445	gb:Homo sapiens mRNA full length insert GDNF family receptor alpha 1	7 <i>.2</i> 7 1.00	1.00
	439926	AW014875	Hs.137007	ESTs	32.58	71.00
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	21.28	9.55
70	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.83	4.02
	440028 440106	AW473675 AA864968	Hs.125843 Hs.127699	ESTs, Wealdy similar to T17227 hypotheti	1.42 1.00	2.54 54.00
	440138	AB033023	Hs.318127	KIAA1603 protein hypothetical protein FLJ10201	24.18	52.00
75	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.21	4.72
-	440289	AW450991	Hs.192071	EST ₈	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
80	440527 440659	AV657117 AF134160	Hs.184164	ESTs, Moderately similar to S65657 alpha claudin 1	10.84 3.18	57.00 2.37
50	440059	M59241	Hs.7327 Hs.162	insulin-like growth factor binding prote	2.89	2.09
	440943	AW082298	Hs.146161	hypothetical protein MGC2408	2.02	1,41
	440994	AJ160011	Hs.272068	ESTs	1.29	1.14
95	441020	AA401359	Hs.190721	ESTs	142.99	17.00
85	441031	Al110684	Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

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	441128	AA570256		ESTs, Wealty similar to T23273 hypotheti	4.13	3.50
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	1.00	1.00
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
5	441377	BE218239 AI692560	Hs.202656 Hs.131175	ESTs ESTs	22.03 3.65	1.00 7.70
,	441390 441497	R51064	Hs.23172	ESTs	1.00	1.00
	441525	AW241857	Hs.127728	ESTs	1.53	1.42
,	441553	AA281219	Hs.121296	ESTs	1.89	1.57
10	441607	NM_005010	Hs.7912	neuronal cell adhesion molecula	1.47	211
10	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	216.22 2.31	363.00 2.05
	441635 441737	AA081846 X79449	Hs.7921 Hs.7957	Homo sapiens mRNA; cDNA DKFZp566E183 (fr adenosine dearninase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721	ESTs	44.15	17.00
	441801	AW242799	Hs.86366	ESTs	1.00	1.00
15	441919	AI553802	Hs.128121	ESTs	1.00	122.00
	441937	R41782	Hs.22279	ESTs	0.86	1.37
	441954	A1744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810	CDA11 protein neural precursor cell expressed, develop	1.00 9.92	46.00 45.00
20	442029 442072	AW956698 AJ740832	Hs.14456 Hs.12311	Homo sagiens clone 23570 mRNA sequence	25.05	77.00
20	442108	AW452649	Hs.166314	ESTs	3.61	3.14
	442117	AW664964	Hs.128899	ESTs	3.00	5.49
	442137	AA977235	Hs.128830	ESTs, Wealthy similar to Z192_HUMAN ZINC	1.00	1.00
25	442159	AW163390	Hs.278554	heterochromatin-like protein 1	1.92 27.22	1.66
25	442179 442328	AA983842 AI952430	Hs.333555 Hs.150614	chromosome 2 open reading frame 2 ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	50.00 3.42
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	181.59	76.00
	442530	A1580830	Hs.176508	Homo sapiens cDNA FLJ14712 fis, clone NT	10.59	144.00
	442547	AA306997	Hs.217484	ESTs, Wealdy similar to ALU1_HUMAN ALU S	109.23	98.00
30	442556	AL137761	Hs.8379	Homo saplens mRNA; cDNA DKFZp586L2424 (f	1.00	53,00
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02	50.00
	442710	A1015631	Hs.23210	ESTs	1.00 1.00	19.00 5.00
	442717 442875	R88362 BE623003	Hs.180591 Hs.23625	ESTs, Wealdy similar to T23976 hypotheti Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
35	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00
••	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.18	4,41
	442942	AW167087	Hs.131562	ESTs	8.45	64.00
	443068	Al188710	11 00010	ESTS	1.00	27.00
40	443204 443211	AW205878	Hs.29643 Hs.143655	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00 12.42	24.00 2.00
70	443247	A1128388 BE614387	Hs.333893	eSTs c-Myc target JPO1	128.84	96.00
	443324	R44013	Hs.164225	ESTs	0.02	4.59
	443383	A)792453	Hs.166507	ESTs	1.00	47.00
15	443400	R28424	Hs.250648	ESTs	18.52	61.00
45	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.02 2.98	1.75 2.57
	443572 443575	AA025610 A)078022	Hs.9605 Hs.269636	cleavage and polyadenylation specific fa ESTs, Wealdy similar to ALU1_HUMAN ALU S	1.00	29.00
	443514	AV655386	Hs.7645	fibrinogen, 8 beta polypeptide	1.00	16.00
	443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	1.00	39.00
50	443648	A1085377	Hs.143610	ESTs	39.81	70.00
	443715	Al583187	Hs.9700	cyclin E1	48.74	7.00
	443723 443802	A1144442	Hs.157144 Hs.9805	syntaxin 6 KIAA1291 protein	1.29 1.75	1.30 1.61
	443859	AW504924 NM_013409	Hs.9914	folistatin	1.35	1.13
55	443892	AA401369	Hs.190721	ESTs	1.00	17.00
	443947	W24187		gb:zb47f09.r1 Soares_fetal_tung_NbHL19W	1.33	1.64
	443991	NM_002250	Hs.10082	potassium Intermediate/small conductance	5.71	6.87
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	1.47 1.00	1.92 77.00
60	444009 444017	A1380792 U04840	Hs.135104 Hs.214	ESTs neuro-oncological ventral antigen 1	1.00	1.00
00	444127	N63620	Hs.13281	ESTs	1.00	29.00
	444129	AW294292	Hs.256212	ESTs	1.00	1.00
	444279	U62432	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239	forkhead box M1	2.91	1.14
65	444378	R41339	Hs.12569	ESTs ESTs, Wealdy similar to S64054 hypotheti	1.00 469.00	1.00 556.00
	444381 444461	BE387335 R53734	Hs.283713 Hs.25978	ESTs, Weakly similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217	KIAA0877 protein	24.91	90.00
	444489	AJ151010	Hs.157774	ESTs	1.00	111.00
70	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	1.00	70.00
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	30.56	139.00
	444707	Al188613	Hs.41690	desmocollin 3 hypothetical protein FLJ13057 similar to	1.00 77.02	1.00 90.00
	444735 444781	BE019923 NM_014400	Hs.243122 Hs.11950	GPI-anchored metastasis-associated prote	1.57	1.31
75	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	77.55	2.00
-	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	1.00	27.00
	445258	Al635931	Hs.147613	EŠTs	1.00	73.00
	445413	AA151342	Hs.12677	CGI-147 protein	28.14	50.00 2.62
80	445417 445443	AK001058	Hs.12680 Hs.322971	Homo saptens cDNA FLJ10196 fis, clone HE ESTs	1.81 1.00	1.00
55	445462	AV653838 AA378776	Hs.288649	hypothetical protein MGC3077	2.09	1.70
	445517	AF208855	Hs.12830	hypothetical protein	1.87	70.00
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.71	2.72
85	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.52	1.34 1.52
0,5	445654	X91247	Hs.13046	thioredoxin reductase 1	1.51	1.04

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	445669	Al570830	Hs.174870	ESTs	10.95	11.45
	445818	BE045321	Hs.136017	ESTs	1.00	1.00
	445873	AA250970	Hs.251946	poty(A)-binding protein, cytoplasmic 1-1	49.42	54.00
_	445885	A1734009	Hs.127699	KIAA1603 protein	1.00	132.00
5	445898	AF070523	Hs.13423	Homo sapiens clone 24458 mRNA sequence	1.00 1.00	1.00 36.00
	445903 445932	A1347487 BE046441	Hs.132781 Hs.333555	class I cytokine receptor Homo sapiens clone 24859 mRNA sequence	2.41	2.88
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.60	1.35
	446078	Al339982	Hs.156061	ESTs	1.00	42.00
10	446102	AW168057	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269 446292	AW263155	Hs.14559 Hs.279682	hypothetical protein FLJ 10540	73.01 1.55	48.00 1.26
	446293	AF081497 AJ420213	Hs.149722	Rh type C glycoprotein ESTs	1.00	2.00
15	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Wealthy similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	Al377320	Hs.150058	ESTs	1.00	5.00
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	1,36	1.31
20	446574 446619	AJ310135 AU076643	Hs.335933 Hs.313	ESTs secreted phosphoprotein 1 (osteopontin,	3,89 32,03	72.00 20.23
20	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82	9.47
	446839	BE091926	Hs.16244	mitotic spindle colled-coil related prot	110.28	28.00
25	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.26	2.94
25	446856 446872	AI814373	Hs.164175	ESTs	6.38 1.98	11.30 2.03
	446880	X97058 Al811807	Hs.16362 Hs.108646	pyrimidinergic receptor P2Y, G-protein c Homo sapiens cDNA FLJ14934 fis, clone PL	94.90	113.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.67	3.90
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	2.82	3.12
30	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	Al357412	Hs.157601	ESTs	7.15	107.00
	447078 447081	AW885727 Y13896	Hs.9914 Hs.17287	ESTs potassium inwardly-rectifying channel, s	47,24 0.12	24.00 17.88
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
35	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
-	447153	AA805202	Hs.315562	ESTs	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	1.00	67.00
	447178	AW594641	Hs.192417	ESTS	3,42 1,60	50.00 1.52
40	447250 447289	A1878909 AW247017	Hs.17883 Hs.36978	protein phosphatase 1G (formerly 2C), ma melanoma antigen, family A, 3	1.00	1.00
	447342	Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	146.62	51.00
	447350	Al375572	Hs.172634	ESTs	1.00	12.00
45	447377	N27687	Hs.334334	transcription factor AP-2 atpha (activat	2.55 0.91	63.00 1.13
43	447415 447425	AW937335 Al963747	Hs.28149 Hs.18573	ESTs, Weakly similar to KF3B_HUMAN KINES acylphosphatase 1, erythrocyte (common)	1.00	35.00
	447519	U46258	Hs.339665	ESTs	59.89	49.00
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.23	1.63
50	447534	AA401369	Hs.190721	ESTs	1.00	17.00
50	447636	Y10043	Hs.19236	high-mobility group (nonhistone chromoso	1.41 1.00	1.11 39.00
	447688 447733	N87079 AF157482	Hs.19400	Target CAT MAD2 (mitotic arrest deficient, yeast, h	1.17	1.12
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	6.47	5.95
	447802	AW593432	Hs.161455	ESTs	0.73	2.34
55	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00
	447924	AIB17226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	1.00 3.50	1.00 4.27
	447973 448030	AB011169 N30714	Hs.20141 Hs.325960	similar to S. cerevisiae SSM4 membrane-spanning 4-domains, subfamily A	4.13	142.00
	448105	A)538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
60	448243	AW369771	Hs.52620	Integrin, beta 8	15.84	1.00
	448278	W07369	Hs.11782	ESTs	0.97	1.90
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00 2.42	1.00 2.17
	448296 448357	BE622756 BE274396	Hs.10949 Hs.108923	Homo sapiens cDNA FLJ14162 its, clone NT RAB38, member RAS oncogene family	1.44	1.08
65	448390	AL035414	Hs.21068	hypothetical protein	1.00	43.00
	448469	AW504732	Hs.21275	hypothetical protein FLJ11011	2.63	2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2.53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672 448733	Al955511 NM_005629	Hs.225106 Hs.187958	ESTs solute carrier family 6 (neurotransmilte	1.00 1.82	21.00 1.08
70	448741	BE614567	Hs.19574	hypothetical protein MGC5469	2.48	1.92
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	23.53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate finked moi	2.34	1.97
75	448826	AJ580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	74.07 1.37	62.67 1.31
75	448830 448844	AL031658 Al581519	Hs.22181 Hs.177164	hypothetical protein dJ310O13.3 ESTs	1.37 1.00	1.31 31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	AJ471630		KIAA0144 gene product	1,63	1.49
90	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00
80	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.97	2.26
	449040 449048	AF040704 Z45051	Hs.149443 Hs.22920	putative turnor suppressor similar to S68401 (catile) glucose induc	0.97 27.13	1.56 90.00
	449053	A1625777	Hs.344766	ESTs	8.33	44.00
0.5	449054	AF148848	Hs.22934	myoneurin	73.85	104.00
85	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00

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	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.36	1.56
	449228	AJ403107	Hs.148590	protein related with psoriasis	1.15	1.15
5	449230	BE613348	Hs.211579	metanoma cell adhesion molecule	206.65	151.00
3	449305 449318	Al638293 AW235021	Hs.78531	gb:tt09b07.x1 NCL_CGAP_GC6 Homo sapiens Homo sapiens, Similar to RIKEN cDNA 5730	17.28 26.39	45.00 35.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
	449467	AW205006	Hs.197042	ESTs	1.00	1.00
10	449523	NM_000579	Hs.54443	chemokine (C-C molif) receptor 5	56.80	216.86
10	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976 450001	H06350 NM_001044	Hs.135056 Hs.406	Human DNA sequence from clone RPS-850E9 solute carrier family 6 (neurotransmitte	2.16 1.17	2.85 1.45
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.79	2.38
	450101	AV649989	Hs.24385	Human hbc547 mRNA sequence	1.00	69.00
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372 450375	BE218107 AA009647	Hs.202436 Hs.8850	ESTs a disintegrin end metalloproteinase doma	1.00 51.26	1.00 93.00
20	450447	AF212223	Hs.25010	hypothetical protein P15-2	123.20	181.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AI701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00 1.89	100.00 1.55
25	450701 450705	H39960 U90304	Hs.288467 Hs.25351	Homo sapiens cDNA FLJ12280 fis, clone MA iroquois homeobox protein 2A (IRX-2A) (1.00	45.00
	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105	AI761324	11- 000000	gb:wi60b11.x1 NCI_OGAP_Co16 Homo saptens	15.02 1.00	124.00 143.00
50	451110 451253	A1955040 H48299	Hs.265398 Hs.26126	ESTs, Wealdy similar to transformation-r claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacylglycerol kinase, zeta (104kD)	2.92	18.00
25	451380	H09280	Hs.13234	ESTs	6.90	6.67
35	451386 451437	AB029006 H24143	Hs.26334	spastic paraplegia 4 (autosomal dominant	35.75 1.00	72.00 69.00
	451462	AK000367	Hs.31945 Hs.26434	hypothetical protein FLJ11071 hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88	1.33
40	451592	AJ805416	Hs.213897	ESTS	1.00	1.00
	451635 451743	AA018899	Hs.127179	cryptic gene	1.52 4.95	1.92 17.00
	451806	AA401369 NM_003729	Hs.190721 Hs.27076	ESTs RNA 3-terminal phosphate cyclase	13.55	31.00
	451807	W52854	110001010	hypothetical protein FLJ23293 similar to	1.55	35.00
45	451871	AJ821005	Hs.118599	ESTs	1.81	2.53
	451952	AL120173	Hs.301663	ESTs	1.00	22.00 2.26
	452012 452046	AA307703 AB018345	Hs.279766 Hs.27657	kinesin family member 4A KIAA0802 protein	3.43 56.59	19.00
	452194	AI694413	Hs.332649	otfactory receptor, family 2, subfamily	1.67	4.09
50	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	9.31	53.00
	452240	AA401369	Hs.190721	ESTs	13.42	17.00
	452256 452281	AK000933 T93500	Hs.28661 Hs.28792	Homo saplens cDNA FLJ10071 fis, clone HE Homo saplens cDNA FLJ11041 fis, clone PL	39.03 153.01	94.00 340.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	1.95	23.00
55	452295	BE379936	Hs.28866	programmed cell death 10	42.33	61.00
	452304	AA025386	Hs.61311	ESTs, Weakly similar to \$10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.00	13.00
	452349 452357	AB028944	Hs.29189 Hs.29279	ATPase, Class VI, type 11A eyes absent (Drosophila) homotog 2	1.09 54.49	1.42 53.00
60	452401	U71207 NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	32.00
•	452410	AL133619		Homo saplens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613 452699	AA461599 AW295390	Hs.23459 Hs.213062	ESTs ESTs	1.39 1.00	1.32 26.00
05	452705	H49805	Hs.246005	ESTs	1.00	1.00
	452747	AF160477	Hs.61460	lg superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
10	452823 452833	AB012124 BE559681	Hs.30696 Hs.30736	transcription factor-like 5 (basic helix KIAA0124 protein	7.91 3.16	75.00 1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell gr	1.55	1.00
75	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.73	1.19
	452946 452976	X95425 R44214	Hs.31092 Hs.101189	EphA5 ESTs	1.00 1.58	1.00 1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
00	453095	AW295660	Hs.252756	ESTs	0.77	1.50
80	453102	NM_007197	Hs.31664	trizzled (Drosophila) homolog 10	1.00	1.00
	453103 453120	Al301052 AA292891	Hs.153444 He 31773	ESTs	1.00 1.23	1.00 1.20
	453120 453153	N53893	Hs.31773 Hs.24360	pregnancy-induced growth inhibitor ESTs	1.00	83.00
0.5	453160	A1263307	Hs.239884	H2B histone family, member L	1.00	30.00
85	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	1.00	134.00

	W	O 02/086	443				DCT/I	US02/12476
	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93	FC1/0	USU2/124/0
	453240	A1969564	Hs.165254	hypothetical protein DKFZp5661133	1.00	1.00		
	453317	NM_002277 AF034102	Hs.41696 Hs.32951	keratin, hair, acidic, 1 solute carrier family 29 (nucleoside tra	1.19 4.90	1 <i>.2</i> 7 4.11		
5	453323 453331	AI240565	Hs.8850	ESTs	199.42	340.00		
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431		Hs.32973	glycine receptor, beta	1.00	1.00		
	453439 453459	AI572438 BE047032	Hs.32976 Hs.257789	guanine nucleotide binding protein 4 ESTs	3.44 2.84	5.17 5.58		
10	453563	AW608906.co		Hs.181163		al protein MGC5629	4.58	90.00
	453633		Hs.34045	hypothetical protein FLJ20764	1.74	1.60		
	453775 453830	NM_002916 AA534296	Hs.35120 Hs.20953	replication factor C (activator 1) 4 (37 ESTs	19.49 24.92	1.00 25.00		
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	167.59	66.00		
15	453867	A1929383	Hs.33032	hypothetical protein DKFZp434N185	1.00	39.00		
	453883	A1538516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884 453900	AA355925 AW003582	Hs.36232 Hs.226414	KIAA0186 gene product ESTs, Wealdy similar to ALUS_HUMAN ALU S	63.89 20.41	20.00 16.00		
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	7.09	22.00		
20	453941	U39817	Hs.36820	Bloom syndrome	29.75	19.00		
	453964 453968	Al961486 AA847843	Hs.12744 Hs.62711	ESTS	1.00 2.06	1.00 1.81		
	453976	BE463830	Hs.163714	Homo sapiens, clone IMAGE:3351295, mRNA ESTs	3.02	131.00		
0.5	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00	131.00		
25	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.23	1.02		
	454042 454059	T19228 NM_003154	Hs.172572 Hs.37048	hypothetical protein FLJ20093 statherin	30.63 1.00	171.00 1.00		
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	1.01	1.45		
20	454098	W27953	Hs.292911	ESTs, Highly similar to \$60712 band-6-pr	1.26	1.11		
30	454241	BE144666 Al244459	Un 44000C	gb:CM2-HT0176-041099-017-c02 HT0176 Homo	6.33 4.30	5.04 7.82		
		AW819152	Hs.110826 Hs.154320	trinucleofide repeat containing 9 DKFZP56601646 protein	1.00	1.00		
	455175			gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
25		Al368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
35	456237 456321	AA203682 NM_001327	Hs.87225	gb:zx52e07.r1 Soares_fatat_liver_spleen_ cancer/testis antigen	1.00 1.14	1.00 1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534 456736	X91195 AW248217	Hs.100623 Hs.1619	phospholipase C, beta 3, neighbor pseudo	2.12 1.15	1.80 1.94		
70	456759	BE259150	Hs.127792	achaete-scute comptex (Drosophila) homol delta (Drosophila)-like 3	1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
45	457234 457465	AW968360 AW301344	Hs.14355 Hs.122908	Homo sapiens cDNA FLJ13207 fis, clone NT DNA replication factor	2.71 46.37	4.15 47.00		
	457489	AI693815	Hs.127179	cryptic gene	1.12	1.35		
		AA725650	Hs.112948	ESTs	1.55	2.51		
		AW974812 AA057484	Hs.291971 Hs.35406	ESTs ESTs, Highly similar to unnamed protein	1.00 4.36	55.00 3.18		
50		BE545684	Hs.343566	KIAA0251 protein	1.00	1.32		
	458098	BE550224		metallothionein 1E (functional)	1.00	22.00		
	458207		Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242 458247	8E299588 R14439	Hs.28465 Hs.209194	Homo sapiens cDNA: FLJ21869 fis, clone H ESTs	1.00 7.00	1.00 9.85		
55		AW975460	Hs.142913	ESTs	1.00	3.00		
		AW451034	Hs.326525	arylsulfatase D	1.31	2.01		
	456933 459352	Al638429 AW810383	Hs.24763 Hs.206828	RAN binding protein 1 ESTs	1.98 12.60	1.71 63.00		
	459670	F01020	Hs.172004	titin	1.00	1.00		
60		Al204995		gb:an03c03.x1 Stratagene schizo brain S1	1.00	237.00		
	TABLE 98	3		•				
		•						
65	Pkey:		s probeset ide	ntifier number	•			
	CAT num Accession	ber: Gene clust	er number ccession num	hom				
	VICTORIA	r Geimanka	CCSSION NUM	ueis .				
70	Pkey	CAT Number						
70	407746	10125_1		962 R69415 BE464605 AA418699 AA053293 AA1490				
				982 AA730033 AA576507 AA991217 AA782067 A198 I T27343 AA306950 AA360989 R58778	3031 AA6U5864 A	AN 168864YA BECCUE	5040 AAS682/9 A	1740U1047 (10332U
	408070	1036688_1		852 BE350895				
75	408660	107294_1	AA525	775 AA056342 Al538978 AW975281 AA664986				
75	409522	113735_1		382 AA075431				
	409866 410032	1156522_1 1170435_1		1152 H41202 H29772 985 BE065944 BE066008 BE066083 BE066093				
	411089	123172_1		454 aa71373d aad91294 aa584921 N86077 aw8367	81 AA501031 AA5	79876 AA551106 AA63	3188 AW905577	A1955808 A1679386
90		_	A16798	95 AA514764 AA454562 A1082382 AA595822 AA551:	351 AA586369 AA	665384 AA188934 AA66	6398 AA551297 A	AA565188
80	411152	1234028_1		199 AW936012 AW877466 AW819782 AW935798 AV 1019 AW935937 BE160180 AW935946 BE069101 BEI				
	412537	1304_1		178 X59711 NM_002505 M59079 A1870439 A1494259				
		· · · · · · · ·	T29403	BE079412 BE079428 N90322 Al631202 Al141758 A	1016793 Al167566	A1862075 A1375230 A12	208445 AW23576	3 AL044113 AA382556
			AW953	918 AA927051 AA889823 BE003094 AW390155 AW	35U8U5 AW360823	AW360810 AA425472	A1694282 AL0441	14 AJ684577 AJ809865

	W	0 02/086443	PCT/US02/12476
	• • • • • • • • • • • • • • • • • • • •	0 02,0001.0	AI478773 AL160445 AI674530 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982
			Al963541 Al469807 Al969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026
	412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 A424991 A1693507 A1863108 AA599060 A1991148 AA598689 R39887 AA813482 AW016452 H06383 R41807 A1364268 AA620528 A1241940 AW089149 AW090733 AW088875 Z38240
5			A12(20) R1734
	413690	1383256_1	BE157489 BE157560
	414883	15024_1	AA926950 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 NB6396 AA001348 BE535736 AA081745 BE566245
			AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314365 AA908783 AI719075 BE270172 BE269819 AA889955 Al204630 W25243 AI935150
10			AA872039 W72395 T99630 A1422691 H98460 N31428 BE255916 H03265 A1857576 AA776920 AA910644 AA459522 AA233140 AW514667
			R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187 AW024595 AW069734 AI828996 AA282997 AA876046
			AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418 AA594628 AI033892 W95096 AI034317 AA398727 AI085031 N95210 A459432 AI041437 AA932124 AA627684 AA935829 AI004827 AI423513 AI094597 H42079 R54703 AI630369 AA617681 AA978045
			AA643280 W44561 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239
15			Al139549 AA633648 Al339996 Al336880 AA399239 Al078708 Al085351 Al362835 Al346618 Al146955 Al989380 Al348243 N92892 AA765850
			A494230 A1278887 AA962596 A492600 W80435 AA001979 R97424 A1129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 A4494211 AW059601 AW886710 R92790 N59755 A361128 AW589407 H47725 H97634 H48076 H48450 T99631 AW300758 H03431 R76789
			AA954344 H77576 R96823 A1457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
20			H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
20	415989	456454 4	W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672
	417324	156454_1 166714_1	Al267700 Al720344 AA191424 Al023543 Al469633 AA172066 AW958465 AA172236 AW953397 AA355086 AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
	418574	17690_1	N28754 N28747 Al568146 Al979339 AA322671 AA322672 AW955043 Al990326 AA776406 Al016250 AA843678 AW451882 N23137 N23129
25	440740	4704405 4	W70051 Al038748 AA831327 Al925845 AW945895
23	418712 419443	1784125_1 184788_1	Z42183 T31621 T97478 - D62703 AA242966 D79798
	419502	18535_1	AU076704 T74854 T74850 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67854 T60630
			T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242
30			T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719
50			T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64305 T71908 T68107
			T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796
			H48353 T71914 T53939 T64121 AA693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 A1064740 T82897 N33594 AA344542 AW805054 Al207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395
35			AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596
			AW470774 AV651256 N54417 AAB12862 AW182929 Al111192 H61463 H72060 AA344503 H38639 Al277511 AV661108 Al207625 T47810
			AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293 T69283 T73931 T72178 T72456 AV645639 AV655476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778
			A344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T68267 T74407 T85778
40			T70475 T64751 AA344441 AA343657 AA345732 AA344328 A1110639 AA344603 AF063513 T64696 T68516 T72223 T60507 T67633 R29500
	•		T72517 R02292 T60599 T69206 T70452 T74577 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344403 T69197 T72057
			T69368 T69358 T69358 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964 T53747 T72042 T62764 Al064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375
4.5			AA345234 T67598 AA011414 T68036 H48262 Al207557 T68219 W86031 T69081 T64232 R93196 T62136 AV650539 H67459 T72978
45			AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862
			AA693592 Al248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835 T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
	419936	189181_1	A/792788 BE142230 AA252019
50	421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818
30			AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126 BE074140 AA514776 AA588034 BE074061 BE074068 AW009769 AW050690 AA858276 R55389 AI001051 AW050700 AW750216 AA614539
			BE074045 Al307407 AW602303 BE073575 Al202532 AA524242 Al970839 Al909751 BE076078 Al909749 R55292
	422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
55	423034 423816	224122_1 23234_1	AL119930 AA320696 AW752565 AL031985 AL137241 AI792386 AI733664 AI857654 AI049911
	424200	236595_1	ALIST 1963 ALIST 241 AT 192500 AT 155004 ALIST 1054 ALIGS 1951 AA337221 AA336756 AW966196
	424999	245835_1	AW953120 R56325 AA349562
	426956 426991	273896_1 27415_1	Al493134 Al498691 AW771508 Al498457 Al768408 Al783624 Al383985 Al580267 D79813 AA393768 AK001536 AA191092 AW510354 Al554256 AL353968 AA134266
60	427260	27415_1 276598_1	AAA01030 AA191032 AYI010304 AI004200 AL003900 AA134200 AA663848 AA400100 AA401424
	428023	28589_2	AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831
			A1936994 W56258 A1653448 A1278611 A1283557 A1824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 A1038904 A1292064
			A034339 AW674593 N72156 A079733 A1038683 A1291616 AA491599 AA993575 AA837380 BE006554 BE006473 A1087090 T33044 AA652743 A1203503 AA583959 W35283 A120906 741844 AM72922 AW675848 A1684622 AAA82907 A148689 A127475 AAA26444

	423034	224122_1	AL119930 AA320696 AW752565
55	423816	23234 1	AL031985 AL137241 Al792386 Al733664 Al857654 Al049911
	424200	236595 1	AA337221 AA336756 AW966196
	424999	245835_1	AW953120 R56325 AA349562
	426956	273896 1	Al493134 Al498691 AW771508 Al498457 Al768408 Al783624 Al383985 Al580267 D79813 AA393768
	426991	27415_1	AK001536 AA191092 AW510354 Al554256 AL353968 AA134266
60	427260	276598 1	AA663848 AA40010D AA401424
	428023	28589 2	AL038B43 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 Al928802 AW182584 AW027872 Al819831
			AJ936994 W56258 AJ653448 AJ278611 AJ283557 AJ824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AJ038904 AJ292064
			A1034339 AW674593 N72156 A1079733 A1038683 A1291616 AA491599 AA993575 AA837380 BE006554 BE006473 A1037090 T33044
			AA652043 Al203503 AA583959 W35283 Al129926 Z41844 AW020925 AW575848 Al684603 AA493297 Al140689 Al277175 AA425444
65			AI932767 W02632 BE396786 R37261
	429220	301384 1	AW207206 AW341473 AA448195 Al951341
	429978	31150 1	AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762
			AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 AJ354442 AA772275 R31663 AJ354441
			Al767525 H92431 Al916735 H93575 Al394255 AW014741 Al573090 C06195 AW612857 AW265195 Al339558 Al377532 Al308821 Al919424
70			AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049
			AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115
	430439	31808_1	AL133561 AL041090 AL117481 AL122069 AW439292 Al968826
	430935	325772_1	AW072916 Al184913 AA489195 AW466994 AW469044 N59350 Al819642 Al280239 Al220572 AA789302 Al473611 AW841126 D60937
	431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102
75	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	432407	34624_1	AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639
			BE061833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945688 C04699 AA205504 AA377241 AW821667 AA055720
			AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859
00	434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
80			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
			T61139 AA149776 AA699829 AW879188 AW813567 AW813538 Al267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
			AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
			AIB29309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
0.5			AW817705 AW817703 AW817659 BE081531 H59570
85	436608	42361_3	AA628980 AI126603 BE504035

	w	O 02/08	6443	PCT/US02/12476
_	438091	44954_1		AW373052 T55662 Al299190 BE174210 AW579001 H01811 W40186 R67100 Al923886 AW952164 AA628440 AW398607 AW898616 AA709126 AW898528 AW898544 AA947932 AW898625 AW898622 Al276125 Al185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 Al288245 Al186932 D52654 D55017 D52715 D52477 D53933 D54679 Al298739 Al146984 Al922204 N38343 BE174213 AA845571 Al813854 Al214518 Al635262 Al139455 Al707807 Al698085 AW884528 Al024768 Al004723 AW087420 Al565133 N94964 Al268939
5	439000	467716_1		AW513280 AU61126 AU453818 AU59106 AU360506 AU24767 AA513019 AA757598 X56196 AA902959 AU34784 AU607207 AW890091 AW513771 AU951391 AU337671 T52499 AA890205 AI640908 H75966 AA463487 AA356588 AU961767 AU866295 AA780994 AU855913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AU220713 AW149306 AU758412 AA045713 R79750 N76096 AW379121 AA847986 AA029098
10	439285 439780	47065_1 47673_1		AL 133916 N79113 AF086101 N76721 AW950828 AA364D13 AW955684 AI346341 AI867454 N54784 AI665270 AI421279 AW014882 AA776552 N62351 N59253 AA626243 AI341407 BE 175639 AA456968 AI368918 AA457077 AL 109688 R23665 R26578
	441128 443068	51021_2 558874_1	1	AA570256 AW014761 AA573721 A473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 A1399627 A1005068 A1356557 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923 A1188710 A1032142 AW078833 N30308 AW675632 A1219028 A1341201 N22181 H95390
15	443947 447636	586160_1 7301_1		W24187 W24194 R17789 Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649 AA369318 AW957081 R05760 AA039903 Al886597 AW630122 AA906264 AA041527 R01145 Al088688 BE463637 AA398795 Al354883 A1768938 AI569996 A452952 Al168552 Al18869 Al086670 AW262560 AW613854 AA862839 AA435840 AA670197 Al024032 Al990659 A1990089 NB1095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582897 AW858854 AW818630 AW818281 AW818433 AW582595
20	448993	79225_1		AA096002 N83992 AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265 AW340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454833 AI982791 AI567270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417 AA911497 BE537702
25	449305 451105 451320	804424_1 859083_1 86576_1		AUS31293 AVV313561 AL761324 AW880941 AW880937 AW118072 AL631982 T15734 AA224195 AL701458 W20198 F26326 AA890570 N90552 AW071907 AL671352 AL375892 T03517 R88265 AL124088 AA224388 AL084316 AL354686 T33652 AL140719 AL720211 T03490 AL372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AL222556 T33511 T33785 AL419606 D55612
30	451807 . 452410	8865_1 9163_1		W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA938634 AI805539 AA351618 AW449522 AI827626 AA904788 AA360381 AA886045 AA774409 BE003229 Z41756 AL133619 AA468118 AA38306A AI476447 T09430 AI673758 AA524895 AISB1435 AI300820 AW498812 AA256162 AI559724 AI685732 AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747
35	454241	1067807_1		R74039 N35031 AI804128 AW513621 AA868351 AID26826 AI493388 AA614641 W81604 AI567080 AI214351 AA730140 A1125754 AI200813 AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316 AI734130 AI734130 AA426284 AA433997 AI741241 AW043563 AI732734 AA437369 AA425820 AA664048 R74130 BE144666 BE184942 AW238414 BE184946
40	455175 456237 458098	1257335_1 168730_1 47395_1		AW993247 AW861464 AA203862 R11968 BE550224 AA832519 N45402 AW885857 N29245 BE465409 W07677 AW970089 AI299731 AA482971 BE503548 H18151 W79223 AF086393 AA461301 W74510 R34182 AI090689 N46003 BE071550 R28075 AW134982 AI240204 AI138906 AW026179 AI572316 BE466182 AI205395 AIZ76154 AIZ73269 AI422817 AI371014 AI421274 AI188525 AA339164 BE549810 AW137865 AI694996 BE503841 AA459718 BE327407 BE467534 BE218421 BE467767 AA989054 BE467063 AI797130 BE327781
45	TABLE 9C			·
50	Pkey: Ref: Strand: Nt_position	Sequence sequence indicates	e source e of hum ONA str	orresponding to an Eos probeset . The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA an chromosome 22." Dunham I. et al., Nature (1999) 402-489-495. and from which excess were predicted. de positions of predicted excess.
55	Pkey 400512 400517 400560 400664	Ref 9796593 9796686 9843598 8118496	Strand Minus Minus Plus Plus	1439-1615 49995-50346 94182-94323,97056-97243,101095-101238,102824-103005 13558-13721,13942-14090,14554-14679
60	400665 400566 400749 400763 401027	8118496 8118496 7331445 8131616 7230983	Ptus Ptus Minus Minus Minus	16879-17023 17982-18115,20297-20456 9162-9293 35537-35784 70407-70554,71060-71160
65	401093 401203 401212 401411	8516137 9743387 9858408 7799787	Minus Minus Plus Minus	22335-23166 172951-173056, 173868-173928 87839-88028 144144-144329
70	401435 401464 401714 401747	8217934 6682291 6715702 9789672	Minus Minus Plus Minus	54508-55233 170688-170834 96484-96681 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866- 131932,132451-132575,133580-134011
75	401760 401780 401781 401785 401797	9929699 7249190 7249190 7249190 6730720	Plus Minus Minus Minus Plus	83126-83250,85320-85540,94719-95287 28397-28517,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573 83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814 165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942 6973-7118
80	401961 401985 401994 402075 402260	4581193 2580474 4153858 8117407 3399565	Minus Ptus Minus Ptus Minus	124054-124209 61542-61750 42904-43124,43211-43336,44607-44763,45199-45281,46337-46732 121907-122035,122804-122921,124019-124161,124455-124610,125672-126076 113765-113910,115653-115765,116808-116940
85	402265 402297 402408	3287673 6598824 9796239	Ptus Ptus Minus	21059-21168 33279-35405,35573-35659 110326-110491

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	402420	9796339	Plus	129750-129919	
	402674	8077108	Minus	39290-39502	
	402802	3287156	Minus	53242-53432	
_	402994	2996643	Minus	4727-4969	
5	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337	
	403306	8099945	Plus	127100-127251	
	403329	8516120	Plus	96450-96598	
	403381	9438267	Minus	26009-26178	
	403478	9958258	Plus	116458-116564	
10	403485	9966528	Plus	2888-3001,3198-3532,3655-4117	
	403627	8569879	Minus	23868-24342	
	403715	7239669	Plus	85128-85292	
	404044	9558573	Minus	225757-225939	
	404076	9931752	Minus	3848-3957	
15	404101	8076925	Minus	125742-125997	
	404140	9843520	Plus	37761-38147	
	404165	9926489	Minus	69025-69128 ·	
	404185	4572584	Minus	129171-129327	•
•	404210	5006246	Plus	169925-170121	
20	404253	9367202	Minus	55675-56055	
	404287	2326514	Plus	53134-53281	
	404298	9944263	Minus	73591-73723	
	404347	9838195	Plus	, 74493-74829	
0.5	404440	7528051	Plus	80430-81581	
25	404721	9856648	Minus	173763-174294	
	404794	4826439	Plus	101619-101898	
	404854	7143420	Plus	14260-14537	
	404877	1519284	Plus	1095-2107	
20	404927	7342002	Phus	68690-69563	
30	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450	
	405449	7622497	Plus	42236-42570	
	405568	6006906	Plus	35912-36065	
	405572	3800891	Plus	85230-85938	
35	405646	4914350	Plus	741-969	
22	405676	4557087	Plus	73195-73917	
	405770	2735037	Plus	61057-62075	
	405932	7767812	Minus	123525-123713	
	406137	9166422	Minus	30487-31058	
40	406360	9256107	Minus	7513-7673 63448-63554	
40	406399 406467	9256288	Minus	182212-182958	
	400407	9795551	Plus	104414-104330	

TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-malignant Lung Disease
Table 2A shows about 307 genes up-regulated in non-malignant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to
normal lung and non-malignant lung disease. These genes were selected from about 59880 probesets on the Eos/Affyrnetrix Hu03 Genechip array. 45

Table 10B show the accession numbers for those Pikey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubteTwist, Oakland Celifornia). The Genbank accession numbers for sequences comprising each cluster are listed in the 50 "Accession" column.

Table 10C show the genomic positioning for those Pikey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed. 55

Pkey: Unique Eos probeset identifier number ExAcon: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number Unigene Title: R1: 60

Unigent gene tille
Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the

average of normal lung samples

Average of non-matignant lung disease samples (including bronchills, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples R2:

65	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	404394		-	ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
	404916			Tarpet Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
70	407568	AA740964	Hs.62699	ESTs	1.00	123.00
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	toll-like receptor 2	39.65	149.00
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
75	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	0.37	2.27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
	414154	AW205314	Hs.323060	ESTs	0.62	2.09
80	414214	D49958	Hs.75819	glycoprotein M6A	0.03	4.55
	414998	NM_002543	Hs.77729	oxidised how density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobutin and	0.67	1.65
0.5	415775	H00747	Hs.29792	ESTs, Wealthy similar to I38022 hypotheti	0.29	2.64
85	415910	U20350	Hs.78913	chemokina (C-X3-C) receptor 1	1.00	145.00

	W	/O 02/086	443			
	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	15.32	237.00
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	0.64	4.00
	417355	D13168	Hs.82002	endothelin receptor type B	0.01	3.90
5	417421 417511	AL138201 AL049176	Hs.82120 Hs.82223	nuclear receptor subfamily 4, group A, m chordin-like	36.30 1.00	357.00 179.00
9	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.02	6.00
	418726	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
10	418883 419086	BE387036 NM_000216	Hs.1211 Hs.89591	acid phosphatase 5, tartrate resistant Kallmann syndrome 1 sequence	0.96 0.62	2.04 2.74
•	419150	T29618	Hs.89640	TEK tyrosine kinase, endothellal (venous	0.03	6.90
	419235	AW470411	Hs.288433	neurotrimin	1.48	5.13
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00
15	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, ctone L	0.80	3.65
13	420656 420729	AA279098 AW964897	Hs.187636 Hs.290825	ESTs ESTs	1.65 2.99	8.07 25.82
	421177	AW070211	Hs.102415	Homo saplens mRNA; cONA DKFZp586N0121 (f	0.46	1.95
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
20	422426	W79117	Hs.58559	ESTs	0.03	7.44
20	422652 423099	AW957969 NM_002837	Hs.118958 Hs.123641	syntaxin 11 protein tyrosine phosphatase, receptor t	0.14 0.01	3.62 3.16
	424433	H04607	Hs.9218	ESTs	0.75	141.75
	424585	AA464840	Hs.131987	ESTs	1.00	167.00
25	424711	NM_005795	Hs.152175	calcitorin receptor-like	0.43	3.01
25	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37	19.45
	425023 425664	AW956889 AJ006276	Hs.154210 Hs.159003	endothelial differentiation, sphingotipi transient receptor potential channel 6	0.14 1.00	3.35 94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
••	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74
30	426753	T89832	Hs.170278	ESTs	1.00	141.00
	427558	D49493	Hs.2171	growth differentiation factor 10	1.00	117.00 2.20
	427983 428467	M17708 AK002121	Hs.2233 Hs.184465	colony stimulating factor 3 (granulocyte hypothetical protein FLJ 11259	0.75 0.76	2.25
	428927	AA441837	Hs.90250	ESTs	0.01	3.62
35	429496	AA453800	Hs.192793	ESTs	1.00	138.00
	430468	NM_004673	Hs.241519	anglopoletin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00 1.00	157.00 157.00
	431728 431848	NM_007351 Al378857	Hs.268107 Hs.126758	multimerin ESTs, Highly similar to AF175283 1 zinc	0.34	2.24
40	432128	AA127221	Hs.117037	ESTs	0.00	1.15
	432519	Al221311	Hs.130704	ESTs, Wealthy similar to BCHUIA S-100 pro	0.01	2.06
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.00	267.00 105.00
	433803 434730	A1823593 AA644669	Hs.27688 Hs.193042	ESTs ESTs	1.00 1.05	3.15
45	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83	1.94
	436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens	1.00	218.00
	437119	A1379921	Hs.177043	ESTs	1.00	133.00
	437140	AA312799 AA382207	Hs.283689 Hs.5509	activator of CREM in testis	0.67 1.00	122.67 142.00
50	437211 437960	A1669586	Hs.222194	ecotropic viral integration site 2B ESTs	1.00	147.00
	438202	AW169287	Hs.22588	ESTs	1.00	141.00
	438873	Al302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875	AA827640	Hs.189059	ESTs	23,32	370.00
55	441048 441188	AA913488 AW292830	Hs.192102 Hs.255609	ESTS ESTS	0.77 3.43	8.50 16.36
33	441499	AW298235	Hs.101689	ESTS	1.00	167.00
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	1.00	151.00
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	46.47	153.00
60	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08 141.00
00	445279 446017	R41900 N98238	Hs.22245 Hs.55185	ESTs ESTs	0.60 0.18	2.39
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	AJ375922	Hs.159367	ESTs	0.46	2.64
UJ	448106 448253	A1800470 H25899	Hs.171941 Hs.201591	ESTS ESTS	18.05 1.00	296.00 141.00
	449275	AW450848	Hs.205457	periaxin	0.56	1.38
	450400	AI694722	Hs.279744	ESTs	0.88	4.33
70	450698	AI654223	Hs.16026	hypothetical protein FLJ23191	0.52	2.08
70	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497 451533	H83294 NM_004657	Hs.284122 Hs.26530	Wnt inhibitory factor-1 serum deprivation response (phosphatidy)	0.35 0.13	2.03 2.25
	453636	R67837	Hs.169872	ESTs	1.00	116.00
75	458332	AI000341	Hs.220491	ESTs	1.00	192.00
75	459580	AA022888	Hs.176065	ESTS	0.20	2.98
	400269			Eos Control NM_016369°:Horno sapisns claudin 18 (CLDN	0.40 0.53	2.40
	403421 407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	1.77 3.18
•	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
80	414517	M24461	Hs.76305	surfactant, putmonary-associated protein	0.64	1.50
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	0.33	1.16
	418307 418935	U70867 T28499	Hs.83974	solute carrier family 21 (prostaglandin carbonic anhydrase IV	0.53 0.20	1.55 1.28
_ =	421502	AF111856	Hs.89485 Hs.105039	solute carrier family 34 (sodium phospha	0.78	1.90
85	421798	N74880	Hs.29877	N-acylsphingosine amidotrydrolase (acid c	0.59	1.54

	W	O 02/086	443			
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0,59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
5	425438	T62216	Hs.270840	ESTs	0.23	9.45
3	426828 427019	NM_000020 AA001732	Hs.172670 Hs.173233	activin A receptor type II-like 1 hypothetical protein FLJ10970	0.03 0.01	1.71 1.49
	428043	T92248	Hs.2240	uteroglobin	0.42	1.26
	430280	AA361258	Hs.237868	Interleukin 7 receptor	0.46	2.43
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DXFZp564B2062 (f	0.29	1.80
	432985 441835	T92363	Hs.178703	ESTS	0.32 0.31	2.27
	442275	AB036432 AW449467	Hs.184 Hs.54795	advanced glycosylation end product-speci ESTs	0.55	1.51 1.78
	443709	A1082692	Hs.134662	ESTs	0.00	3.02
15	444325	AW152618	Hs.16757	ESTs	0.32	2.49
	450954	A1904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmille	0.00 0.01	3.30
20	456855 444342	AF035528 NM_014398	Hs.153863 Hs.10887	MAD (mothers against decapentaplegic, Dr similar to hysosome-associated membrane	0.66	2.31 2.20
20	400754	148_014030	113.10007	Target Exon	1.00	297.00
	401045			C11001883*:gij6753278 ref[NP_033938.1 c	1.00	109.00
	401083			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
25	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
25	402808			ENSP00000235229:SEMB.	1.00 1.00	1.87 149.00
	403021 403438			C21000030:gij9955960[ref]NP_063957.1 AT NM_031419*:Homo sapiens molecule possess	1.06	2.96
	403687			NM_007037*Homo saplens a disintegrin-li	0.04	4.89
	403764			NM_005463:Homo sapiens heterogeneous nuc	1.00	225.00
30	404277			NM_019111°:Homo sapiens major histocompa	0.97	1.93
	404288	. 104 0004		NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518 405106	Al815601		CD83 antigen (activated B lymphocytes, i	0.02 1.00	1.83 235.00
	405381			C11001637*:gi]5032241 ref NP_005732.1 z Target Exon	1.00	93.00
35	406387			Target Exon	1.37	6.02
	406646	M33600		major histocompatibility complex, class	0.86	2.48
	406714	Al219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973 407248	M34996 U82275	Hs.198253 Hs.94498	major histocompatibility complex, class teukocyte immunoglobulin-like receptor,	1.03 1.00	2.04 64.00
40	407510	U96191	113.34430	gb:Human trophoblast hypoxia-regulated f	1.00	90.00
	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	1.00	67.00
	407830	NM_001086	Hs.587	arytacetamide deacetylase (esterase)	1.00	102.00
15	408045	AW138959	Hs.245123	ESTs	1.00	70.00
45	408074	R20723	11- 455504	ESTs	1.00	112.00
	408374 409064	AW025430 AA062954	Hs.155591 Hs.141883	forkhead box F1 ESTs	0.07 0.39	10.17 2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00	95.00
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.01	4.55
50	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	0.01	3.72
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389 409718	AB007979 D86640	Hs.301281 Hs.56045	Homo sapiens mRNA, chromosome 1 specific	0.14 1.00 .	27.35 113.00
	410798	BE178622	Hs.16291	src homotogy three (SH3) and cysteine it gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64	2.47
55	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	0.55	2.40
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172 Hs.73853	ESTs	1.00	87.00 8.07
60	412420 412564	AL035668 XB3703	Hs.31432	bone morphogenetic protein 2 cardiac ankyrin repeat protein	1.43 0.02	3.07
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	0.93	1.72
	412870	N22788	Hs.82407	CXC chemokine ligand 16	0.97	1.51
	413529	U11874	Hs.846	interteukin 8 receptor, beta	0.02	2.42
65	413533	BE146973	Us noons	gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
05	413689 413724	BE157286	Hs.20631 Hs.23767	zinc finger protein, subfamily 1A, 5 (Pe	20.87 1.00	232.00 80.00
	413800	AA131465 AJ129238	Hs.192235	hypothetical protein FLJ12666 ESTs	1.00	85.00
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	1.00	213.00
70	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	0.02	3.93
70	414376	BE393856	Hs.66915	ESTs, Wealdy similar to 16.7Kd protein [1.00	115.00
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700 415078	H63202 AA311223	Hs.38163 Hs.283091	ESTs found in inflammatory zone 3	0.03 0.86	3.75 1.95
	415120	N64464	Hs.34950	ESTs	1.00	120.00
75	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60	2.48
	415335	AA847758	Hs.111030	ESTs	1.00	95.00
	415582	W92445	Hs.165195	Homo sapiens cDNA FLJ14237 fis, clone NT	1.00	136.00
	416030	H15261	Hs.21948	ESTs Resident? mustine exchange factor (GER)	0.02	8.07 73.00
80	416427 416464	BE244050 NM_000132	Hs.79307 Hs.79345	Rac/Cdc42 guardine exchange factor (GEF) coagulation factor VIII, procoagulant co	1.00 0.70	73.00 3.36
-	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	0.70	3.66
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	1.00	114.00
85	417370	T28651	Hs.82030	tryptophanyl-IRNA synthetase	0.85	1.30
55	417673	T87281	Hs.16355	ESTS	0.15	15.54

	W	O 02/086	443			
	418067	Al127958	Hs.83393	cystatin E/M	0.81	1.74
	418296	C01566	Hs.86671	ESTs	1.00	99.00
	418543	J03798	Hs.86948	small nuclear ribonucleoprotein D1 polyp	1.00	60.00
-	418832	X04011	Hs.88974	cytochrome b-245, beta polypeplide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261	X07876	Hs.89791	wingless-type MMTV Integration site fami	1.00	73.00
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	1.00	192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (Interferon, bela 2)	61.16	500.00
10	420256	U84722	Hs.76205	cadherin 5, type 2, VE-cadherin (vascula	0.52	1.70
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	1.00	172.00
	420577	AA278436	Hs.186649	ESTs	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88	1.51
15	421470	R27496	Hs.1378	ennexin A3	0.05	11.26
	421478	Al683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50	31 <i>.</i> 57 129.00
20	421855	F06504	Hs_27384	ESTs, Moderately similar to ALU4_HUMAN A	1.00	
20	421913	Al934365	Hs.109439	osteoglycin (osteoinductive factor, mime	1.00	101.00 63.60
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	148.00
	422232	D43945	Hs.113274	transcription factor EC	1.00	3.98
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-0-sulfot	1.40 0.34	3.59
25	423168	R34385	Hs.124940	GTP-binding protein	0.55	2.00
23	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.09	2.13
	423387	AJ012074 AF150241	Hs.128433	vasoactive intestinal peptide receptor 1	1.00	141.00
	423424			prostaglandin D2 synthase, hematopoietic	1.00	66.00
	423456	AL110151	Hs.128797	DKFZP586D0824 protein	0.73	1.27
30	423696	Z92548	Hs.201591	Sushi domain (SCR repeat) containing ESTs	0.54	2.58
50	424027	AW337575	Hs.143131	glycoprotein A33 (transmembrane)	0.77	2.47
	424212 425087	NM_005814 R62424	Hs.126059	ESTs	1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56
35	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DXFZp586B0220 (f	1.00	76.00
55	427507	AF240467	Hs.179152	toll-like receptor 7	1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42
	427952	AA765368	Hs.293941	ESTs, Moderately similar to A53959 throm	1.00	105.00
40	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	1.00	80.00
	428769	AW207175	Hs.106771	ESTs	0.09	2.55
	428780	Al478578	Hs.50636	ESTs	1.00	98.00
	428833	AI928355	Hs.185805	ESTs	1.00	113.00
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	1.00	52.00
45	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11	15.60
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	1.00	103.00
	430414	AW365665	Hs.120388	ESTs	0.50	6.96
	430656	AA482900	Hs.162080	ESTs	1.00	70.00
50	430843	AJ734149	Hs.119514	ESTs	1.00	90.00
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.29	1.84
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
	432176	AW090386	Hs.112278	arrestin, beta 1	0.66	2.63
55	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.00	76.00
	432231	AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25
	432522	D11466	Hs.51	phosphatidylinositol glycan, class A (pa	1.93	4.83
60	432596	AJ224741	Hs.278461	matritin 3	0.04	5.79
60	432850	X87723	Hs.3110	anglotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04	9.16
	433563	Al732637	Hs.277901	ESTs	1.00	91.00
	433588	AI056872	Hs.133386	ESTs	120.16	315.00
65	434445	AI349306	Hs.11782	ESTs	0.60 1.00	1.84 128.00
UJ	435496	AW840171	Hs.265398	ESTs, Wealdy similar to transformation-r Homo sapiens beta-1 adrenergic receptor	1.00	108.00
	435974	U29690 A1248584	Hs.37744		1.00	91.00
	436061	BE048860	Hs.190745 Hs.120655	Homo sapiens cDNA: FLJ21326 fis, clone C ESTs	1.00	87.00
	437157 437207	T27503	Hs.15929	hypothetical protein FLJ12910	1.00	105.00
70	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	1.00	71.00
, 0	437439	H29795	Hs.269622	ESTs	1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112	ESTs	0.30	3.10
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	1.00	77.00
75	440887	AI799488	Hs.135905	ESTs	1.00	85.00
. •	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	0.79	1.89
	441735	AI738675	Hs.127346	ESTs	1.00	75.00
	442200	AW590572	Hs.235768	ESTs	0.78	5.83
80	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957	AI949952	Hs.49397	ESTs	1.00	70.00
	443282	T47764	Hs.132917	ESTs	1.00	197.00
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	1.00	253.00
	443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
85	444330	Al597655	Hs.49265	ESTs	1.00	90.00

WO 02/086443 PCT/US02/12476 84.00 444515 AW204908 Hs.169979 ESTs 0.02 4.38 445769 A1741471 Hs 23666 **FSTs** Hs.13436 97.00 445908 Homo saplens clone 24425 mRNA sequence 1.00 R13580 Hs.14623 interferon, gamma inducible protein 30 0.93 1.69 446291 BE397753 5 106.00 446917 AJ347863 Hs.156672 **ESTs** 1.00 0.40 extracellular link domain-containing 1 nudix (nucleoside diphosphate linked moi 47.20 447261 NM_006691 Hs.17917 1.00 100.00 AW958473 447432 Hs.301957 447482 AB033059 Hs.18705 KIAA1233 protein 8.21 Hs.29792 ESTs, Wealthy similar to 138022 hypotheti 0.02 5.42 447997 H00656 10 79.00 448299 AA497044 Hs.20887 hypothetical protein FLJ10392 1.00 KIAA0758 protein Hs.22039 1,56 AL050295 0.42 448782 purine-rich element binding protein A ESTs 11.33 Hs.29117 0.17 NM 005859 450575 Hs.60371 94.00 450584 AA040403 1.00 450693 AW450461 Hs.203965 1.00 91.00 **ESTs** 15 152.00 450715 AJ266484 Hs.31570 ESTs, Weakly similar to KIAA1324 protein 1.00 DKFZP564D206 protein 1.00 86.00 451103 R52804 Hs.25956 Hs.26054 novel SH2-containing protein 3 0.60 1.30 AF124251 Z43948 451220 Hs.326444 0.54 1.91 451668 cartilage acidic protein 1 Hs.232048 1.00 67.00 452197 AW023595 20 AA598509 purine-rich element binding protein A 452331 Hs.29117 4.53 11.07 2.24 epithelial membrane protein 2 0.72 452353 C18825 Hs.29191 Hs.30343 1.00 68.00 BE537217 453049 **ESTs** 453107 NM_016113 Hs.279746 vaniiloid receptor-like protein 1 0.83 1.70 Hs.31412 Homo sapiens cDNA FLJ11422 fis, clone HE 1.00 132.00 453355 AW295374 25 453390 AA862496 Hs.284B2 **ESTs** 1.00 72.00 ESTs, Wealdy similar to JC\$795 CDEP prot gb:CM2-HT0342-091299-050-b05 HT0342 Homo 68.00 1.00 453531 AA41794D BE154398 454741 0.57 456579 AA287827 Hs.284205 up-regulated by BCG-CWS 1.00 82.00 Homo sapiens, clone MGC:16327, mRNA, com 456672 AK002016 Hs.114727 0.79 1.96 30 457400 AF032906 Hs.252549 cathepsin Z 1.03 3.25 113.00 457718 F18572 Hs.22978 ESTs. Weakly similar to ALU4_HUMAN ALU S 1.00 gb:HSC1KA072 normalized Infant brain cDN 1.00 544.00 459696 F03027 TABLE 10B 35 Unique Eos probeset identifier number CAT number. Gene cluster number Accession: Genbank accession numbers 40 Accession Pkey 408074 **CAT Number** R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AIB10530 D31302 AW134897 AAB30127 AA046953 AI668930 103684_1 BE160193 AW935898 T11520 AW935930 AW856073 AW861034 BE146973 BE146972 BE147042 BE147018 BE146783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146797 BE146776 BE146985 BE146793 BE146768 BE146771 BE146954 BE146760 BE147048 BE147025 BE147030 411667 1253334_1 413533 1375344_1 45 AJ012074 U11087 L13288 X75299 L20295 AW630780 H1488D T28037 AJ872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 423387 22779_1 AD1014 D1107 C13286 X3255 12023 H0507 H050 50 423696 Z92546 AA330586 AI570568 AW341487 AI827050 AW298668 AI792189 AI015693 AI733599 AI572251 AI672488 AW193262 AI244716 23112 1 Al864375 Al206100 AA912444 Al269365 Al640254 AW772466 Al867336 AA627604 H16914 AA358477 AA338009 430212 314437_1 AA469153 AI718503 AA469225 AA721522 AW975443 T93070 436532 421802_1 55 97026 1 AA417940 AA036735 T07025 453531 BE154396 AW817959 BE154393 454741 1232559_1 TABLE 10C 60 Pkey: Ref: Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons. 65 Nt_position 400754 401045 7331445 8117619 Plus 144559-144684 90044-90184,91111-91345 Plus 70 401083 3242744 33192-33360 Pius 7547175 53526-53628,55755-55920,57530-57757 402474 114964-115136,115461-115585,115931-116047,117666-117771,118004-118102 402808 6456148 Minus 7547270 9665041 120799-120966 403021 Plus 126609-126773,139986-140205 403421 Minus 75 403438 9719679 Plus 90792-90938 403687 7387384 9009-9534 118692-118853 403764 7717105 Minus 91665-91946 404277 1834458 Minus 404288 2769644 Phrs 3512-3691 80 404394 3135305 Minus 37121-37205,37491-37762,41053-41140,41322-41593,41773-41919 404518 8151988 84494-84603 404916 7341826 Plus 91057-91188 80877-81418 405106 8079395 Minus 7329310 Plus 73121-73273 405257

7636-8054

85

405381

6006920

Table 11A shows about 84 genes upregulated in tung adenocarcinomas relative to other tung tumors, non-malignant tung disease, and normal tung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 118 show the accession numbers for those Pkey's lacking UnigenetD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland Catifornia). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 11C show the genomic positioning for those Pikey's lacking Unigene ID's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: 15 ExAcon:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number Unigene Tille: Unigene gene title

5

10

Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the R1:

average of normal lung samples

Average of normalignant lung disease samples (including bronchilis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples 20 R2:

	Pkey 403329	ExAccn	UnigenelD	Unigene Tille Target Exon	R1 1.00	R2 61.00
25	406399 406690	M29540	Hs.220529	NM_003122*:Homo sapisns serine protease carcinoembryonic antigen-related cell ad	1.00 226.37	39.00 350.00
	407869	A1827976	Hs.24391	hypothetical protein FLJ13612	0.77 1.00	1.18 10.00
	407881 408908	AW072003 BE296227	Hs.40968 Hs.250822	heparan sulfate (glucosamine) 3-0-sulfot serine/threonine kinase 15	7.76	1.00
	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
30	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89 0.92	1.00 1.06
35	410399	8E068889 L27943	Hs.72924	synuclein, gamma (breast cancer-specific cytidine deaminase	1.00	1.00
33	411908 412612	NM_000047	Hs.74131	aryisulfatase E (chondrodysplasia puncta	1.02	1.03
	414075	U11862	Hs.75741	amilaride binding protein 1 (amine oxida	0.84	1.07
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
40	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
40	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419502	AU076704	U- 202454	fibrinogen, A alpha polypeptide	13.05 1.00	115.00 13.00
	419631 420931	AW188117 AF044197	Hs.303154 Hs.100431	popeye protein 3 small inducible cytokine B subfamily (Cy	1.00	8.00
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
45	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	1.00	3.00
	421582	Al910275		trefoll factor 1 (breast cancer, estroge	1.23	1.00
50	422026	U80736	Hs.110826	trinucleofide repeat containing 9	1.00 4.37	52.00 2.34
50	422095 422311	AI868872 AF073515	Hs.282804 Hs.114948	hypothetical protein FLJ22704 cytokine receptor-like factor 1	1.15	1.78
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.69	3.17
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
55	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
	424905 424960	NM_002497 BE245380	Hs.153704 Hs.153952	NIMA (never in mitosis gene a)-related k	21.35 1.00	1.00 1.00
	425523	AB007948	Hs.158244	5' nucleotidase (CD73) KIAA0479 protein	1.00	35.00
60	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
	427701	AA411101	Hs.243886	nuclear autoanligenic sperm protein (his	7.41	34.00
	428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1,13
65	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
UJ	429263 429610	AA019004 AB024937	Hs.198396 Hs.211092	ATP-binding cassette, sub-family A (ABC1 LUNX protein; PLUNC (palate lung and nas	1.07 1.59	1.00 1.69
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430985	AA490232	Hs.27323	ESTs, Weakly similar to 178885 serine/th	0.94	1.28
	431548	AJ834273	Hs.9711	novel protein	5.66	15.00
70	431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	1.19	1.47
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432677 433556	NM_004482 W56321	Hs.278611 Hs.111460	UDP-N-acetyl-alpha-D-galactosamine:polyp calcium/calmodulin-dependent protein kin	1.00 1.00	48.00 19.00
75	433819	AW511097	Hs.112765	ESTs	3.71	8.00
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29,31	72.00
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	1.00	64.00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
οΛ	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
80	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
	436972 437866	AA284679 AA156781	Hs.25640	claudin 3 metallothioneln 1E (functional)	1.59 3.62	1.46 101.00
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
85	439451	AF086270	Hs.278554	heterochromalin-like protein 1	23.28	52.00

	w	O 02/086	443				PCT/US02/12476
5	441377 443614	Al110684 BE218239 AV655386	Hs.67709 Hs.7645 Hs.202656 Hs.7645	Homo saptens mRNA full tength insert cDN fibrinogen, 8 beta polypeptide ESTs fibrinogen, 8 beta polypeptide	1.00 1.41 22.03 1.00	21.00 99.00 1.00 16.00	
,	443991 444570	AA876372 NM_002250 H58373 AV652066	Hs.93961 Hs.10082 Hs.332938 Hs.75113	Homo sapiens mRNA; cDNA DXFZp6670095 (fr potassium intermediatelsmall conductance hypothetical protein MGC5370 general transcription factor INA	1.20 5.71 1.98 1.00	1.99 6.87 33.00 54.00	
10	446163 446469 447388	AW168067 AA026880 BE094848 AW630534 AK000614	Hs.317694 Hs.25252 Hs.15113 Hs.76277 Hs.18791	ESTs Homo sagiens cDNA FLJ13603 fis, clone PL homogentisate 1,2-dioxygenase (homogenti Homo sagiens, clone MGC:9381, mRNA, comp hypothetical protein FLJ20607	1.00 1.00 1.00 1.24 1.23	1.00 36.00 11.00 1.16 1.63	
15	448243 448844 449444 451807	AW369771 AL581519 AW818436 W52854	Hs.52620 Hs.177164 Hs.23590	integrin, beta 8 ESTs solute carrier family 16 (monocarboxylic hypothetical protein FLJ23293 similar to	15.84 1,00 1,00 1,55	1.00 31.00 83.00 35.00	
20	453392 453464	F33868 U23762 Al884911 Al066629	Hs.284176 Hs.32964 Hs.32989 Hs.125073	transferrin SRY (sex determining region Y)-box 11 receptor (calcitonin) activity modifying ESTs	1.54 · 1.00 1.55 1.01	1.44 16.00 2.45 1.30	
	TABLE 11	В					
25	Pkey: CAT numb Accession:	er: Gene dust		nlifier number bers			
30	Pkey 410399	CAT Number 11995_1	BE068 Al9365	lon 189 BE068882 AF044311 AF017256 NM_003087 A1 27 AA804675 AA394097 A1139933 AA946606 BE17 737 H49348 AA486472 AA411094 AA235594 AA40	1313 AA722407	7 AA293803 A146848	30 AA056035 AA055968 AW796957 Al637713
	419502	18535_1	AU076	704 T74854 T74860 T72098 T73265 T73873 T6918 7 T68401 T53959 T72360 T72099 T60377 T58961 T	0 T74658 T5878	36 T60385 T73410 T	68781 T67845 T67593 T73952 T67864 T60630
35			T68220 T73203 T74756 T71916	173693 173690 183855 161227 162738 163931 1 1774673 171800 168355 161227 162738 163317 1 1770498 161409 158925 NM_000508 M64982 1685 1760477 174863 161109 168329 158850 171857 1 1773787 156035 164425 171870 160476 161376 1 177914 153393 164121 AA693398 172525 16777	53850 T64692 1 301 T73729 T69 73425 T53736 1 67820 T71895 1	173768	382 T68914 T70975 T73400 T60631 T73277 T67736 T68716 T67755 T74765 T73819 T58719 309 T72031 T72079 T64305 T71908 T68107 170 T74617 T71958 T69440 T61875 R05796
40			N33594 AA312 AW470 AA2352	1 AA344542 AW805054 A1207457 T61743 AA02573 919 T40156 H66239 AV852989 H38728 P88521 AV 774 AV851256 N54417 AA812882 AW182829 Al11 9252 T27853 T47778 R95748 H70620 AA701463 AW 1 T73931 T72178 T72456 AV645639 AV653476 T72	7 H94389 AA38 655200 R95790 1192 H61463 H 1827166 R98475	12695 AA918409 T68 1 W03250 W00913 A 72060 AA344503 H3 5 C20925 AV657287	2044 S82092 T39959 A1017721 AA312395 A344136 AV660126 R97923 AA343596 18639 A1277511 AV661108 A1207625 T47810 T71959 T71313 T73920 T73333 T61618 T69293
45	•		AA3447 T70475 T72517 T69368	726 127854 174485 174101 173868 171518 17230 164751 A3344441 A3343657 A3345732 A33432 1 (802292 160599 169206 170452 174677 R29366 1 1 169358 168258 A4650429 173341 161702 174593	4 AA343853 T7: 8 Al110639 AA: 161277 T74914 8 T40095 K0227	3909 T68070 T7206: 344603 AF063513 T6 T60352 R29675 T74 72 T40106 AA34304:	5 H72149 T73493 T73495 AV645993 R02293 54696 T68516 T72223 T60507 T67633 R29500 843 AV645792 AA344408 T69197 T72057 5 AA341908 AA341907 AA342807 AA341964
50			AA345 AA344 AA693	* T72042 T62764 A1054899 AA343080 T67832 T724 234 T67598 AA011414 T68036 H48262 A1207557 T1 583 T60362 H58121 T95711 T72803 T68055 T7171 592 A1248502 R29454 T64764 T57001 T73052 T711 * T73317 T74273 T69420 T68245 T74380 T67862 T	68219 W86031 [*] 5 R29036 T727 129 T51176 T58	T69081 T64232 R93 93 T69122 T64595 T	196 T62136 AV650539 H67459 T72978 62888 T69139 T68291 T64652 T67971 T46862
55	421582	2041_1	AA5583 BE0741	75 X00474 X52003 X05030 NM_003225 AA314326 812 AA614409 AA307578 A1925552 AW950155 AI9 140 AA514776 AA588034 BE074051 BE074068 AW 145 A1307407 AW602303 BE073575 A1202532 AA5	10083 M12075 I 009769 AW050	BE074052 AW00466 690 AA858276 R553	8 AA578674 AA582084 BE074053 BE074126 189 Al001051 AW050700 AW750216 AA614539
	437866	44433_2	AA156	781 AW293839 U52054 AA024963 AA778446 BE07 181 AW468444 BE185091 AW468002 AA687333 AA	3977 AW44490	4 AW602574 BE164	040 BE164012 BE163972 BE163974 BE163992
60	451807	8865_1	AA8124 W5285	IS9 AW874142 AI471883 W84421 AA156850 4 AL117600 BE208116 BE208432 BE206239 BE08: 652 AW449519 AA993634 AI806539 AA351618 AW	2291 AW953423	3 AA351619 BE1806	48 BE140560 W60080 AA865478 N90291
65	TABLE 11	С					
	Pkey: Ref:			nding to an Eos probeset digit numbers in this column are Genbank Identifier	(GI) numbers. '		, ers to the publication entitled "The DNA
70	Strand: Nt_position	sequence of Indicates D	of human chro NA strand from	mosome 22.° Dunham I. et al., Nature (1999) 402:40 n which exons were predicted. tions of predicted exons.			
	~						

Ref 8516120 9256288

75

Nt_position 96450-96598 63448-63554 WO 02/086443 PCT/US02/12476

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung turnors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechtp array. 5

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the 10 "Accession" column.

Table 12C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15

Pkey:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number ExAcon: UnigenelD:

Unigene Title: Unigene gene title

20 Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the R1:

average of normal lung samples

Average of normal lung disease samples (Including bronchilis, emphysema, fibrosis, atelectasis, esthma) divided by the average of normal lung samples R2:

	KZ:	Average	or non-maugn	and rung disease samples (including dronchlus, emphy	sema, morosis, a	Leierzesis, es
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
25	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
	400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
	401780			NM_005557*:Homo saplens keratin 16 (foca	26.47	10.50
	401781			Target Exon	10.33	4.61
	401785			NM_002275*:Homo saptens keratin 15 (KRT1	4.13	2.70
30	401994			Target Exon	61.84	47.00
	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
	404996			Target Exon	1.00	1.00
	407839	AA045144	Hs.161566	ESTs	173.91	108.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00
35	408522	AJ541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	10.04	1.00
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1.00
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00
40	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00
70	417366	BE185289	Hs.1076	small proline-rich protein 18 (comifin)	8.97	3.27
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00
			Hs.87225	cancerflestis artigen	1.18	1.10
	418678	NM_001327			1.00	1.00
45	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	3.04	1.25
43	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.12	1.14
	421773	W69233	Hs.112457	ESTs		
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25
	421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91
50	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10
30	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	47.53	32.00
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
E E	424012	AW368377	Hs.137569	turnor protein 63 kDa with strong homolog	233.42	68.00
55	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00
	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00
60	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00
60	427335	AA448542	Hs.251677	G antigen 7B	51.83	4.00
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428645	AA431400	Hs.98729	ESTs, Wealthy similar to 2017205A dilhydro	1.00	16.00
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00
15	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
65	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
70	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00
70	431846	BE019924	Hs.271580	uroplakin 1B	4.49	2.51
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20	1.09
	434360	AW015415	Hs.127780	ESTs	40.98	27.00
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00
	435505	AF200492	Hs.211238	interteukin-1 homolog 1	1.00	38.00
75	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436511	AA721252	Hs.291502	ESTs	16.76	14.00
	438403	AA806607	Hs.292206	ESTs	1.00	1.00
	439285	AL133916		hypothetical protein FLJ20093	46.23	139.00
	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
80	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	62.88	147.00
	441525	AW241867	Hs.127728	ESTs	1.53	1.42
	443162	T49951	Hs.9029	DKFZP434G032 protein	31.11	38.00
85	444378	R41339	Hs.12569	ESTs	1.00	1.00

	WC	02/086	443		PCT/US02/12476							
		AF081497	Hs.279682	Rh type C glycoprotein	1.55 47.24	1.26 24.00						
		AW885727 Al199268	Hs.9914 Hs.19322	ESTs Homo saplens, Similar to RIKEN cDNA 2010	28.63	1.00						
		X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	1.00	1.00						
5	449101	AA205847	Hs.23016	G protein-coupled receptor	2.58	27.00						
		AW970602	Hs.105421	ESTs	25.17	36.00						
		AJ591147 NM_002277	Hs.61232 Hs.41696	ESTs keratin, hair, acidic,1	13.42 1.19	1.00 1.27						
		AA534296	Hs.20953	ESTs	24.92	25.00						
10		W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26	1.11						
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00						
	TABLE 12B											
1.5												
15	Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number											
	Accession:		cession numb	ers								
20	Pkey 439285	CAT Number 47065_1	Accession At 1339	27 16 N79113 AF086101 N76721 AW950828 AA36401:	3 AW955684 AI34	6341 Al867454 N54784 A	1655270 Al421279 AW014882					
	AA775552 N62351 N59253 AA626243 AJ341407 BE175639 AA456968 AJ358918 AA457077											
0.5	TABLE 120	TABLE 12C										
25	Pkey:	Liniano era	ther come non	ding to an Ene embased								
	Ref:	Sequence s	Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA									
		sequence o	f human chron	rosome 22.° Dunham I. et al., Nature (1999) 402:48	9-495.							
30	Strand:			which exons were predicted.								
30	Nt_position:	indicates n	ociecuue posiu	ons of predicted exons.		·						
	Pkey	Ref	Strand	NI_position								
	400666	8118496	Plus	17982-18115,20297-20456 28397-28617,28920-29045,29135-29296,29411-2	0557 20705 2070	7 20224 20572						
35	401780 401781	7249190 7249190	Minus Minus	83215-83435.83531-83656.83740-83901.84237-8								
55	401785											
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-4								
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,								
40	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-4	0014,42331-4243	v						

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

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Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechtip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the ofigoruc/ecitides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 13C show the genomic positioning for those Pikey's lacking Unigens ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15		11-1	- Cb	akida affica assanka a			•				
13	Pkey:		Unique Eos probeset identifier number								
	ExAcon:			n number, Genbank accession number							
	UnigenelD: Unigene number										
	Unigene Ti		ne gena title								
20	R1:				nomas, small cet	carcinomas, granulomatous and carcinoid tumors) divided t	by the				
20			ge of normal l								
	R2:	Avera	ge of non-ma	lignant lung disease samples (including bronchitis, err	iphysema, fibrosis	, atelectasts, asthma) divided by the average of normal lung	sample				
	Pkey	ExAcon	UnigenelD	Unigene Title	RI	R2					
		Al436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00					
25		AA376836	Hs.76728	ESTs	1.00	128.00					
		R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00					
		U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00					
		AL049176	Hs.82223	chordin-like	1.00	179.00					
		AA228776	Hs.191721	ESTs		140.00					
30					1.00						
30		R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00					
		AA464840	Hs.131987	ESTs	1.00	167.00					
		T89832	Hs.170278	ESTs	1.00	141.00					
		AA453800	Hs.192793	ESTs	1.00	138.00					
25		AA488988	Hs.293796	ESTs	1.00	133.00					
35		BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00					
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00					
		NM_007351	Hs.268107	multimerin	1.00	157.00					
	436532	AA721522		gb:nv54h12.r1 NCl_CGAP_Ew1 Homo sapiens	1.00	218.00					
	437960	AJ669586	Hs.222194	ESTs	1.00	147.00					
40	438202	AW169287		ESTs	1.00	141.00					
	441499	AW298235	Hs.101689	ESTs	1.00	167.00					
		AL120214	Hs.7117	glutamate receptor, tonotropic, AMPA 1	1.00	151.00					
		H25899	Hs.201591	ESTs	1.00	141.00					
		R67837	Hs.169872	ESTs	1.00	116.00					
45		Al000341	Hs.220491	ESTs	1.00	192.00					
		AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00					
	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			Barrison in London Tradition Comments		10 1100					
	TABLE 138	3									
50 ⁻	-										
20	Pikey:			entifier number .							
		er: Gene dus		•							
	. Accession:	Genbank	accession nu	mbers							
	Pkey	CAT Num	ber Accessio	•							
55	431089	327825_1		5 AA491826 AA621946 AA715980 AA666102							
00	436532	421802_1		2 AW975443 T93070							
	100002	421002_1	1 7002102	2 A11313440 130010							
	TABLE 130	;									
60											
	Pkey:	Unique nu	umber corresp	onding to an Eos probeset							
	Ref:				(GI) numbers. "E	ounham I, et al." refers to the publication entitled "The DNA					
				romosome 22.° Dunham I. et al., Nature (1999) 402:4		• • • • • • • • • • • • • • • • • • • •					
	Strand:			om which exons were predicted.							
65	Nt_position			sitions of predicted exons.							
	Pkey	Ref	Strand	NL position							
70	402075	8117407	Plus	121907-122035,122804-122921,124019-124161	,124455-124610,	125672-126076					
70											

WO 02/086443 PCT/US02/12476 TABLE 14A: Preferred Utility and Subcellular Localization for Polential Lung Disease Targets

Table 14A shows the subcetular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecute, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. 5

Table 148 show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleofide locations of each predicted exon are also listed.

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Pkey: Unique Eos probeset identifier number

Presy: Unique Eos procesei identitater number
Exacon: Exemplar Accession number, Genbank accession number
Unique Title: Unique gene title
Pref. Utility: Preferred Utility
Pred. Loc: Preferred utility

	Pkey	ExAcon	UnipenelD	Unigene Title	Pref Utility	Pred. Loc
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	mAb & diag & s.m.	extracellular
25	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
-	402075			ENSP00000251056":Plasma membrane calcium	mAb & diag	secreted
	407811	AW190902	Hs.40098	cystelne knot superfamily 1, BMP antagon	diag	secreted
	408243	Y00787	Hs.624	interleukin 8	diag	secreted
••	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
30	408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
	409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	diag	secreted
25	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
35	409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL	nuclear .
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	diag	extracellular
	410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
40	410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
40	410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	s.m.	
	412719	AW016610	Hs.816	ESTs	s.m.	nuclear
	414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
15	414883	AA926960		CDC28 protein kinase 1	s.m.	
45	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag	extracellular
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	mAb & diag & s.m.	secreted
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrana
	41665B	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
50	417034	NM_006183	Hs.80962	neurotensin	diag	extracellular
50	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
	417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	πAb	plasma membrane
5 5	417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
22	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	6.M.	cytoplasm
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
60	419171	NM_002846	Hs.89655		mAb & s.m.	plasma membrane
UU	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
	419216	AU076718	Hs.164021		diag	secreted
	419235	AW470411	Hs.288433		mAb & diag	plasma membrane
	419452	U33635	Hs.90572		mAb & s.m.	plasma membrane
65	419556	U29615	Hs.91093	chilinase 1 (chitotriosidase)	mAb & diag	extracellular*
03	420610	AI683183 AJ250717	Hs.99348	distal-less homeo box 5	CTL	nuclear
	421110	Y15221	Hs.1355	cathepsin E	sm & diag	extracellular
	421379 421474	U76362	Hs.103982		diag	secreted
	421474	AF026632	Hs.104637 Hs.105700		mAb & s.m.	plasma membrane secreted
70	421753	BE314828	Hs.107911		diag	
70	421753	AF146074	Hs.108660		mAb & s.m.	plasma membrane
	422109	S73265	Hs.1473		mAb & s.m. diao	plasma membrane secreted
	422158	L10343	Hs.112341			
	422282	AF019225	Hs.114309		diag diag	secreted secreted
75	422283	AW411307	Hs.114305			nuclear
, ,	422424	A1186431	Hs.296638		s.m. diao	extracellular
	422765	AW409701	Hs.1578			cytoplasm
		AK001379	Hs.121028		s.m. s.m.	nuclear
	422867	L32137	Hs.1584		s.n. điao	extracellular
80	422956	BE545072	Hs.122579		CTL & s.m.	DAU GERHAIDI
50	423634	AW959908	Hs.1690		qisa Cire sur	
	423573	BE003054	Hs.1695		mAb & diag & s.m.	secreted
	423961	D13666	Hs.136348		mAb & diag	extracellular
	424046	AF027856	Hs.138202		diag	secreted
85	424381	AA285249	Hs.146329		S.M.	nuclear
	(L 100)		1 1	Province Mark	V412	

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	W	O 02/086	443			
	424502	AF242388	Hs.149585	tengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687 425247	J05070 NM_005940	Hs.151738 Hs.155324	matrix metalloproteinase 9 (gelatinase 8 matrix metalloproteinase 11 (stromelysin	diag mAb & diag & s.m.	extracellular secreted
5	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	S.M.	cytoplasmic
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	mAb	plasma membrane
	425734 425776	AF056209 U25128	Hs.159396 Hs.159499	peptidylglycine alpha-amidating monocxyg	s.m. mAb & diag	plasma membrane
	425852	AK001504	Hs.159651	parathyroid hormone receptor 2 death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
10	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.159840	TTK protein kinase	CTL & s.m.	nuclear
	426514 427335	BE616633 AA448542	Hs.170195 Hs.251677	bone morphogenetic protein 7 (osteogenic G antigen 7B	mAb & diag CTL	secreted cytoplasmic
	427747	AW411425	Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330 428450	L22524 NM_014791	Hs.2256 Hs.184339	matrix metalloproteinase 7 (matrilysin, KIAA0175 gene product	mAb & diag & s.m. s.m.	extracellular nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	S.M.	nuclear
00	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	mab & s.m.	plasma membrana
20	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
	428698 428748	AA852773 AW593206	Hs.334838 Hs.98785	KIAA1866 protein Ksp37 protein	mAb diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; much 16	diag	mitochodria*
25	428969	AF120274	Hs.194689	artemin	diag	extracellular
23	429211 429263	AF052693 AA019004	Hs.198249 Hs.198396	gap junction protein, beta 5 (connexin 3 ATP-binding cassette, sub-family A (ABC1	mAb & s.m. mAb & s.m.	plasma membrane plasma membrane
	429547	AW009166	Hs.99376	ESTs	diag	secreted
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
30	429903 430486	AL134197 BE062109	Hs.93597	cyclin-dependent kinase 5, regulatory su chloride channel, calcium activated, fam	s.m. mAb & s.m.	plasma membrane
50	431462	AW583672	Hs.241551 Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m.	plasma membrane
	431846	BE019924	Hs.271580	uroplakin 1B	mAb & diag	plasma membrane
35	431958 432201	X63629 Al538613	Hs.2877 Hs.298241	cadherin 3, type 1, P-cadherin (placenta Transmembrane protease, serine 3	mAb & diag mAb & diag & s.m.	plasma membrane plasma membrane
55	433001	AF217513	Hs.279905	clone HQ0310 PR00310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	diag	secreted
	436481° 437016	AA379597 AU076916	Hs.5199 Hs.5398	HSPC150 protein similar to ubiquifin-con guarrine monphosphate synthetase	s.m. s.m.	cytoplasm
40	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	CTL	ER
-	437789	AJ581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheli	CIL	nuclear
	437852	BE001836	Hs.256897	ESTs, Wealdy similar to dJ365012.1 [H.sa	mAb & s.m. mAb	plasma membrane plasma membrane
	439223 439477	AW238299 W69813	Hs.250618 Hs.58042	UI.16 binding protein 2 ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	piasina memorane
45	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m.	plasma membrane
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	mAb & s.m.	plasma membrane nuclear
	440006 441362	AK000517 BE614410	Hs.6844 Hs.23044	NALP2 protein; PYRIN-Containing APAF1-ti RAD51 (S. cerevisiae) homolog (E coli Re	s.m. s.m.	Inucical
	442117	AW664954	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
50	443247	BE614387	Hs.333893	c-Myc target JP01	CTL	extracellular*
•	443426 443859	AF098158 NM_013409	Hs.9329 Hs.9914	chromosome 20 open reading frame 1 follistatin	CTL diag	extracellular
	444005	BE395085	Hs.10086	type I transmembrane protein Fn14	mAb	plasma membrane
55	444371	BE540274	Hs.239	forkhead box M1	s.m.	nuclear
55	444381 444781	BE387335 NM_014400	Hs.283713 Hs.11950	ESTs, Weakly similar to \$64054 hypotheti GPI-anchored metastasis-associated prote	điag mAb & diag	secreted plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag	secreted
60	446921 447033	AB012113 Al357412	Hs.16530 Hs.157601	small inducible cytokine subfamily A (Cy ESTs	diag CTL & diag	extracellular secreted
00	447342		Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL	SCHOLOU
	448243	AW369771	Hs.52620	Integrin, beta 8	mAb&s.m	plasma membrane
	448844 449048	Al581519	Hs.177164	ESTs	mAb & s.m. mAb	plasma membrana
65	449722	Z45051 BE280074	Hs.22920 Hs.23960	similar to S68401 (cattle) glucose induc cyclin B1	s.m.	cytoplasm
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmille	mAb & s.m.	ptasma membrane
	450375	AA009647	11- 00040	a disintegrin and metalloproteinase doma	mAb & diag & s.m.	plasma membrane
	450701 450983	H39960 AA305384	Hs.288457 Hs.25740	hypothetical protein XP_098151 (leucine- ERO1 (S. cerevisiae)-like	mAb & diag diag	plasma membrene secreted
70	451668		Hs.326444	cartilage acidic protein 1	mAb & diag	plasma membrane
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	diag	automa a Nod
	452401 452747	NM_007115 BE153855	Hs.29352 Hs.61460	tumor necrosis factor, alpha-induced pro to superfamily receptor LNIR	diag mAb	extracellular plasma membrana
~ -	452838	U65011	Hs.30743	preferentially expressed antigen in meta	CTL	nuclear
75	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	CTL & s.m.	nuclear
	457489	Al693815	Hs.127179	cryptic gene	diag	secreted
	TABLE 1	48				
80	Dieser	I below 5				
δU	Picey: CAT num	Unique Eo: iber: Gene chist	s probeset ident er number	iner nurrider		
	Accessio		ocession numb	ers		

Pkey CAT Number Accession

	wo	02/086443	3	PCT/US02/12476
F	414883	15024_1	AA082436 AA292753 AA872039	0 AA926959 W76521 W24270 W21526 AA031712 BE267636 H83186 AA469909 NB6396 AA001348 BE535736 AA081745 BE566245 5 H72525 H77575 N49786 W88665 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 8 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889355 AI204630 W25243 AI935150 9 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA176920 AA910644 AA459522 AA293140 AW514667
5			AW61300 N95210 A AA643280	W682396 AA662522 AUB65147 A423163 AW562230 AA584410 AA563187 AW024595 AW069734 AUB28996 AA282997 AA876046 2 AA527373 AW972459 AUB31360 AA621337 AA100926 AA772418 AA594628 AU033892 W95098 AU034317 AA398727 AU085031 J459432 AU041437 AA932124 AA627684 AA935829 AU004827 AV23513 AU094597 H42079 R54703 AU630399 AA617681 AA978045 D W44561 AU991988 AU537692 AU090262 AA740817 AU312104 AU911822 AA416871 AU185409 AA129784 AA701623 AU075239
10			A1494230 A1494211 AA954344 H03266 B	AA633648 A339998 A335880 AA39239 A076708 A085351 A356283 A346618 A1146955 A1989380 A346243 N92892 AA765850 A1278887 AA962596 A492600 W80435 AA001979 R97424 A1129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AW059501 AW886710 R92790 N59755 A361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 H77576 R96823 A4457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923 E261919 AA769633 AA480310 AA507454 A4910686 A1203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99155 R97470 AA70275 T77561 A4911982 H22966 N33673 AA283672
15	450375	B3327_1	AA009647	CHAYO AAVU22/3 17/351 AA911592 H02936 N036/3 AA2036/2 7 AA131254 AA374293 AW954405 H04410 AW605294 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 3 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AJ161014 AA099554 R69067
20	TABLE 14C			
	Pkey: Ref:	Sequence sour	rce. The 7 di	ing to an Eos probeset gli numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA Isome 22." Dunham I. et al., Nature (1999) 402-489-495.
25	Strand: Nt_position:	Indicates DNA	strand from v	which exons were predicted, is of predicted exons.
	Pkey	Ref S	Strand	N1_position
30	402075	8117407 F	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No. Pkey, ExAcon, UnigeneID, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pixey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the eligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Toots (DoubleTwist, Oaldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 5

Table 15C show the genomic positioning for those Pkey's tacking Uniquene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleofide locations of each predicted exon are also listed. 10

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Seq ID No: Sequence ID number
Pkey: Unique Eos probeset identifier number
ExAcor: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number

Unigene Title: Unigene gene title

20	Seq 1D No:	Pkey	ExAcon	UnigenelD	Unigene Titla
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
~ =	Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
25	Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 13 & 14	407788	BE514982	Hs.38991	S100 catclum-binding protein A2
20	Seq ID No: 15 & 16	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
30	Seq ID No: 17 & 18	439285	AL133916	11. 75547	hypothetical protein FLJ20093
	Seq ID No: 19 & 20	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
	Seq ID No: 21 & 22	120486 425650	AW368377	Hs.137569 Hs.1925	tumor protein 63 kDa with strong homolog desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 23 & 24 Seq ID No: 25 & 26	412140	NM_001944 AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
35	Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
55	Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito
40 ·	Seq ID No: 37 & 38	429510	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 39 & 40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 41 & 42	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
4.5	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	AJ085377	Hs.143610	ESTB
	Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
	Seq ID No: 50 & 51	408522	Al541214	Hs.46320	Small profine-rich protein SPRK (human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
50	Seq ID No: 54 & 55	435505 417366	AF200492 BE185289	Hs.211238 Hs.1076	interleukin-1 homolog 1 small proline-rich protein 1B (comitin)
50	Seq ID No: 56 & 57 Seq ID No: 58 & 59	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 60 & 61	441020	W79283	Hs.35962	ESTs
	Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys
	Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
	Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 74 & 75	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911	Plakophilin
	Seq ID No: 80 & 81	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu
	Seq ID No: 82 & 83	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
65	Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
03	Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
	Seq ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 90 & 91 Seq ID No: 92 & 93	417389 423634	BE260964 AW959908	Hs.82045 Hs.1690	midkine (neurite growth-promoting factor heparin-binding growth factor binding pr
	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telangieclasia group D-associated
70	Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
, 0	Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Sea ID No: 100 & 101	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o
	Seq ID No: 102 & 103	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3
	Seq ID No: 104 & 105	409103	AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 106 & 107	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifin
	Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
	Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
00	Seq ID No: 114 & 115	418203	X54942	Hs.B3758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
	Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guarine monphosphate synthetase
	Seq ID No: 119 & 120	449230	BE613348	Hs.211579	malanoma cell adhesion molecule
	Seq ID No: 121 & 122	446989	AK001898	Hs.16740 Hs.35406	hypothetical protein FLJ11036
85	Seq ID No: 123 & 124	457819	AA057484 J05070	Hs.151738	ESTs, Highly similar to unnamed protein matrix metalloproteinase 9 (gelatinase B
0,5	Seq ID No: 125 & 126	424687	300010	19.101100	Incrembiorentese a filesemiese o

	WO 02/080	9443			
	Seq ID No: 127 & 128	414430	Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 131 & 132	100668	L05424	Hs.169610	CD44 antigen (homing function and Indian
	Seq ID No: 133 & 134	458933	AI638429	Hs.24763	RAN binding protein 1
5	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
9		418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 137 & 138				cyclin-dependent kinase inhibitor 2A (me
	Seq ID No: 139 & 140	418478	U38945	Hs.1174	
	Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ 10540
10	Seq ID No: 145 & 145	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur
	Seq ID No: 147 & 148	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con
	Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
	Seq ID No: 153 & 154	453884	AA355925	Hs.36232	KIAA0188 gene product
15	Seq ID No: 155 & 156	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877			NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 163 & 164	413129	AF292100	Hs.104613	RP42 homolog
20	Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
20		444781	NM_014400	Hs.11950	GPI-anchored metastasts-associated prote
	Seq ID No: 167 & 168			Hs.80205	
	Seq ID No: 169 & 170	416819	U77735	NS.00200	pim-2 oncogene
	Seq ID No: 171 & 172	451320	AW118072	LL genen	diacylglycerol kinase, zeta (104kO)
25	Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyahronan synthase 3
23	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	Seq ID No: 179 & 180	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
20	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
30	Seq ID No: 185 & 186	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-l
	Seq ID No: 187 & 188	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-l
	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	Al471630	Hs.8127	KIAA0144 gene product
25	Seq ID No: 193 & 194	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
35	Seq ID No: 195 & 195	430393	BE185030	Hs.241305	estrogen-responsive B box protein
	Seq ID No: 197 & 198	425057	AAB26434	Hs.1619	achaete-scute complex (Drosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin I precursor
	Seq ID No: 201 & 202	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta
40	Seq ID No: 203 & 204	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid
40	Seq ID No: 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766	selzure related gene 6 (mouse)-like
	Seq ID No: 209 & 210	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 211 & 212	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
15	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortex; lissencephaly, X-linked (d
45	Seq ID No: 215 & 216	428182	BE386042	Hs.293317	ESTs, Wealdy similar to GGC1_HUMAN G ANT
	Seq ID No: 217 & 218	427335	AA448542	Hs.251677	Gantigen 7B
	Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (niceln (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li
50	Seq ID No: 223 & 224	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9 NM_021048:Homo sapiens melanoma antigen,
50	Seq ID No: 225 & 226	404440	ADA COECCE	Hs.78589	
	Seq ID No: 227 & 228	415669	NIM_005025		serine (or cysteine) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomal Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 231 & 232	320843	BE069288	Hs.34744	Homo sapiens cDNA FLJ13103 fis, clone NT
55	Seq ID No: 233	429065	AI753247	Hs.29643	
55		446400			
	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 234 & 235 Seq ID No: 236 & 237	330495	U47924	Hs.71642	ESTs guardne nucleotide binding protein (G pr
	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238	330495 413573	U47924 AI733859	Hs.71642 Hs.149089	ESTs guanine nucleotide binding protein (G pr ESTs
	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 Seq ID No: 239 & 240	330495 413573 428479	U47924 AI733859 Y00272	Hs.71642 Hs.149089 Hs.334562	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242	330495 413573 428479 428479	U47924 AI733859 Y00272 Y00272	Hs.71642 Hs.149089 Hs.334562 Hs.334562	ESTs guantne nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244	330495 413573 428479 428479 332180	U47924 AI733859 Y00272 Y00272 AF134160	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1
60	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245	330495 413573 428479 428479 332180 437915	U47924 AI733859 Y00272 Y00272 AF134160 AI637993	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca
60	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 Seq ID No: 245 Seq ID No: 246 & 247	330495 413573 428479 428479 332180 437915 441553	U47924 AI733859 Y00272 Y00272 AF134160 AI637993 AA281219	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sepiens clone N11 NTera2D1 teratoca ESTs
60	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 & 244 Seq ID No: 245 & 247 Seq ID No: 246 & 247 Seq ID No: 248 & 249	330495 413573 428479 428479 332180 437915 441553 331692	U47924 AI733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213	ESTs guantne nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami
	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 & 244 Seq ID No: 246 & 247 Seq ID No: 246 & 249 Seq ID No: 250 & 251	330495 413573 428479 428479 332180 437915 441553 331692 429413	U47924 A1733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877	ESTs guarine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein
60 65	Seq ID No: 234 & 235 Seq ID No: 238 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 248 & 249 Seq ID No: 250 & 251 Seq ID No: 250 & 251 Seq ID No: 252 & 253	330495 413573 428479 428479 332180 437915 441553 331692 429413 422283	U47924 A1733859 Y00272 Y00272 AF134160 A1637993 AA281219 A1683487 NIM_014058 AW411307	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sepiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.ceravis
	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 Seq ID No: 245 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 248 & 249 Seq ID No: 253 Seq ID No: 253	330495 413573 428479 428479 332180 437915 441553 331692 429413 422283 448357	U47924 A1733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sepiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogene family
	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 & 244 Seq ID No: 246 & 247 Seq ID No: 246 & 247 Seq ID No: 250 & 251 Seq ID No: 250 & 251 Seq ID No: 255 & 253 Seq ID No: 256 & 255 Seq ID No: 256 & 257	330495 413573 428479 428479 332180 437915 441553 331692 429413 422283 448357 446292	U47924 A1733859 Y00272 Y00272 AF134160 A1537993 AA281219 A1683487 NM_014058 AW411307 N20169 AF081497	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279682	ESTs guarine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogene family Rh type C glycoprotein
	Seq ID No: 234 & 235 Seq ID No: 238 & 237 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 248 & 249 Seq ID No: 250 & 251 Seq ID No: 252 & 253 Seq ID No: 254 & 255 Seq ID No: 255 & 257 Seq ID No: 256 & 257 Seq ID No: 256 & 255	330495 413573 428479 428479 332180 437915 441553 331692 429413 42223 448357 446292 416209	U47924 A1733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA235776	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279682 Hs.79078	ESTs guantine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogane family Rh type C glycoprotein MAD2 (mittofic arrest deficient, yeast, h
65	Seq ID No: 234 & 235 Seq ID No: 238 Seq ID No: 238 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 245 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 246 & 249 Seq ID No: 250 & 251 Seq ID No: 252 & 253 Seq ID No: 254 & 255 Seq ID No: 256 & 257 Seq ID No: 256 & 257 Seq ID No: 258 & 259 Seq ID No: 258 & 259	330495 413573 428479 428479 332180 437915 441553 331692 429413 422283 448357 446292 416209 453922	U47924 AI733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA236776 AF083306	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279562 Hs.79078 Hs.35708	ESTs guarine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogene family Rh type C glycoprotein MAD2 (mitodic arrest deficient, yeast, h budding uninhibited by berzimidazoles 1
	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 245 Seq ID No: 255 Seq ID No: 255 Seq ID No: 255 Seq ID No: 256 & 257 Seq ID No: 256 & 256	330495 413573 428479 428479 332180 437915 441553 331692 429413 422283 448357 446292 416209 4539222 424046	U47924 A1733859 Y00272 Y00272 AF134160 AI537993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA236776 AF083306 AF027866	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279682 Hs.79078 Hs.38708 Hs.38708 Hs.138202	ESTs guarine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogane family Rh type C glycoprotein MAD2 (mitotic arrest deficient, yeast, h budding uninhibited by bernzimidazoles 1 serine (or cysteine) proteinase inhibitio
65	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 & 240 Seq ID No: 241 & 242 Seq ID No: 243 & 244 Seq ID No: 243 & 244 Seq ID No: 246 & 247 Seq ID No: 250 & 251 Seq ID No: 250 & 251 Seq ID No: 256 & 255 Seq ID No: 256 & 257 Seq ID No: 256 & 257 Seq ID No: 256 & 257 Seq ID No: 256 & 255 Seq ID No: 256 & 253	330495 413573 428479 428479 32180 437915 441553 331692 429413 4422283 448357 446292 416209 4539223	U47924 A1733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA236776 AF083306 AF027866 AW238299	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279682 Hs.79078 Hs.332022 Hs.332022 Hs.250618	ESTs guarine nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogane family Rh type C glycoprotein MAD2 (mittate arrest deficient, yeast, h budding uninhibited by benzimidazoles 1 serine (or cysteine) proteinase inhibito UL16 binding protein 2
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65 70 75	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 & 240 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 245 & 253 Seq ID No: 250 & 251 Seq ID No: 250 & 251 Seq ID No: 256 & 259 Seq ID No: 256 & 257 Seq ID No: 256 & 258 Seq ID No: 257 & 258	330495 413573 428479 332180 4379153 331692 429213 448357 446292 453922 424046 439223 42928 409757 411089 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969	U47924 AI733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA2365776 AF023306 AF027866 AW238299 AI553633 NM_001898 AA456454 AA721252 AF120274 AF120274 AF120274 AF120274 T97307 AA648459 H39960	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279562 Hs.79078 Hs.35708 Hs.138202 Hs.250618 Hs.250618 Hs.250618 Hs.214291 Hs.214291 Hs.214291 Hs.214291 Hs.214291 Hs.194689 Hs.194689 Hs.194689 Hs.194689	ESTs guantne nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogene family Rh type C glycoprotein MAD2 (mitotic arrest deficient, yeast, h budding uninhibited by benzimidazoles 1 serine (or cysteine) proteinase inhibito UL16 binding protein 2 ESTs cystatin SN cell division cycle 2-like 1 (PITSLRE pr ESTs artemin artemin artemin gbye53h05.s1 Soares fetal liver spleen hypottretical protein XP_098151 (leucine- NM_002362Homo sapiens melanoma antigen,
65 70 75 80	Seq ID No: 234 & 235 Seq ID No: 238 & 237 Seq ID No: 238 & 240 Seq ID No: 241 & 242 Seq ID No: 241 & 242 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 250 & 251 Seq ID No: 250 & 255 Seq ID No: 250 & 257 Seq ID No: 250 & 251 Seq ID No: 250 & 250 Seq ID No: 250 & 250	330495 413573 428479 332180 437915 331692 429413 42223 429413 446292 416292 424046 439223 42923 42924 42925 42929 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 4367170 435770 435770	U47924 AI733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA236776 AF023306 AF027856 AW238299 AI5553633 NM_001898 AA456454 AA721252 AF120274	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279682 Hs.79078 Hs.138202 Hs.79078 Hs.3250518 Hs.3250518 Hs.3250518 Hs.3250518 Hs.3250518 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274291 Hs.274	ESTs guanha nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-lype MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogane family Rh type C glycoprotein MAD2 (mitodic arrest deficient, yeast, h budding uninhibited by benzimidazoles 1 serine (or cysteine) proteinase inhibito UL16 binding protein 2 ESTs cystatin SN cell division cycle 2-like 1 (PITSLRE pr ESTs artemin artemin artemin gbyeS3h05.s1 Soares fetal liver spleen hypothetical protein XP_09B151 (leucine- NM_002362Horno sapiens melanoma amtigen, thyroid hormone receptor interactor 13
65 70 75	Seq ID No: 234 & 235 Seq ID No: 236 & 237 Seq ID No: 238 & 240 Seq ID No: 239 & 240 Seq ID No: 241 & 242 Seq ID No: 245 Seq ID No: 246 & 247 Seq ID No: 245 & 253 Seq ID No: 250 & 251 Seq ID No: 250 & 251 Seq ID No: 256 & 259 Seq ID No: 256 & 257 Seq ID No: 256 & 258 Seq ID No: 257 & 258	330495 413573 428479 332180 4379153 331692 429213 448357 446292 453922 424046 439223 42928 409757 411089 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969 428969	U47924 AI733859 Y00272 Y00272 AF134160 AI637993 AA281219 AI683487 NM_014058 AW411307 N20169 AF081497 AA2365776 AF023306 AF027866 AW238299 AI553633 NM_001898 AA456454 AA721252 AF120274 AF120274 AF120274 AF120274 T97307 AA648459 H39960	Hs.71642 Hs.149089 Hs.334562 Hs.334562 Hs.7327 Hs.202312 Hs.121296 Hs.152213 Hs.201877 Hs.114311 Hs.108923 Hs.279562 Hs.79078 Hs.35708 Hs.138202 Hs.250618 Hs.250618 Hs.250618 Hs.214291 Hs.214291 Hs.214291 Hs.214291 Hs.214291 Hs.194689 Hs.194689 Hs.194689 Hs.194689	ESTs guantne nucleotide binding protein (G pr ESTs cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to cell division cycle 2, G1 to S and G2 to claudin 1 Homo sapiens clone N11 NTera2D1 teratoca ESTs wingless-type MMTV integration site fami DESC1 protein CDC45 (cell division cycle 45, S.cerevis RAB38, member RAS oncogene family Rh type C glycoprotein MAD2 (mitotic arrest deficient, yeast, h budding uninhibited by benzimidazoles 1 serine (or cysteine) proteinase inhibito UL16 binding protein 2 ESTs cystatin SN cell division cycle 2-like 1 (PITSLRE pr ESTs artemin artemin artemin gbye53h05.s1 Soares fetal liver spleen hypottretical protein XP_098151 (leucine- NM_002362Homo sapiens melanoma antigen,

	Seq ID No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No. 295 & 296	437789	AI581344	Hs.127812	ESTs, Wealty similar to T17330 hypotheti
	Seq ID No. 297 & 298	437789	AI581344	Hs.127812	ESTs, Wealty similar to T17330 hypotheli
5	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
5	Seq ID No: 301 & 302 Seq ID No: 303 & 304	437789 437789	AI581344 AI581344	Hs.127812 Hs.127812	ESTs, Wealthy similar to T17330 hypotheti ESTs, Wealthy similar to T17330 hypotheti
	Seq ID No. 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
10	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
10	Seq ID No. 310 & 311	434105	AW952124	Hs.13094	presentlins associated rhomboid-like pro
	Seq ID Nox 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315 Seq ID No: 316 & 317	413691 423934	AB023173 U89995	Hs.75478 Hs.159234	ATPase, Class VI, type 118 forkhead box E1 (thyroid transcription f
	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
15	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTs .
	Seq ID No: 326 & 327 Seq ID No: 328 & 329	403329 409893	AW247090	Hs.57101	unnamed protein product (Homo sapiens) minichromosome maintenance deficient (S.
20	Seq ID Not 330 & 331	119073	BE245360	Hs.279477	v-ets erythroblastosis virus E26 oncogen
	Seq ID No: 332 & 333	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 334 & 335	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 335 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
25	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
23	Seq ID No: 340 & 341 Seq ID No: 342 & 343	102012 105729	BE259035 H46612	Hs.118400 Hs.293815	singed (Drosophila)-like (sea urchin fas Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
20	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
30	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353 Seq ID No: 354 & 355	100486 419121	T19006 AA374372	Hs.10842 Hs.89626	RAN, member RAS oncogene family parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
	Seq ID No: 358 & 359	330493	M27826	,	endogenous retroviral protease
35	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365 Seq ID No: 366 & 367	437016 429612	AU076916 AF062649	Hs.5398 Hs.252587	guanine monphosphate synthetase pitultary tumor-transforming 1
	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
40	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470	Hs.260622	butyrate-Induced transcript 1
	Seq ID No: 374 & 375	431565	AF161470	Hs.260622	bulyrate-induced transcript 1
	Seq ID No: 376 & 377 Seq ID No: 378 & 379	132354 424441	BE185289 X14850	Hs.1076 Hs.147097	small proline-rich protein 1B (comitin) H2A histone family, member X
45	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425265	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387 Seq ID No: 388 & 389	424503 400289	NM_002205 X07820	Hs.149609 Hs.2258	integrin, alpha 5 (fibronectin receptor, matrix metalloproteinase 10 (stromelysin
50	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloprotetnase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (callonic amino
	Seq ID No: 396 & 397 Seq ID No: 398 & 399	415138 418506	C18356 AA084248	Hs.295944 Hs.85339	tissue factor pathway inhibitor 2 G protein-coupled receptor 39
55	Seq ID No: 400 & 401	423961	D13666	Hs.136348	periostin (OSF-2os)
	Seq ID No: 402 & 403	414812	X72755	Hs.77367	monokine induced by gamma interferon
	Seq ID No: 404 & 405	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
60	Seq ID No: 408 & 409 Seq ID No: 410 & 411	422867 428227	L32137 AA321649	Hs.1584 Hs.2248	cartilage ofigomeric matrix protein (pse small inducible cytokine subfamily B (Cy
•	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adlican
65	Seq ID No: 418 & 419 Seq ID No: 420 & 421	428698 -450098	AA852773 W27249	Hs.334838 Hs.8109	KIAA1866 protein hypothetical protein FLJ21080
05	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	lg superfamily receptor UNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
70	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
70	Seq ID No: 430 & 431 Seq ID No: 432 & 433	425247 432201	NM_005940 AI538613	Hs.155324 Hs.298241	matrix metalloproteinase 11 (stromelysin Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
75	Seq ID No: 440 & 441	447033	AI357412	Hs.157601	ESTs ESTs
	Seq ID No: 442 & 443 Seq ID No: 444 & 445	447033 447033	Al357412 Al357412	Hs.157601 Hs.157601	ESTs ESTs
	Seq ID No: 446 & 447	115522	BE614387	Hs.333893	c-Myc target JPO1
00	Seq ID No: 448 & 449	410418	D31382	Hs.63325	transmembrane protease, serine 4
80	Seq ID No: 450 & 451	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq ID No: 452 & 453 Seq ID No: 454 & 455	409041 452461	AB033025 N78223	Hs.50081 Hs.108106	Hypothetical protein, XP_051860 (KIAA119 transcription factor
	Seq ID No: 454 & 455 Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
0.5	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

	WO 02/086	6443			
	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa
	Seq ID No: 464 & 465	402075			ENSP00000251056*:Plasma membrane calcium
	Seq ID No: 456 & 457	421110	AJ250717	Hs.1355	cathepsin E
_	Seq ID No: 468 & 469	451668	Z43948	Hs.326444	cartilage acidic protein 1
5	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475	422282	AF019225	Hs.114309	apolipoprotein L
	Seq ID No: 476 & 477	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member
	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),
10	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281	A1623693	Hs.323494	Predicted cation efflux pump
	Seq ID No: 484 & 485	405932			C15000305;gij3806122[gb]AAC69198.1] (AF0
	Seq ID No: 486 & 487	405932			C15000305:gij3806122[gb]AAC69198.1] (AF0
	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
15	Seq JD No: 490 & 491	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	Seq ID No: 492 & 493	417079	U65590	Hs.81134	interleukin 1 receptor antagonist
	Seq ID No: 494 & 495	430890	X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein
20	Seq ID No: 500 & 501	413053	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	Seq ID No: 502 & 503	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro
25	Seq ID No: 508 & 509	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte
25	Seq ID No: 510 & 511	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 512 & 513	309931	AW341683	11-040	gbthd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183	Hs.80962 Hs.241551	neurotensin chloride channel, calcium activated, fam
30	Seq ID No: 518 & 519	430486	BE062109		laminin, beta 3 (nicein (125kD), katinin
3 0	Seq ID No: 520 & 521	413753	U17760	Hs.75517 Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 522 & 523	425650 423673	NM_001944 BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 524 & 525 Seg ID No: 526 & 527	418663	AK001100	Hs.41690	desmocalin 3
	Seq ID No: 528 & 529	418663	AK001100	Hs.41690	desmocollin 3
35	Seq ID No: 530 & 531	429510	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
55	Seq ID No: 532 & 533	406590	M29540	Hs.220529	carcingembryonic antigen-related cell ad
	Seq ID No: 534 & 535	431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 536 & 537	422158	L10343	Hs.112341	protesse inhibitor 3, skin-derived (SKAL
	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
40	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 542 & 543	428484	AF104032	Hs.184501	solute carrier family 7 (cationic amino
	Seq ID No: 544 & 545	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap Junction protein, beta 6 (connextin 3
45	Seq ID No: 550 & 551	417542	J04129	Hs.82269	progestagen-associated endometrial prote
	Seq ID No: 552 & 553	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
£Λ	Seq ID No: 558 & 559	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 560 & 561	418462	BE001596	Hs.85266	integrin, beta 4
	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxla-inducible protein 2 ·
	Seq ID No: 564 & 565	439605	W79123	Hs.58561	G protein-coupled receptor 87 NM_005365:Homo sapiens melanoma antigen,
	Seq ID No: 566 & 567	404877	NM 014400	Hs.11950	GPI-anchored metastasis-associated prote
55	Seq ID No: 568 & 569	444781		Hs.85962	hyaturonan synthase 3
55	Seq ID No: 570 & 571	418543	NM_005329 U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 572 & 573	415817 415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577 Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Sea ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
00	Seq ID No: 582 & 583	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
•	Seq ID No: 584 & 585	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR
	Seg ID No: 586 & 587	418678	NM_001327	Hs.157379	cancer/testis antigen (NY-ESO-1)
	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancerflestis antigen (NY-ESO-1)
65	Seq ID No: 590 & 591	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
• •	Seq ID No: 592 & 593	332180	AF134160	Hs.7327	claudin 1
	Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 598 & 599	439223	AW238299	Hs.250618	UL16 binding protein 2
70	Seq ID No: 600 & 601	409757	NM_001898	Hs.123114	cystatin SN
	Seq ID No: 602 & 603	428969	AF120274	Hs.194689	arlemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	arternin
	Seq ID No: 606 & 607	428969	AF120274	Hs.194689	artemin
75	Seq ID No: 608 & 609	428969	AF120274	Hs.194689	erternin
75	Seq ID No: 610 & 611	450701	H39960	Hs.288457	hypothetical protein XP_098151 (leucine-
	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine- plasminogen activator, urokinase
	Seq ID No: 614 & 615	414774	X02419	Hs.77274	piasminogen activator, trokinase desmocollin 2
	Seq ID No: 616 & 617	407944	R34008	Hs.239727	
80	Seq ID No: 618 & 619	407944 457489	R34008 A1693815	Hs.239727 Hs.127179	desmocalin 2
50	Seq ID No: 620 & 621 Seq ID No: 622 & 623	429547	AW009166	Hs.99376	cryptic gene ESTs
	Seq ID No: 624 & 625	407242	M18728	1 100001 0	gb:Human nonspecific crossreacting antig
	שטע זוו וזעג שבד ע עצט	TU1 474			Bon town introduction and
		407747	M18728		ob:Human nonspecific crossreacuru anuo
	Seq ID No: 626 & 627	407242 407242	M18728 M18728		gb:Human nonspecific crossreacting antig rb:Human nonspecific crossreacting antig
85		407242 407242 444005	M18728 M18728 BE395085	Hs.10086	gb:Human nonspecific crossreacting antig gb:Human nonspecific crossreacting antig type I transmembrane protein Fn14

	wo	02/0864	143			PCT/US02/12476
	Seq ID No: 6		429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
	Seq ID No: 6		422109	S73265	Hs.1473	gastrin-releasing peptide
	Seq ID No: 6		419235	AW470411	Hs.288433	neurotrimin
_	Seq ID No: 6	338 & 639	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc
5	Seq ID No: 6		419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy
	Seq ID No: 6		431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu
	Seq ID No: 6		448243	AW369771	Hs.52620	integrin, beta 8
	Seq ID No: 6		426427	M86699	Hs.169840	TTK protein kinase
10	Seq ID No: 6		445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6
10	Seq ID No: 6		422278	AF072873	Hs.114218	trizzled (Drosophila) homolog 6
	Seq ID No: 6		428450 446619	NM_014791 AU076643	Hs.184339 Hs.313	KIAAD175 gene product secreted phosphoprotein 1 (osteopontin,
	Seq ID No: 6 Seq ID No: 6		453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	Seq ID No. 6		426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
15	Seq ID No: 6		425776	U25128	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 6		425776	U2512B	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 6		431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
	Seq ID No: 6	66 & 667	419452	U33635	Hs.90572	PTK7 protein tyrosine ktnase 7
~~	Seq ID No: 6	£8 & 659	432653	N62095	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
20	Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Wealdy similar to JC7328 amino aci
	Seq ID No: 6		432653	N62098	Hs.293185	ESTs, Weakly similar to JC7328 amino ad
	Seq ID No: 6		432653	N62096	Hs.293185	ESTs, Wealthy similar to JC7328 amino aci
	Seq ID No: 6		410001	AB041035	Hs.57771	kallibrein 11
25	Seq ID No: 6		426501 408369	AW043782 R38438	Hs.293616	ESTS
23	Seq ID No: 6		445413	AA151342	Hs.182575 Hs.12677	solute carrier family 15 (H??? transport CGI-147 protein
	Seq ID No: 6 Seq ID No: 6		422424	AJ186431	Hs.296638	prostate differentiation factor
	Seq ID No: 6		428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
	Seq ID No: 6		420610	AI683183	Hs.99348	distal-less homeo box 5
30	00412					
	TABLE 15B					
	Pkey:			dentifier number		•
35		: Gene clust				
33	Accession:	Genoank a	ocession nu	mbers		
	Pkey	CAT Numb	er Acce	ssion		
	309931	AW341683				
	330493	33264_5		326 R78416 AA30	7645 AW957879	AW957800 AA633529 H03662
40	439285	47065_1	AL13	3916 N79113 AF	086101 N76721 A	AW950828 AA364013 AW955684 Al346341 Al867454 N54784 Al655270 Al421279 AW014882
						Al341407 BE175639 AA456968 Al358918 AA457077
	450375	83327_1				4405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
						852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
45	451320	86576_1				5 Al701458 W20198 F26326 AAB90570 N90552 AW071907 Al671352 Al375892 T03517 R88265
45.						36 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230
			AAU	17 13 1 AV4433U3	1 330Z3 MIZZZSSC	5 T33511 T33785 Al419606 D55612
	TABLE 15C					
50						·
	Pkey:			ponding to an Eos		
	Ref:					Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
						Nature (1999) 402:489-495.
55	Strand:			rom which exons		
22	Nt_position:	Indicates n	ucleotide po	sitions of predicte	ed exons.	
	Pkey	Ref	Strand	Nt position		
	402075	81 17407	Plus		n35.1228n&.1220	921,124019-124161,124455-124610,125672-126076
	403329	8516120	Plus	96450-9659		Amilians a satisfication into introduction reports
60	403478	9958258	Plus	116458-116		
	404440	7528051	Plus	80430-8158		
	404877	1519284	Pius	1095-2107		•
	405770	2735037	Plus	61057-6207	'5 ·	
~	405932	7767812	Minus	123525-123	713	
65						

Table 16

Seq ID NO: 1 DNA sequence Nucleic Acid Accession #: NM_001216 5 Coding sequence: 43..1422 GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 10 AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120 CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180 TOCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240 AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 15 TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCAG 420 AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480 COSCCCTGGC CCCGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC 540 OGCCCCCAGC TOGCCGCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600 CTCCCGCCGC TCCCAGAACT GCGCCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCCTG CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 660 20 720 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780 CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900 AGTECCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 960 25 1020 TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG 1140 1200 1260 30 AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCCTGT CCTGCTCATT 1440 1500 ATGCCACTIC CTTTTAACTG CCAAGAAATT TTTTAAAATA AATATITATA AT 35 Seq ID NO: 2 Protein sequence: Protein Accession #: NP 001207 40 MAPLCPSPWL PLLIPAPAPG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180 ELLGPOLPPL PELRLRNNGH SVOLTLPPGL EMALGPGREY RALOLELEWG AAGRPGSEET 240 45 VEGHRPPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA 300 EEGSETQVPG LDISALLPSD PSRYPQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420 GLLFAVTSVA FLVOMRROHR RGTKGGVSYR PAEVAETGA 50 Seq ID NO: 3 DNA sequence Nucleic Acid Accession #: BC013923 Coding sequence: 438-1391 55 GTGTTTGCAA AAGGGGGAAA GTAGTTTGCT GCCTCTTTAA GACTAGGACT GAGAGAAAGA AGAGGAGAGA GAAAGAAAGG GAGAGAAGTT TGAGCCCCAG GCTTAAGCCT TTCCAAAAAA 160 TAATAATAAC AATCATCGGC GGCGGCAGGA TCGGCCAGAG GAGGAGGGAA GCGCTTTTTT 240 60 TGATCCTGAT TCCAGTTTGC CTCTCTCTTT TTTTCCCCCA AATTATTCTT CGCCTGATTT
TCCTCGCGGA GCCCTGCGCT CCCGACACCC CCGCCCGCCT CCCCTCCTCC TCTCCCCCCG 300 360 420 COSCICACAG CICCOGCATG TACAACATGA TIGAGAACIGA GCTIGAAGCCI COGGGCCOGC AGCAAACTTC GGGGGGGGG GGCGCAACT CCACCIGCGC GGCGGCCGGC GGCAACCAGA 480 540 65 AAAACAGCCC GGACCGCGTC AAGCGGCCCA TGAATGCCTT CATGGTGTGG TCCCGCGGGC AGOGGOGCAA GATGGCCCAG GAGAACCCCA AGATGCACAA CTCGGAGATC AGCAAGCGCC 660 TEGGCECCEA GTEGAAACTT TTGTCEGAGA CEGAGAAGGG GCCGTTCATC GACGAGGCTA
AGCEGCTECG AGCECTECAC ATGAAGGAGC ACCCGGATTA TAAATACCEG CCCCGGCEGA 720 780 AAACCAAGAC GCTCATGAAG AAGGATAAGT ACACGCTGCC CGGCGGGCTG CTGGCCCCCG 70 GCGGCAATAG CATGGCGAGC GGGGTCGGGG TGGGCGCCGG CCTGGGCGCG GGCGTGAACC 900 AGCGCATGGA CAGTTACGCG CACATGAACG GCTGGAGCAA CGGCAGCTAC AGCATGATGC 960 AGGACCAGCT GGGCTACCCG CAGCACCCGG GCCTCAATGC GCACGGCGCA GCGCAGATGC 1020 AGCCCATGCA CCGCTACGAC GTGAGCGCCC TGCAGTACAA CTCCATGACC AGCTCGCAGA 1080 CCTACATGAA CGGCTCGCCC ACCTACAGCA TGTCCTACTC GCAGCAGGGC ACCCCTGGCA 1140 75 TOGCTCTTGG CTCCATGGGT TCGGTGGTCA AGTCCGAGGC CAGCTCCAGC CCCCCTGTGG
TTACCTCTTC CTCCCACTCC AGGGCGCCCT GCCAGGCCGG GGACCTCCGG GACATGATCA 1200 1260 GCATGTATCT CCCCGGCGCC GAGGTGCCGG AACCCGCCGC CCCCAGCAGA CTTCACATGT CCCAGCACTA CCAGAGCGGC CCGGTGCCCG GCACGGCCAT TAACGGCACA CTGCCCCTCT 1380 CACACATGTG AGGGCCGGAC AGCGAACTGG AGGGGGGAGA AATTTTCAAA GAAAAACGAG 1440 80 GGAAATGGGA GGGTGCAAA AGAGGAGAGT AAGAAACAGC ATGGAGAAAA CCCGGTACGC 1500 TCARAAAAA AAAAAAAAA AAAATCCCAT CACCCACAGC AAATGACAGC TGCAAAAGAG AACACCAATC CCATCCACAC TCACGCAAAA ACCGCGATGC CGACAAGAAA ACTTTTATGA 1620 GAGAGATCCT GGACTTCTTT TKGGGGGACT ATTTTTGTAC AGAGAAAACC TGGGGAGGGT 1680 GGGGAGGGG GGGGAATGGA CCTTGTATAG ATCTGGAGGA AAGAAAGCTA CGAAAAACTT 1740 85 TTTAAAAGTT CTAGTGGTAC GGTAGGAGCT TTGCAGGAAG TTTGCAAAAG TCTTTACCAA 1800 TANTATITAG AGCTAGTCTC CAAGCGACGA AAAAAATGTT TTAATATTTG CAAGCAACTT 1860 TIGIACAGTA TITATORAGA TARACATOGC ARTCARAGTG TOCATIGITI ATRAGCTGAG 1920

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        2580
        CACAACAA AAACAAAAAA AAAAAAAAGA AACAAACACA CAACACAACA CAACACAAAA 2640
        CCACAACACA AACAACAACA CACAGAGGG
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        Protein Accession #: CAA83435.1
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        KKDKYTLPGG LLAPGGNSMA SGVGVGAGLG AGVNQRMDSY AHMNGWSNGS YSMMQDQLGY
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        Nucleic Acid Accession #: U91618
        Coding sequence: 29-541
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                                                                                   240
        AGCTGAGGAA ACAGGAGAAG TTCATGAAGA GGAGCTTGTT GCAAGAAGGA AACTTCCTAC
        TGCTTTAGAT GGCTTTAGCT TGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAAATCTG
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TGACAAAAAT GGAAAGGAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAAACGGCA
                                                                                   420
40
                                                                                   480
        GCTGTATGAG AATAAACCCA GAAGACCCTA CATACTCAAA AGAGATTCTT ACTATTACTG
        AGAGAATAAA TCATTTATTT ACATGTGATT GTGATTCATC ATCCCTTAAT TAAATATCAA
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        VCSLVNNLNS PARETGEVHE EELVARRKLP TALDGPSLEA MLTIYOLHKI CHSRAFOHWE
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       Nucleic Acid Accession #: NM_006536.2
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       Coding sequence: 109-2940
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        AGCATTGCAG GTCCTATTTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA
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       GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC
ATTGCAATTA ATCCTCAGGT ACCTGAGAAT. CAGAACCTCA TCTCAAACAT TAAGGAAATG
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TCATATGAAA AGGCAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA
                                                                                   420
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CIACAGAACC AGAIGIGCAG COTCAGAAGI GCAIGGGAIG TAAICACAGA CICIGCIGAC
                                                                                   900
                                                                                   960
80
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       GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAATTTT ATTTGATGCA GATTGTTGAA
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                                                                                  1200
       CACCAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA
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	1 -	11 ntregal din	21 SSTSLEKNINV	31	41	51 TEMEVECALM	60
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WO 02/086443

Seq ID NO: 38 Protein sequence: Protein Accession #: NP_057667

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TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 540 600 AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTTATC ACAATCAGGG CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720 20 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG 780 AATTGAATAT TAAGAA Seq ID NO: 42 Protein sequence: Protein Accession #: NP_008883.1 25 MAKDNSTVRC FOGLLIFGNV IIGCCGIALT ABCIPFVSDQ HSLYPLLEAT DNDDIYGAAW IGIPVGICLF CLSVLGIVGI MKSSRKILLA YPILMPIVYA FEVASCITAA TORDFPTPNL FLKOMLERYO NNSPPNNDDO MKNNGVTKTW DRLMLODNCC GVNGPSDWOK YTSAFRTENN 120 30 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GPYHNQGCYE LISGPMNREA WGVAWPGFAI LCWTFWVLLG TMFYWSRIEY 35 Seq ID NO: 43 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 83-2605 40 GCCGGACAGA TCTGCGCGTA TCCTGGAGCC GGCCCAGTTG TGAACTAGGA GAGCTTTGGG ACCTCTGTCC CAAGCAAGAG AGATGAATGG AGAGTATAGA GGCAGAGGAT TTGGACGAGG AAGATTTCAA AGCTGGAAAA GGGGAAGAGG TGGTGGGAAC TTCTCAGGAA AATGGAGAGA 180 AAGAGAACAC AGACCTGATC TGAGTAAAAC CACAGGAAAA CGTACTTCTG AACAAACCCC 240 45 ACAGTITITG CTTTCAACAA AGACCCCACA GTCAATGCAG TCAACATTGG ATCGATTCAT ACCATATAAA GGCTGGAAGC TTTATTTCTC TGAAGTTTAC AGCGATAGCT CTCCTTTGAT 300 360 TGAGAAGATT CAAGCATTTG AAAAATTTTT CACAAGGCAT ATTGATTTGT ATGACAAGGA 420 TGAAATAGAA AGAAAGGGAA GTATTTTGGT AGATTTTAAA GAACTGACAG AAGGTGGTGA 480 AGTARCTARC TIGATACCAG ATATAGCARC TGRACTARGA GATGCACCTG AGARARCCTT 540 50 GGCTTGCATG GGTTTGGCAA TACATCAGGT GTTAACTAAG GACCTTGAAA GGCATGCAGC 600 TGAGTTACAA GCCCAGGAAG GATTGTCTAA TGATGGAGAA ACAATGGTAA ATGTGCCACA TATTCATGCA AGGGTGTACA ACTATGAGCC TTTGACACAG CTCAAGAATG TCAGAGCAAA TTACTATGGA AAATACATTG CTCTAAGAGG GACAGTGGTT CGTGTCAGTA ATATAAAGCC TCTTTGCACC AAGATGGCTT TTCTTTGTGC TGCATGTGGA GAAATTCAGA GCTTTCCTCT 720 780 B40 55 TCCRGATGGA AAATACAGTC TTCCCACAAA GTGTCCTGTG CCTGTGTGTC GAGGCAGGTC 900 ATTTACTGCT CTCCGCAGCT CTCCTCTCAC AGTTACGÀTG GACTGGCAGT CAATCAAAAT 960 CCAGGAATTG ATGTCTGATG ATCAGAGAGA AGCAGGTCGG ATTCCACGAA CAATAGAATG 1020 TGAGCTTGTT. CATGATCTTG TGGATAGCTG TGTCCCGGGA GACACAGTGA CTATTACTGG 1080 AATTGTCAAA GTCTCAAATG CGGAAGAAGG TTCTCGAAAT AAGAATGACA AGTGTATGTT 60 CCTITTGTAT ATTGAAGCAA ATTCTATTAG TAATAGCAAA GGACAGAAAA CAAAGAGTTC 1200 TGAGGATGGG TGTAAGCATG GAATGTTGAT GGAGTTCTCA CTTAAAGACC TTTATGCCAT CCAAGAGATT CAAGCTGAAG AAAACCTGTT TAAACTCATT GTCAACTCGC TTTGCCCTGT 1260 1320 CATTITIGGT CATGAACTIG TTAAAGCAGG TTTGGCATTA GCACTCTTTG GAGGAAGCCA GARATACSCA GATGACAAAA ACAGAATTCC AATTCSGSGA GACCCCCACA TCCTTGTTGT TGGAGATCCA GGCCTAGGAA AAAGTCAAAT GCTACAGGCA GCGTGCAATG TTGCCCCACG 1440 65 1500 TGGCGTGTAT GTTTGTGGTA ACACCACGAC CACCTCTGGT CTGACGGTAA CTCTTTCAAA 1560 AGATAGTTCC TCTGGAGATT TTGCTTTGGA AGCTGGTGCC CTGGTACTTG GTGATCAAGG 1620 TATTIGIGA ATCGATGAAT TIGATAAGAT GGGGAATCAA CATCAAGCCT IGTIGGAAGC 1680 CATGGAGCAG CAAAGTATTA GTCTTGCTAA GGCTGGTGTG GTTTGTAGCC TTCCTGCAAG AACTTCCATT ATTGCTGCTG CAAATCCAGT TGGAGGACAT TACAATAAAG CCAAAACAGT 1740 70 1800 TTCTGAGAAT TTAAAAATGG GGAGTGCACT ACTATCCAGA TTTGATTTGG TCTTTATCCT 1860 GTTAGATACT CCAAATGAGC ATCATGATCA CTTACTCTCT GAACATGTGA TTGCAATAAG AGCTGGAAAG CAGAGAACCA TTAGCAGTGC CACAGTAGCT CGTATGAATA GTCAAGATTC 1920 1980 AAATACTTCC GTACTTGAAG TAGTTTCTGA GAAGCCATTA TCAGAAAGAC TAAAGGTGGT 2040 75 TCCTGGAGAA ACAATAGATC CCATTCCCCA CCAGCTATTG AGAAAGTACA TTGGCTATGC 2100 TOGGCAGTAT GTGTACCCAA GGCTATCCAC AGAAGCTGCT OGAGTTCTTC AAGATTTTTA 2160 CCTTGAGCTC CGGAAACAGA GCCAGAGGTT AAATAGCTCA CCAATCACTA CCAGGCAGCT 2220 GGAATCTTTG ATTCGTCTGA CAGAGGCACG AGCAAGGTTG GAATTGAGAG AGGAAGCAAC 2280 CAAAGAAGAC GCTGAGGATA TAGTGGAAAT TATGAAATAT AGCATGCTAG GAACTTACTC 2340 80 TGATGAATTT GGGAACCTAG ATTTTGAGCG ATCCCAGCAT GGTTCTGGAA TGAGCAACAG 2400 GTCARCAGG AAAGATTTA TTTCTGCTCT CAACAACGTT GCTGAAAGAA CTTATAATAA
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Seq ID NO: 41 DNA sequence

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85

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Seq ID NO: 59 Protein sequence:

Protein Accession #: NP_001784.2

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	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT	CAAGGAGGGC TGGCCCTCAG CCTTGCCGGG GGGAGAGGCA	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAT GAGAGAGGGG	GGGGGACTCA ACGCGGGCTG TGGGGAGAGG TCCCGGGCTC AGAACGGGGA	AAGGGCGACC GGCCCCCCG CCAGGCAGGG GAGAAAGGAG	6120 6180 6240 6300
	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA	CAAGGAGGC TGGCCTCAG CCTTGCCGGG GGGAGAGGCA ACAGGGCAGA	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAT GAGAGAGGGG CTGGACTCCC	GGGGGACTCA ACGCGGGCTG TGGGGAGAGG TCCCGGGCTC AGAACGGGGA TGGAACCCCT	AAGGGCGACC GGCCCCCCG CCAGGCAGGG GAGAAAGGAG GGGCCCCCCG	6120 6180 6240 6300 6360
70	GCCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA GACCCCCTGG	CAAGGAGGGC TGGCCCTCAG CCTTGCCGGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC	GGGGGACTCA ACGCGGGCTG TGGGGAGAGG TCCCGGGCTC AGAACGGGGA TGGAACCCCT TGGACTCTCT	AAGGGCGACC GGCCCCCCG CCAGGCAGGG GAGAAAGGAG GGGCCCCCCG GGAGAACAGG	6120 6180 6240 6300 6360 6420
70	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA GACCCCCTGG GACCCCCTGG	CAAGGAGGGC TGGCCCTCAG CCTTGCCGGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATCGCCCTC TCTGTGGATG GCTAAGGGGG	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAT GAGAGAGGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG	GGGGGACTCA ACGCGGGCTG TGGGGAGAGG TCCCGGGCTC AGAACGGGGA TGGAACCCCT TGGACTCTCT CAATGGTGAC	AAGGGCGACC GGCCCCCCG CCAGGCAGGG GAGAAAGGAG GGGCCCCCCG GGAGAACAGG CAAGGTCCCA	6120 6180 6240 6300 6360 6420 6480
70	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA GACCCCCTGG GACCCCCTGG AAGGAGACAG	CAAGGAGGGC TGGCCCTCAG CCTTGCCGGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT GGGTGTGCCA	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGGG GGCATCAAAG	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAT GAGAGAGGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG GAGACCGGGG	GGGGGACTCA ACGCGGGCTG TGGGGAGAGG TCCCGGGCTC AGAACGCGGT TGGAACCCCT TGGACTCTCT CAATGGTGAC AGAGCCTGGA	AAGGGCACC GGCCCCCG GCCCCCG CCAGGCAGGG GAGAAAGGAG GGGCCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGCCC	6120 6180 6240 6300 6360 6420 6480 6540
70	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAG GACCCCTGG GACCCCTGG AAGGAGACAG AGGAGGCAA	CAAGGAGGGC TGGCCCTCAG CCTTGCCGGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGGT ACTCAAGGGT GGGTTGCCA CCCGGGTCTA	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGGG GCCATCAAAG CCAGGAGAGC	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAT GAGAGAGGGG CTGGACTCCC AGCCAGGTCC AGCCAGGTCA GAGACCGGGG GTGGTATGGC	GGGGGACTCA ACGCGGGCTC TGGGGCTC AGAACGGGA TGGAACCCCT TGGACTCTC CAATGGTGA AGAGCCTGGA TGGGCCTGAA	AAGGGCACC GGCCCCCG CCAGGCAGG GAGAAAGGAG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAAGCCGG	6120 6180 6240 6300 6360 6420 6480 6540 6600
70	GCCCCCAGG GTGGAGACCC GCCCTTCCG CTGGGGTGT AACGTGGAGA GACCCCCTGG GACCCCCTGG AAGGAGACA AGGACGCAA GTCTGCAGGG	CAAGGAGGC TGGCCTCAG TGGCCTTGCCGG GGGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT GCGTGTGCCTA TCCAAGAGGC TCCAAGAGGG	CCCATCGGCT GGGCCACCTG GAGCCTGGA GGAGGCCCTC TCTGTGGATG GCTAAGGGGG GGCATCAAG CCAGGAGAGC CCCCTGGCC	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAG GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG GAGACCGGG GTGGTATGGC CAGTGGGTGG	GGGGGACTCA ACGCGGGCTC TGGGGAGGGA TGGAACGGGA TGGAACCCCT TGGACTCTCT CAATGGTGAC AGAGCCTGGA TGGGCCTGGA TGGGCCTGAA	AAGGGCACC GGCCCCCCG CCAGCAGGG GAGAAAGGAG GGGCCCCCCG GGAGACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCGG CCTGGACCAC	6120 6180 6240 6300 6360 6420 6480 6540 6600 6660
	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACCTGGAGA GACCCCCTGG GACCCCCTGG AAGGAGACAGC AGGACGGCA AGGACGGCA GTCTGCAGGG CTGGTGCCCC	CAAGGAGGC TGGCCTCAG CCTTGCCGGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT GGGTGTGCCA CCCGGGTCTA TCCAAGAGGC GGGTCTTGCT	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAC TCTGTGGATG GCTAAGGGG GCCATCAAAG CCAGGAGAGC CCCCCTGGCC GGCCTGCAC	TTCCTGGAGA GTCTGGCCCT AGCCTGGTAT GAGAGAGGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG GAGACCGGGG GTGGTATGGC CAGTGGGTGG GACCCCAAGG	GOGGGACTCA ACGCGGGCTC TGGGGGCTC AGAACGGGA TGGAACCCCT TGGACTCTCT CAATGGTGAC AGAGCCTGGA TGGGCCTGAA TCATGGAGAC ACCTTCTGG	AAGGGCGACC GGCCCCCG GGAGAAAGGAG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGACACCG CCTGGACCAC CCTGAAGGGG	6120 6180 6240 6300 6360 6420 6480 6540 6600 6660 6720
70 75	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA GTCTGCAGGG CTGGTGCCCC AGCCTGGAGA	CAAGGAGGC TGGCCTCAG CCTTGCCGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT GGGTGTGCCA CCCGGGTCTA TCCAAGAGGC GGGTCTTGCT GACAGGACCT	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGG GGCATCAAAG CCAGGAGAGC CCCCTGGCC GGCCCTGGCC	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT AGCCTGGTAT AGCCAGTCC AGCCAGGTCC AGCCAGGTCG GAGACCGGGA GAGACCGGGG GTGGTATGGC CAGTGGGTGG GACCCCAAGG GACCCCAAGG	GGGGACTCA ACGGGGCTG TGGGGAGAGG TCCCGGGCTC AGAACGGGA TGGAACCCCT TGGACTCTC CAATGGTGAC AGGCCTGAA TCATGGAGAC ACCTTCTGGC ACCTACTGGA	AAGGGCACC GGCCCCCG GGCAGGAAAGGAG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCAG CCTGGACCAC CCTGAAGGGGG GCTGTGGACAC	6120 6180 6240 6300 6360 6420 6480 6540 6600 6660 6720 6780
	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA GACCCCCTGG GACCCCCTGG AAGGAGACAG AGGAGGCAA GTCTGCAGGG CTGGTGCCCC AGCCTGGAGA CTTCCTGGACC	CAAGGAGGC TGGCCTCAG CCTTGCCGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT CCCGGGTCTA TCCAAGAGGC GGGTCTTACT GACAGGACCT GACAGGACCT CCCCGGCCCT	CCCATCGGCT GGGCCACCTG GAGCCTGGA GATGGCCCTC TCTGTGGATG GCTAAGGGG GGCATCAAAG CCAGGAGAGC CCCCTGGCC GGCCCTGCAG CCAGGACAGGC TCAGGCCTTGCAG TCAGGACGGG TCAGGCCTTTG	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GGAGAGGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCG GAGACCGGGGG GTGGTATGGC CAGTGGTATGGC GACCCCAAGG GCCTGACTGG TGGGTCCACA	GGGGACTCA ACGGGGCTC TGGGGAGAGG TCCCGGGCTC AGAACGGGA TGGAACCCCT TGGACCTCTC CAATGGTGAC AGGCCTGGA TCATGGAGC ACGTTCTGG ACGCCTGAA TCATGGAGAC ACCTTCTGGC ACCTACTGGA GGGGTCTCCA	AAGGGCACC GGCCCCCG GGCACAGG GAGAAAGGAG GGGCCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCAC CTGAACGCG CCTGGACCAC GCTTTGCCTG GGTTTGCCTG	6120 6180 6240 6300 6360 6420 6540 6660 6660 6720 6780 6840
	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA AGGACGCAA AGGACGCAA AGTGGCCCC AGCCTGGAGA TTCCTGGACC ACCTGGAGC ATCCTGGACG CACAGTGGCCA	CAAGGAGGC TGGCCTCAG TGGCCGG GGGAGAGGCA ACAGGGCAGA ACTCAAGGGT GGGTGTGCCA CCCGGGTCTA TCCAAGAGG GGGTCTTGCT GACAGGACCC CCCGGCCCT CCCCGCCCCC	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGGG GCCATCAAAG CCAGGAGAGGC CCCCCTGGCC GGCCCTGCAG CCAGGACGGG TCAGGCCTTG AAGCCGGAA	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG GAGACCGGG GTGGTATGGC CAGTGGTGG GACCCCAAGG GCCTGACTGC CCCCAGGTCC CCCCAGGTCC CCCCAGGTCC	GGGGACTCA ACGGGGCTC TGGGGAGAGG TCCGGGCTC AGAACGCGGA TGGACCCTC CAATGGTGAC AGAGCCTGGA TGGGCCTGGA TGGGCCTGGA TCATGGGCAC ACCTTCTGGC ACCTACTGGA ACGAGTCTCCA AGATGGTGCCA AGATGGTGCCA AGATGGTGCCA AGATGGTGCCA AGATGGTGCC	AAGGGCACC GGCCCCCG GGCCCCCG CAGGAAAGGAG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCCG GCTGGACCAC CTGAAGGGG GCTGTGGGAC AGTTGCCTG AGTGGAAAAG	6120 6180 6240 6300 6360 6420 6480 6540 6660 6720 6720 6780 6840 6990
	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA AGGACGCAA AGGACGCAA AGTGGCCCC AGCCTGGAGA TTCCTGGACC ACCTGGAGC ATCCTGGACG CACAGTGGCCA	CAAGGAGGC TGGCCTCAG TGGCCGG GGGAGAGGCA ACAGGGCAGA ACTCAAGGGT GGGTGTGCCA CCCGGGTCTA TCCAAGAGG GGGTCTTGCT GACAGGACCC CCCGGCCCT CCCCGCCCCC	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGGG GCCATCAAAG CCAGGAGAGGC CCCCCTGGCC GGCCCTGCAG CCAGGACGGG TCAGGCCTTG AAGCCGGAA	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG GAGACCGGG GTGGTATGGC CAGTGGTGG GACCCCAAGG GCCTGACTGC CCCCAGGTCC CCCCAGGTCC CCCCAGGTCC	GGGGACTCA ACGGGGCTC TGGGGAGAGG TCCGGGCTC AGAACGCGGA TGGACCCTC CAATGGTGAC AGAGCCTGGA TGGGCCTGGA TGGGCCTGGA TCATGGGCAC ACCTTCTGGC ACCTACTGGA ACGAGTCTCCA AGATGGTGCCA AGATGGTGCCA AGATGGTGCCA AGATGGTGCCA AGATGGTGCC	AAGGGCACC GGCCCCCG GGCCCCCG CAGGAAAGGAG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCCG GCTGGACCAC CTGAAGGGG GCTGTGGGAC AGTTGCCTG AGTGGAAAAG	6120 6180 6240 6300 6360 6420 6480 6540 6660 6720 6720 6780 6840 6990
75	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACGTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA GTCTGCAGGG CTGGTGCCCC AGCCTGGAGA TTCCTGGACC GACAAGTGGG ATGGAGACAG CTAAAGGAGA	CAAGGAGGC TGGCCTCAG CCTTGCCGG GGGAGAGGCA ACAGGGCAGA CCCCAAGGTG ACTCAAGGGT CCCGGGTCTA TCCAAGAGGC GGGTCTTGCT GACAGGACCT CCCCGGCCCT CCCCGGCCCT ACCTGGCCCCC ACCTGGCCCCC	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAGGCCAC GATGGCCCTC TCTGTGGATG GCTAAGGGG GCATCAAAG CCAGGAGAGC CCCCCTGGCC GGCCCTGGCC CGGCCCTGCCA GGCCCTCCAG CCAGGACGGG TCAGGCCTTC AAGCCGGAA ACGGGGGCCCA	TTCCTGGAGA GTCTGGCCT AGCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCAGGTCC AGCAGGGG GTGGTATGGC CAGTGGGTG GACCCCAAGG GCCTGACTGG TGGGTCACAC CCCCAGGTCC CGTCACCAG CGTCACCAGG CGTCACCAGG CTGGACCAGG CTGGACCAGG CTGGACAGG CTGGACAGG	GGGGACTCA ACGGGGCTC TGGGGAGAGG TCCCGGGCTC AGAACGGGA TGGACCCCT TGGACTCTCT CAATGGTGAC AGGGCCTGAA TCATGGAGAC ACCTACTGAGAC ACCTACTGAGAC ACCTACTGAGAC ACGTACTGAGAC TCTGGACTCCA AGATGGTGCC TCTGGCCTGCA TCTGGTGCC TGTGGTCGGG TGTGGTCGGG	AAGGGCACC GGCCCCCG GGCAGCAGG GAGAAAGGAG GGGCCCCCG GGAGACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCAC GCTGGACCAC GCTGTGGACCAC GCTTTGGAC GCTTTGGAC GCTGTAGAGGG CCTGCAGAGGGC CCTGCAAGGGC CCTGCAAGGGC CCTGCAAGGGC CCTGCAAGGGC CCTGCAAGG	6120 6180 6240 6300 6360 6420 6480 6540 6660 6720 6780 6840 6960 7020
	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGAGACAG GTCTGCAGGG CTGGTGCCC AGCCTGGAGA TTCCTGGACA TTCCTGGACA GTCTGGACA CTAAGGAGACAG ATGGAGACAG ATGGAGACAG ATGGAGACAG CTAAAGGGAGA CAAAGGGAGA	CAAGGAGGC TGGCCTCAG GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA ACTCAAGGGT GGGTGTGCCA CCCGGGTTCTA TCCAAGAGG GGGTCTTGCT GACAGAGCC GGGTCTTGCT GACAGACAC CCCGGCCCT CCCCGCCCCT CCCCGGCCCT ACCTGGCCCT ACCTGGCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCT ACCTGGCCCCCT ACCTGGCCCCCT ACCTGGCCCCC	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGGG GCCATCAAAG CCAGGAGAGGC CCCCCTGGCC GGCCCTGCAG CCAGGACGGG TCAGGCCTTC AAGCCGGAA GGTGTGCCAG ACGGGGGCCC CCTGGAGGCCC	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCC AGCCAGGTCC AGCCAGGTCA GAGACCGGG GAGACCGGG GAGACCGAGG GACCCCAAGG GCCTGACTGG GCCCAGGTCG GCCCAGGTCG GTGGGTCG GTGGGTCG GTGGGTCG GTTCACCAG CTGGCAGG CTGGACAGG CTGGACAGG CTGGACAGG	GGGGGACTCA ACGGGGCTC ACGGGGCTC AGAACGGGA TCCCGGGCTC TGGACCTCTC CAATGGTGAC TGGACCTGGA TCATCGGACCTGA TCATCGGAC TCATCGGAC ACCTACTGGA ACCTACTGGA ACCTACTGGA ACCTACTGGA ACCTACTGGA ACCTACTGGA ACCTACTGGA CCTGCTGGC TCTGCCTGGC CCTGGTGGGC CCTGGTGGGC CCTGGTGGGC	AAGGCGACC GGCCCCCGG GGCCCCCGG GCAGGAGAGGG GGGCCCCCG GGAAACAGG CAAGGTCCCA CCGAGGGTC GGGAACCCG GCTGGACCAC CTGAAGGGGG GCTTGGACAC CTGAAGGGGG GCTTTGGAC AGTTGGAC AGTTGGAC AGTTGGAC AGTTGGAC AGTTGGAC CTGTTGGAC CCTCTGAAGGGGG CCTTTGAAGGGGG CCTTTGGAAC CCTCCTGGAG CCTCCTGGAG GAGCCGGAG	6120 6180 6240 6300 6420 6480 6540 6660 6720 6780 6840 6900 6960 7020 7080
75	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA GTCTGCAGGG CTGGTGGCCC AGCCTGGAGA TTCCTGGACG ATGGAGACAG ATGGAGACAG CTAAAGGAGA CTAAAGGAGA CCAAAAGGTGA	CAAGGAGGC TGGCCTTCAC GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA ACTCAAGGGT GGGTGTGCCA CCGGGTCTA CCAGAGGC GGGTCTTGCT GACAGGACCT CCCCGGCCCT GACAGAGGC AGGGAGCCCT ACCTGGCCCC GAAGGAGCCC GAAGGAGCC CCGAGGACCT CCCGGGCCT CCCGGCCCT CCCGGCCCT CCCGGCCCT CCCGGCCCT CCCGGCCCT CCGGGAGACCCC CAAGGAGCCC CCGAGGACCCC CCGAGGGACCCC CCGAGGGACCCC CCGAGGGACCCC CCGAGGGACCCC CCGAGGGACCCC CCGAGGGACCCC CCGAGGGACCCC CCGAGGACCCC CCGAGGGACCCC CCGAGGACCCC CCGAGGGACCCC CCGAGGACCCC	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCTC TCTGTGGAT GCTAAGGGGG GGCATCAAAG CCAGGAGAGCC CCCCCTGGCC GGCCCTGCAG CCAGGACGGG TCAGGCCTTG AAGCCGGAG GGTGTGCCAG ACGGGGGAG CCTGGAGGCCC CCTGGAGGCCC CCTGGAGGCCC CCTGGAGGCC	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCAGGTCG GAGACCGGG GAGACCGGG GAGACCGGG GACCCAAGG GCCTGACTGG CCCCAAGG CCCAAGGTCG GCTCACCAGGTCG GTCACCAGGTCG GTTACCAGG CTGGACAGG CTGGACAGG GAGGCGAGAA GAGGCGAGAA	GGGGACTCA ACGGGGCTTC TGGGGAGAGG TCCCGGGCTC AGAACGCGGA TGGACCTCT TGGACTCTCT CAATGGTGAC AGAGCCTGGA TGGGCCTGGA TGGGCCTGGA TCATGGGAC ACCTTCTGGC ACCTACTGGA AGATGGTCTCCA AGATGGTGCC TCTGCCTGGC TGTGGTGGGG GGGTGAGAGCT GGGGTGGGGG	AAGGGCACC GGCCCCCG GGCCCCCG GAGAAAGGAG GGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC CCTGAACGCG CCTGAACGG GCTTTGGAC GGTTTGCCTG AGTGGAAAAG CCTGCTGGAC CTGCTCGGAC CCTCCTGAAGGGG CCTGCAGAC CCTCCTGAAGG CCTCCTGAAG CCTCCTGAAG CCTCCTGAAG CCTCCTGAAG GAGCCGGAA	6120 6180 6240 6300 6360 6420 6540 6540 6600 6660 6720 6780 6980 6990 6960 7020 7080 7080 7140
75	GCCCCCAGG GTGGAGACCC GGCCTTCCGG GACCCCTGG GACCCCTGG AAGGAGACAG AGGACGCAA GTCTGCAGG CTGGAGA TTCCTGGACC GACAAGTGG CAAAGGGACAG CTAAAGGAGA CTAAAGGAGA CAAAGGGAGA CAAAAGGGAGA CAAAAGGGAGA CCAAAAGGGAGA GCCAGAGGACCCGG	CAAGGAGGC TGGCCTTCAC GCTTGCCGG GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA CCCCAAGGTG GGGTGTGCCA CCCGGGTCTA CCCGGGTCTGC GACAGGACCT CCCCGGACACGG AGGGACAGGG AGGGACCCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCC CAAGGGACCT ACCTGGCCC CAAGGGACCT AGACCCTGGGG	CCCATCGCT GGGCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCTC TCTGTGGATG GCTAAGGGG GGCATCAAAG CCAGGAGAGGC CCCCTGGCAG CCAGGACGGG CCAGGACGGG CCAGGACGGC CCAGGACGC CCAGGACGC CCAGGACGC CCAGGACGC CCAGG	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGGG CTGGACTCCC AGCCAGGTCC GAGACCGGG GTGGTATGGC CAGTGGTTGG GACCCAAGG GCCTGACTGG TGGGTCACA CCCCAGGTCG CGTCACCAGG CTTGCTGGAGA CTGGACAGG CTGGACAGG CTGGACAGG CTGGACAGG AGAGGGAGAA AGGAAAGGGGC	GGGGACTCA ACGGGGCTC TGGGGACAGGGGCTC TGGACCCCT TGGACTCTCT CAATGGTGAC TGGACCTGA TGGACCTGA TGGACCTGA TGGACCTGA TGGACCTGA TCATGGAGA TCATGGAGA ACCTACTGGA GGGTCTCA AGATGGTGCC TGTGGTCGGG TGTGGTGGGT TCTGCTGGGC TGTGGTGGGT TCCAGGACCC	AAGGGCACC GGCCCCCG GGCAGGAAAGAG GGGCCCCCG GGAGAAACAGG CAAGGTCCA CCGAGGGTC GGGAACCAG CCTGAACGAC CCTGAACGAC GGTTTGCAC GGTTTGGAC GGTTTGGAC GGTTTGGAAC CCTGTAGAGAC GGTTTGGAAC CCTGTAGAGAC CCTGCAGAG GAGCCGGAG GAGCCGGAG AAAGGTTTCA	6120 6180 6240 6300 6360 6420 6480 6540 6660 6720 6780 6840 6900 7020 7080 7140
75	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGAGACAG ATTCCTGAGGG CTGGTGCCC AGCCTGGAGA ATTCCTGGACA ATTCCTGGACA ATTCCTGGACA ATTCCTGACGA ATTCAAGGAGACAG CTAAAGGAGA CTAAAGGAGA CAAAGGTGA CAAAGGTGA CGGAGACCCCG AGGCTGACCCC	CAAGGAGGC TGGCCTCAG GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA ACAGGGCAGA CCCCAAGGTCA ACTCAAGGGT GGGTGTGCCA CCCGGGTCTA TCCAAGAGGC GGGTCTTGCT GACAGGACCT GACAGGACAG	CCCATCGGCT GGGCCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCCTC TCTGTGGATG GCTAAGGGGG GCCATCAAAG CCAGGAGGGG CCCCCTGCAG CCAGGACGGG TCAGGCCTGCAG GGTGTGCCAG GGTGTGCCAG CCAGGGCCCC CCAGGCCCC CCAGGCCCC CCAGGCCCC CCAGGCCCC CCAGGCCCC CCACGCCCC CCACCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCAGGTCA AGCCGGGCAG GAGACCGGG GTGTATGGC CAGTGGGTGG GCCCCAAGG GCCTGACTGG CTGGCCAC CCCAGGTCC GGTCACCAGG CTGGACAGG CTGGACAGG CTGGCAGAG AGAAAGGGG AAGAGGCGAGAA AGAAAGGGG CCCCTGGGCC CCCCTGGGCC	GGGGACTCA ACGGGGCTC ACGGGGCTC AGAACGGGA TCCCGGGCTC TGGAACCCCT TGGACCTGTC CAATGGTGAC ACGACCTGA ACGACCTGA ACCACTGAA TCATGGAGAC ACCTTCTGGC ACCTACTGGA ACCTACTGGA ACCTACTGGA ACCTACTGGA ACCTACTGGA TCTGCCTGGC TCTGCCTGGC CCTGGTGGGT GGGTGAGCCT TCTGGGAGACC TCTGTGGGACCT TCTGTGGGCCCT TCTCTGGCCCT	AAGGCGACC GGCCCCCG GGCCCCCG GGAGAAAGGAG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CGGAACCAG CCTGGACCAC CTGAAGGGGC CTGGACCAC CTGAAGGGGG GGTTTGGAC AGTGGAACAG CCTGTTGGAC CCTGTTGGAC CCTGCTGGAC AGTGGAAAAG CCTGTTGGAC CCTCCTGGAG GGCCTGCAG AAAGGTTTCA CCAGGTTTCA	6120 6180 6240 6300 6360 6420 6540 6660 6780 6780 6960 6960 7020 7080 7140 7200
75 80	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA AGGACGCAA AGGACGCAA AGCTGGAGA CTGGTGCCCC AGCCTGGAGA ATCCTGGAGA ATCCTGGACA ATCAGAGACA CTAAAGGAGA CTAAAGGAGA CCAAAGGTGA CCAAAGGTGA AGGAGACCCGG AGGGTGACCTGAGAGACCCAGAGAGACCTGAAGAGACA AGGAGACCCGG AGGGTGACCTGAGAGACCCAGAGAGACCTGAAGAGACA AGGGTGACCCGG AGGGTGACCTGAGGACACCTGAAGGTGAA	CAAGGAGGC TGGCCTTCAC GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA ACTCAAGGGT GGGTGTGCCA CCCGGCCTT GACAGGACCT GGAGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGGACAGGG AGGAGACTGG AGACCTGGCCC CAAGGGACTGG AGGACTCGG AGGACTCGG AGGACTCGGG AGGACTCCGG	CCCATCGGCT GGGCACCTG GAGCCTGGAA GAAGGCCAG GATGGCCTC TCTGTGGATG GCTAAGGGGG GCCATCAAAG CCAGGAGAGAGC CCCCCTGCCAG CCAGGACGGG CCAGGACGGA GGTGTGCCAG CCTGGAGGCCC CCTGGAGGCC CCTGGAGGCC CCAGGGCCCC CCAGGGCCCC CCAGGGCCCC GAAGATGGTC GTCCCGGGCC GAAGATGGTC GTCCCGGCCCC	TTCCTGGAGA GTCTGGCCT AGCCTGGACTCCC AGCCAGGTCC AGCCAGGTCC AGCCAGGCAG GAGACCGGG GAGACCGGG GAGACCGAG GCCCAAGG GCCTGACTGC GGTCACCACA CCCCAGGTCG GTCACCAGG CTGGACAGG CTGGACAGG CTGGACAGG CTGGACAGG CAGGGCGAGAA AGAAAGGGC CCCCGGGC	GGGGACTCA ACGGGGCTC AGAACGGGA TCCCGGGCTC TGGACCTCTCTGGACTCTCTCT CAATGGTGAC AGAGCCTGA TGGACCTGA TGGGCCTGA TGGGCCTGA ACATGGTGC ACCTACTGGA ACCTTCTGGC ACCTACTGGA ACCTTCTGGC TCTGCTGGC TGTGCTGGG GGGTGAGCT TCCTGGCCT TCCTGGCCT TCTTGGCCCT TCTTGTTGGC	AAGGGCACC GGCCCCCG GGCCCCCG GGAGAAGGG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCGG GCTGGACCAC CTGAAGGGGC GTTTGCCTG AGTGGAC GGTTTGCCTG AGTGGAC CTCCTGGAG CCTCCTGGAG GAGCCGGGAG CCTCCTGAG AAGGTTCCA AAAGGTTCCA AAAGGTTCA TCCCGGGTC TCACGGGTCCAG AAAGGTTCA TCCCGGGTC	6120 6180 6240 6300 6420 6480 6540 6660 6720 6780 6840 6990 7020 7080 7200 7260 7320
75	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGTGT AACGTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA GTCTGCAGGCAA GTCTGCAGGA TTCCTGGACC GACAAGTGGG ATGGAGACAGG CTAAAGGAGA CTAAAGGAGA CCAAAGGGGA AGGACCCCG AGGGTGACCC AGGGAGATCT AGACAGGCCC	CAAGGAGGC TGGCCTTCAC GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA ACAGGGCAGA CCCCAAGGTG GGGTGTGCCA CCCGGGTCTA TCCAAGAGG GGGTCTTGCT GACAGGACCT CCCGGCCT ACCTGGCCCT ACCTGGCCCC GAAGGACCCC CCAAGGGCCCC CCAAGGGCCCC CCAAGGCCCC CCAAGGCCCC CCAAGGCCCC CCAAGGCCCC CCAAGGCCCC CCAAGGCCCC CCAAGGCCTCC CCAAGGCCTCC AGACCCTGGG AGGCCTCCCT AGGCCCCCTCTCTCAAGGCACGC AGGACTCGGC AGGACTCGGG AGGACTCGGG AGGACTCCGGC AGGACTCCGCC TCCAAGGACTCC TCCAAGGACTC TCCAAGGACTCC TCCAAGGACTC TCCAAGGACT TCCAAGGACTC TCCAAGGACT TCCAAGACT TCCAAGGACT TCCAAGCACT TCCAAGGACT T	CCCATCGCT GGGCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCTC TCTGTGGATG GCTAAGGGG GGCATCAAAG CCAGGAGAGGC CCCCTGGC GGCCTGCAG CCAGGACGGG CCAGGACGGG CCAGGACGGG CCAGGACGGG CCAGGACGGG CCAGGACGGG CCAGGACGGG CCAGGACGGG CCAGGACGGC CCAGGACGC CCAGGACGC CCAGGCCC GAAGATGGTC GGCCTGCCAG ATGGCCTGCAG	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCGGGCAG GAGACCGGG GAGACCGGG GACCCAAGG GCCTGACTGG TGGGTAC GCCCAAGG GCCTGACTGG TGGACAGG CTGGACAGG CTGCTGGACAG AGGAGAGAA AGGAAAGGGC CCCTGGCCC CTGCTCCTGG	GGGGACTCA ACGGGGCTC TGGGGACAGGGGCTC TGGACCCCT TGGACTCTCT CAATGGTGAC TGGACCTGA TGGACCTGA TCATGGAGAC ACGTCTGGAC TGGGCCTGA TCATGGAGAC TCATGGAGAC TCTGGGC TGTGGTCGG TGTGGTGGG TCTGGGC TCTGGGCCT TCTGGCGC TCTGGGCCT TCCAGGACC TCCTGGCCCT TCTTGTGTGGT TGTGTTGGG TGGGACCC TCTTGGCCCT TCTGAGACCC TCTGAGACCC TGTGAGGCCC TGTGAGCCG TGGAGACCG TGGAGACCG TGGAGACCG TGGAGACCG TGGAGACCG	AAGGGCACC GGCCCCCG GGCAGGAAAGAG GGGCCCCCG GGAGAAAGAG GGGCCCCAC CCGAGGGTCCA CCGAGGGTC GGGAACCAG GCTGACCAC CTGAAGGGC GCTGGACCAC CTGAAGGGG GCTTTGCAC GGTTTGGAC CTGCTGAAAAG CCTGTCGGAC CTCCTGAAG GAGCCGGAG GAGCCGGAG AAAGGTTCA CCAGGTTTAC CCAGGTTTAC CCAGGTTCAC GCTCCGGAG GCCGTCCAG AAAGGTTTCA CCAGGTTCAG CCAGGTTCAG GGTCTGGCAG	6120 6180 6240 6300 6360 6420 6540 6660 6720 6780 6840 6900 7020 7080 7140 7200 7320 7380
75 80	GCCCCCAGG GTGGAGACCC GGCCTTCCGG CTGGGGGTGT AACCTGGAGA GACCCCCTGG AAGGAGACAG AGGACGCAA AGGACGCAA AGCCCCCCAGG CTGGTGCCC ACCCTGGAGC CTAAAGGGACAC CTAAAGGAGACAG CCAAAGGTGA CCAAAGGTGA CCAAAGGTGA CCAAAGGTGA CCAGGAGACCCC AGGGGAGACCC AGGGGAGACCC AGGGAGACCC AGGCACCCCAGG	CAAGGAGGC TGGCCTTCAG GGGAGAGGCA ACAGGGCAGA ACAGGGCAGA ACTCAAGGGT GGGTGTGCCA CCCGGGTCTTA CCAGAGGGC GGGTCTTGCT GACAGAGGC GGGACAGGC GGACACAGGC GAGACAGGC GAAGGACCC GAAGGACCC GAAGGACCT GAAGGACCT CCAGGCCCT TCGAGGACT GGAGGACT GGAGGACT GGAGGACT TGGGAGGACT TCGAGGAGGA GGGACTCGGG GGGCTCCCT TCGAGGAGAG GGGCTCCCT CGAGGAGAGAGGA GGGAGAGAGGA GGAGGAGAGGA	CCCATCGGCT GGGCACCTG GAGCCTGGAA GGAAGGCCAG GATGGCCTC GCTAAAGGGG GCCATCAAAG CCAGGACGGC GCCCTGGAC GCCCTGGAC GCCCTGGAC GCCCTGGAC GCCCTGGAC GCCCTGGAC GGCCTTGCAG GCTGAGGCCC CCTGGAGGCCC CCTGGAGGCCC CCTGGAGGCCC CCTGGAGGCCC GAGATGGTC GCCTGCCGGCT GGCCTGCCG	TTCCTGGAGA GTCTGGCCT AGCCTGGTAT GAGAGAGGG CTGGACTCCC AGCCAGGTCC AGCCAGGTCC AGCCAGGTCG GAGACCGGG GTGGTATGG CAGTGGTTGG GCCCAAGG GCCTGACTGG CTGGTCACA CCCCAGGTCG GTCACAGG CTGGCAGGA CCCCAGGTCG GTCACAGG CTGGCAGGA CCCCGGCC GTGCTCTGG CAGGCGCAGA CCCTGGGCC CTGGCCTAG CCCTGGGCC CCCTGGCCC CCCTGGGCC CCCTGGGGCC CCCTGGGGCC CCCTGGGGCC CCCTGGGGCC CCCTGGGGCC CCCTGGGCC CCCTGGGGCC CCCTGGGCC CCCTGGGCC CCCTGGGCC CCCTGGGCC CCCTGGGCC CCCTGGGCC CCCTGGGCC CCCTGGGCC CCCTGGCC CCCTGGCC CCCTGGCC CCCTGCC CCCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	GGGGACTCA ACGGGGCTC ACGGGGCTC AGAACGGGGA TCCCGGGCTC TGGACTCTCT TGGACTCTCT CAATGGTGAC AGGCCTGAA TCATGGAGC ACCTACTGAG ACCTACTGAG ACCTACTGAG GGGGTCTCCA AGATGGTGCC TCTGGCCTGGA TCTGGGGCTGAAC TCCTGGCCCT TCTTGGCCCT TCTGGCCCT TCTTGGCCCT TCTGGCCCT TGTGTTTTGGG ACCTGGACCC ACCTGGACCC ACCTGGACCC	AAGGGCACC GGCCCCCG GGCCCCCG GGAGAAGGG GGGCCCCCG GGAGAACAGG CAAGGTCCCA CCGAGGGGTC GGGAACCGG GCTGGACCAC CTGAAGGGGC GTTTGCCTG AGTGGAC GGTTTGCCTG AGTGGAC CTCCTGGAG CCTCCTGGAG GAGCCGGGAG CCTCCTGAG AAGGTTCCA AAAGGTTCCA AAAGGTTCA TCCCGGGTC TCACGGGTCCAG AAAGGTTCA TCCCGGGTC	6120 6180 6240 6360 6420 6420 6540 6660 6720 6780 6960 7020 7080 7140 72260 7320 7320 7340

WO 02/086443 PCT/US02/12476 CTGGGCCCCG AGGCGAGCCTG GCGTCCGGGC TGAAGATGGC CGCCCCGGCC 7560

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Seq ID NO: 69 Protein sequence: Protein Accession #: NP_068772.1

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PCT/US02/12476

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                                                                                     1440
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STEQMLSSEA VAVDFGNYHL GVMSWIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGELP
                                                                                       240
                                                                                       300
30
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        RKPELERPIK VNLALPVFFI LACLFLIAVS PWKTPVECGI GFTIILSGLP VYFFGVWWKN
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                                                                                       480
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                                                                                       720
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                                                                                       960
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        CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC
                                                                                      1080
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                                                                                      1140
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GCTCGGTTTC CTTTTCTAGA ATGGAAATAG TGAGGGCCAA TGC
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        Protein Accession #: NP_005259.1
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        CECCCTECTE GCECTCACCT CCGCGETCGC CARARAGARA GATRAGGTGA AGRAGGGCGG CCCGGGGRGC GAGTGCGCTG AGTGGGCCTG GGGGCCCTGC ACCCCCAGCA GCARGATTG
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85
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                                                                                       240
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        TGCGTGTGAT GGGGGCACAG GCACCAAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA
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		7000443	003 800000	G1 GG1 1 GGGG	2001 200001		400
		TGCCAGGAGA					420
		GCCAAGAAAG TCACATGGGG					480
		TCACATGGGG					540
5		CCCACCCCTA					600 660
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15	MOHRGFLLLT	LLALLALTSA	VAKKKOKVKK	GGPGSECAEW	AWGPCTPSSK	DCGVGFREGT	60
	CGAQTQRIRC	RVPCNWKKEP	GADCKYKFEN	WGACDGGTGT	KVRQGTLKKA	RYNAQCQETI	120
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	CTCTACCTGA	CACAGCTGCA	GCCTGCAATT	CACTCCCACT	GCCTGGGATT	GCACTGGATC	60
		GAACAAGGTG					120
		CTCCTACTGG					180
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		CACACAGCTA					1080
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45	TTTTTCAAAA	AAAAAAAAA	AAA				
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		93 Protein					
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50	1 MKICSLTLLS	 PLLLAAQVLL	ABCKKKAKNIC 	 LHSKVVSEQK	 DTLGNTQIKQ	 KSRPGNKGKP	60 120
	1 MKICSLTLLS VTKDQANCRW	1	TEACL OFF	 LHSKVVSEQK EFSCVFAGNP	 DTLGNTQIKQ TSCLKLKDER	 KSRPGNKGKP VYWKQVARNL	
50 55	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS	 PLLLAAQVLL AATEQEEGIS	VEGKKKVKNG LKVECTQLDH KDFPESSLKL	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK	 DTLGNTQIKQ TSCLKLKDER PRKEKTEMSP	 KSRPGNKGKP VYWKQVARNL REHIKGKETT	120
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55 60	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTQTM Seq ID NO: Nucleic Ac: Coding sequents	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession sence: 125-1	VEGKKKVKNG LKVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG	LHSKVVSEOK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC	DTLENTOIKQ DTLENTOIKQ DTSCLKLEDER PRIEKTENSP LCTFFLSIVQ 41 CCACTCCCTG	KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACGCC	120 180
55 60	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTQTM Seq ID NO: Nucleic Ac: Coding sequents	PLILIAAQVIL AATEQEEGIS RTAVKTRVCR ATKAPECVED 94 DNA sequid Accession 11	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA	LHSKVVSEQK EPSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG	KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACCCC CCCAAGCACCC	120 180 60 120
55	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequent 1 CTCCTCACAG TGCCAGAAAG	PLILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession sence: 125-1 11 GTGTGTCTCT GTCACCTATC GCTGCAGATG	VEGKKKVKNG VEGKKKVKNG LKVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 LAGTCCTCGTG CTGAACCCCA CCTCCAGGAG	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG	KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACGCC CCCAGGGATGC	120 180 60 120 180
55 60	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTQTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCGATGGAA	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession tence: 125-1 GTGTGTCTCT GTCACCTATC GCTGCAGATG TCGGGCCCCA	VEGKKKVKNG LKVECTQLDH KKPFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT	LHSKVVSEOK EPSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGAGAATGGC	DTLENTQIKQ DTLENTQIKQ TSCLKLKDER PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGAGGTAG ACCAAGAGGTAG	KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC ACGCAAGGA	120 180 60 120 180 240
55 60	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTQTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCGATGGAA	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession tence: 125-1 GTGTGTCTCT GTCACCTATC GCTGCAGATG TCGGGCCCCA	VEGKKKVKNG LKVECTQLDH KKPFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT	LHSKVVSEOK EPSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGAGAATGGC	DTLENTQIKQ DTLENTQIKQ TSCLKLKDER PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGAGGTAG ACCAAGAGGTAG	KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC ACGCAAGGA	120 180 60 120 180 240
556065	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequ 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCGATGGAA CCGGAGCCCG CCCAGAAGCC	PLILIAAQVIL PLILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ence: 125-1 11 GTGTGTCTCT GTCACCTATC GCTGCAGATG TCGGGCCCCA ACCGACGGC GGGGAAGGTA	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGGA GGAGCGCCCT	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA GCAAGCCTGA GGCAGATGGC GGCAGCTGAG GTTCGCGGGC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTCAG AGCAAGGGCC AATGAGTGGC	KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC CCAGGATGC ACGGCAAGGA TGGGCAGGGC GGCGGCACCAT	60 120 180 240 300 360
556065	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG CCGGAGCCCG TGCCAGAGCCC CCTGAAGCC	FLILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession tence: 125-1 GTGTGTCTT GTCACCTATC GCTGCAGATG TCGGGCCCA ACCAACGGGC GGGGAAGGTA GTCGAGTCCG	VEGKKKVKNG VEGKKKVKNG LKVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT ACGGCGGGGA ACGGCGCCT GGGACGACAA	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEFCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGAGAATGGC GGCAGCTGAG GTTCGCGGGC GAACTCCAAC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER FREEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAG ACCAAGGCTG GGCAAGAGCC AATGAGTGCC TACTTCAGCA	KSRPGNKGKP KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACCCC CCAAGCACCC CCAAGCACCC CCAGGATGC ACGCCAAGGA TGGGCAGGA TGGGCACCAT TGGACTCTAT	60 120 180 240 300 360 420
55 60	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAACC CCTGAAGCCA CATCCAGTTT GGAAGGCAAG TACCTTTGCC	PLILIAAQVIL PLILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ence: 125-1 11 GTGTGTCTCT GCTGCACTATC GCTGCAGATG TCGGGCCCCA ACCGGC GCGGAAGGTA GTCGAGTCGCG AGGTCGCCGT AGGTCGCCGT AGGTCGCCGT AGGTCGCCGT AGGTCGCCGT AGAAGGGCC GAAAGGGCCG AGGTCGCCGT AGGTCGCCGT AGAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCCA AGAAAGGGCCA AGAAAGGGCCCA AGAAAGGGCCA AGAAAGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGAA	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGA GGAGCGCCCT GGGACGACCA ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGTGCGCAA	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCTCGAC GGCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGGGC GAACTCCAAC CCAGCTGGGC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTCAG AACAGGTTCAG CGAAGAGGC AATGAGTGGC AATGAGTGGC TACTTCAGCA GCTGCCAAGA	KSRPGNKGKP VYWKQVARNIL REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCCC CCAGGCATGC ACGGCAGGGA TGGGCAGCGC GGCACCCAT TGGACTCTAT AGCCACCCGT GGAAGCCCAC	60 120 180 60 120 240 300 360 420 480 540
556065	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAACC CCTGAAGCCA CATCCAGTTT GGAAGGCAAG TACCTTTGCC	PLILIAAQVIL PLILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ence: 125-1 11 GTGTGTCTCT GCTGCACTATC GCTGCAGATG TCGGGCCCCA ACCGGC GCGGAAGGTA GTCGAGTCGCG AGGTCGCCGT AGGTCGCCGT AGGTCGCCGT AGGTCGCCGT AGGTCGCCGT AGAAGGGCC GAAAGGGCCG AGGTCGCCGT AGGTCGCCGT AGAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCG AGGTCGCCGT AGAAAGGGCCG AGAAAGGGCCCA AGAAAGGGCCA AGAAAGGGCCCA AGAAAGGGCCA AGAAAGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGGGCCA AGAAAGAA	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGA GGAGCGCCCT GGGACGACCA ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGCAGGGCT ACGTGCGCAA	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCTCGAC GGCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGGGC GAACTCCAAC CCAGCTGGGC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTCAG AACAGGTTCAG CGAAGAGGC AATGAGTGGC AATGAGTGGC TACTTCAGCA GCTGCCAAGA	KSRPGNKGKP KSRPGNKGKP VYWKQVARNL REHIKGKETT DTSC 51 CCGAGACCCC CCAAGCACCC CCAAGCACCC CCAGGATGC ACGCCAAGGA TGGGCAGGA TGGGCACCAT TGGACTCTAT	60 120 180 60 120 240 300 360 420 480 540
556065	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence TCCCTCACAG TGCCAGAAAG TGCCAGAAAG CCGGAGCCCG TGCCAAGACC CCTGAAGACC CCTGAAGCCA CATCCAGTTT GGAAGGCAAG GACCTTTGCC GGTGTCCATC	PLILIAAQVIL PALLIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ence: 125-1 11 GTGTGTCTCT GCTGCAGATG TCGGCCCCA TCGGGCCCCA GCGGAAGGTA GTCGAGTCG AGGTCGCGT AGGTCGCGT AAAGGGCC AAGGTGGCCCCA AAGGGCCCCA ATGGAGCCCCC	VEGKKKVKNG VEGKKKVKNG LKVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCAGGAG GTGGCAGCT ACGCGGGGGA ACGCGGGGCAA ACGCAGGGCT GGGACGACAA ACGCAGGGCTA ACGCAGGGCAA ACGCAGGGCAA ACGCAGGGCAA ACGCAGGACCAA	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC CAACGGGTCG GGCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGGGG GTCCATTTC GCGGAACAGC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAAGGCTC AATGAGTGGC TACTTCAGCA GCTGCCAAGA TCGGAGTCCC TACCCCCGGG	KSRPGNKGKP VYWKQVARNIL REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCCC CCAGGCATGC ACGGCAGGGA TGGGCAGCGC GGCACCCAT TGGACTCTAT AGCCACCCGT GGAAGCCCAC	60 120 180 240 300 360 420 480 540 600
55606570	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequ 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAAGACC CCTGAAGCCA CATCCAGTTT GGAAGGCAAG TACCTTTGCC GGTGTCCATC CCTTTTTTCA CAAGGCAAG	PLILIAAQVIL PALILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ence: 125-1 11 GTGTGTCTCT GTCACCTATC GCTGCAGATG TCGGGCCCCA ACCAACGGC GCGGAAGGTA GTCGAGTCCCAGT GAAAAGGGCCG ATGGAGCCCG ATGGAGCCCG ATGGAGCCCG GCGTCCAAGT GCTGTCAAGT GCTGTCAAGT GCTGTCAAGT GCTGTCAAGT GCTGTCAAGT GCTGTCAAGT GCTGTCAAGT GCTGTCAAGT	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT GGAGCGCCCT GGGAGCGCCCT GGGAGCGCCCT GGGAGCCCCC CCGCAGGAC ACGCAGGGCCCCC CCGGAGCCCCC CCGGAGCCCCC	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCCTGAC GCAGCTGAG GTTCGCGGC GAACTCCAAC CCAGCTGGG GTCCATTTTC GCGGAACAGC GCAGGTGGGG GTCCATTTTC GCGGAACAGC GCAGGTGCTG GCAGGTGCTG GTTGCTGGGC	DTLGNTQIKQ DTLGNTQIKQ TSCLIKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTTCAG AGCCAGAAG ACCAAGGCTCAG AACAGGCTCAG TACTTCAGCA GCTGCCAAGA TCGGAGTCCC TACCCCGGG TGGGACTCCT TACCCCCGGG	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC CCAGGATGC ACGGCAGGGA TGGGCAGGGC GGCGACCCAT TGGACTCTAT AGCCACCCGT GGAAGCCCAC CCGACACGGG GCATCGGCAA	60 120 180 240 300 360 420 480 540 600 660
556065	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG CCGGAGCCG TGCCAAGACC CCTGAAGCCA CATCCAGTTT GGAAGGCAAG CAGCTTTGCC GGTGTCCATC CCTTTTTTCA	PLILIAAQVIL PALILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ence: 125-1 11 GTGTGTCTCT GCTGCAGATG TC3GGCCCCA ACCGGC GGGAAGGTA GTCGAGTCGCGT GAAAGGGCC AAGGTCGCCGT ATGAGTCCCC AGGTCGCAGT GCGGTCCAAGT GCGGTCCAAGT GCGGTCAAGT GCGGTCAAGT GCGGTCAAGT CTGGAGGCCG CTGGAGGCCG CTGGAGGCCG CTGGAGGCCG CTGGAGGGCG CTGGAGGGCCG CTGGAGGCCG CTGGAGGCCG CTGGAGGCCG CTGGAGGCCG CTGGAGGCCG CTGGAGGGCCG CTGGAGGCCG CTGAGGCCG CTGGAGGCCG CTGGAGGCCCCA CTGGAGGCCG CTGGAGGCCG CT	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGAGCCCT GGGACGACCA ACGCAGGGCCCT GGGACGACCA ACGCAGGGCCCC CCGGCTCCGA CCTGCCTGGT CCGCCTTCCC	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCTGAG GGCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGGGG GTCCATTTTC GCGGAACAGC GGAGGTGCTG GTGCCAGGCC AGACCACCAG	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTCAG AGCCCAGAAG ACCACTCACCT TACTCAGCA TCGGAGTCCC TACCCCCGGG TGGGAACTCCT TCCTCTCTGCG CTGCTCAGAG CTGCTCCAGC CTGCTCCAGAG CTGCTCCAGC	KSRPGNKGKP VYWKQVARNIL REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC CCAGGATGC ACGGCAAGGA TGGCACCCT TGGACTCTAT AGCCACCCT CGGAAGCACCAC CCGACACGGG GCATCGCAC CCGACACGGG GCATCGCAC CCGACACGGG CCATCGCAC CCGACACGGG CCATCGCAC CCGACACGGG CCATCCCGGA	60 120 180 240 300 420 480 540 660 660 720 780
55606570	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAGACC CCTGAAGCCC CCTGAAGCCC CCTGAAGCCAGACC CCTTTTTTCA CAAGCAGAAAG CAAGCAGAAG CAAGCACCAC CTTTGAGGCC	FLILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession tence: 125-1 11 GTGTGTGTCTCT GTCACCTATC GCTGCAGATG TCGGGCCCA ACCAACGGGC AGGTCGAGTCG AGGTCGAGTCG CGGTCCAAGT GCGGTCCAAGT CTGAGGCCC CGGTCCAAGT CTGAGGCCC CGGTCCAAGT CTGAGGCCC CCGAGGGCC CCGAGGGCC CCGAGGGCC CCGAGGGCC CCGAGGGCC CCGAGGGCC CCGAGGGCC CCGAGGGCC CCCAAGTGTC CTGAGGGCC CCCAAGTGTC CTGAGGGCC CCCAAGTGTC CCCAAGTC CCCAAGTGTC CCCAAGTGTC CCCAAGTGTC CCCAAGTGTC CCCAAGTGTC CCCAAGTC	VEGKKKVKNG VEGKKKVKNG LKVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CCTGAACCCCA CCTCCAGGAG GTGGCAGCCT ACGGCGGGGA ACGCGGGGCA ACGCAGGGCCT ACGGAGGCCCT ACGTGCCCAA CCGGCTCCGA CCTGCCTGGT CCGCCTTCCG CCGCTTCCG	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGAGAATGGC GGCAGCTGAG GTTCGCGGG GTCCATCTTC GCGGACCACC GCAGCTGGGG GTCCATTTC GCGGACACGC GCAGCTGGG GTCCATCTTC GCGGACACGC GCAGCTGGG GAACCACCA CAAGACCACCA CAAGACCACCA CAAGACCACCAC CAAGACCACCAC CAAGACCACCAC CAAGACCACCAC CAAGACCACCAC CAAGACCACCAC CAAGCCACCACCAC CAACCACCACCAC CAACCACCACCACCA	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGGCTCAG AGCCCAGAAG ACCAAGGCTC GGCAAGAGCC TACTTCAGCA GCTGCCAAGA TCGGAGTCCC TACCCCGGG TGGGACTCCT TCCTTCTGCG TCCTTCTGCG GGAGCTCCT TCCTTCTGGGG GAGCTCTTCTCTGGGG GAGCTCTTCTTCTGGGG GAGCTCTTCTTCTGGGG GAGCTCTTCTT	KSRPGNKGKP KSRPGNKGKP VYWKQVARNIL REHIKGKETT DTSC 51 CCGAGACCCC CCAGGGATCC ACGCAAGGA TGGCACCCC TGGAGACCCAT TGGACTCTAT AGCCACCGT GGAAGCCCAC CCGACACGGG GCATCGCAA AGCTCCACGG GCATCGCAA AGCTCCACGA AGCTCCACGA GCCACCGA	60 120 180 240 300 420 480 540 660 720 780 840
55606570	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequity I CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAGACC TGCCAGAGACC TGCCAGAGCCCG TGCCAAGACC TGCCAGAGCCCG TGCCAAGACC CCTTTATTCA CAAGCAGAAG CAAGCCCAC CTTTGAGGCA CAAGCCCAC CCTTTGAGGCA CAAGCCCAC CCTTTGAGGCAC CCTTTGAGGCCCC CCAGACCTGC	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession lence: 125-1.	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGGA GGAGCCCT ACGCGGGGA GGAGACCCA ACGTGCCTCGA CCTGCCTGGC CCGCTTCCG CCGCTTCCG CCGTGCATGG TTTGCATGTT	LHSKVVSEQK EPSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGCAGCTGAG GTTCGCGGG GAAATCCAAC CCAGCTGAG GTCATTTTC GCGGAACAGC GGAGGTGGT GTGCCAGGCC AGACCACCAG CCAGCTGAG CCAGCTGAG CCAGCAGCC AGACCACCAC CCAGCACACCAC CCAGCACCAC CCAGCACACCAC CCAGCACACC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAAGAGC AATAGTIGG GCTACCAAGA TCGGAGTCCC TACCCCGGG TACTCCCGGG TTGCGACTCT TCCTTCTGCG CTGCTCGAGC TGCGACTCTTCT AAGAATCATA	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CGGAGACGCC CCAAGCACCC CCAAGGATGC ACGGCAAGCA TGGGCAGCC GGGATCC GGAGACCGC GGGACCCT GGAAGCCCAT GGAACCGC GCATCGCAA AGCTGCATC CCATCGGGAA AGCTGCATC CCATCGGGAA AGCTGCATC CCATCGGGAA AGCTGCATCAC AGCACCGGA AGCACCGGAA AGCACCATGAC GCACCGGAA AGCACCATGAC GCACCGGAA AGCACCATGAC	120 180 60 120 240 300 360 420 480 540 660 720 780 840 900
55606570	1 MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequ 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAGCC CCTGAAGCCA CATCCAGTTT GGAAGGCAA TACCTTTGCC GGTGTCCATC CCTTTTTTCA CAAGCAGAAG CAAGCAGAAC	PLILIAAQVIL PALLIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession lence: 125-1 11 GTGTGTCTCT GCTGCACCTATC GCTGCAGATG TCGGGCCCCA ACCAACGGC GCGGAAGGTA GTGGAGTCCCAGT GAAAAGGCCG ATGGAGCCCG TCGAGTCAACT CTGGAGCCCG CGGTCCAAGT CTGGAGGCCC CGCAAGTTC CTGCAAGGCCC GCCAAGTGTC ATCTGCTACC GCCAAGGCCCG GCCAAGGCCCG GCCAAGGCCCG GCCAAGGCCCG GCCAAGGCCCC GCCAAGGCCCC	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT GGAGCGCCT GGAGCGCCT GGAGCGCCC GGGAGCCCC CCGCTCCAG CCGCTCCAG CCGCTCCAG CCGCTCCAG CCGCTTCCA CCGCTTCCA CCGCTTCCA CCGCTTCCA CCGCCTTCCA CCGGCTTCCA CCGCCTTCCA CCGCCTTCCA CCGGTGCAAG CCGCCTTCCA CCGGCTTCCA CCGGCTTCCA CCGGCTTCCA CCGCCTTCCA CCGCCTTCCA CCGGCTTCCA CCGCCTTCCA CCGCCTCCA CCGCCTTCCA CCGCCTCCA CCGCCTTCCA CCGCCTCCA CCGCCCCCCCCCC	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA GCAAGCCTGAG GCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGGGG GTCCATTTTC GCGGAACAGC GGAGGTGCTA GTGCCAGGCC AGACCACCAG CCAGGACCACCAG CCAGGACCACCAG CCAGGACCACCAG CCAGGACCACCAG CCAGGACCACCAG CCAGGACCACCAG CCAGGACCAC CCAGCACC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGCAC CCAC	DTLGNTQIKQ DTLGNTQIKQ TSCLIKLXDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTC AATGAGTCGC AATGAGTCGC TACTCCAGGG TCGGAGTCCC TACCCCGGG TGGGACTCCT TCCTTCTGGG CTGCTCGAGC GAGCTCTTCT AACAAAGG CTGCAAAAAG CTGCAAAAAAG CTGCAAAAAAG CTGCAAAAAAG CTGCAAAAAAG CTGCAAAAAAG	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC CCAGGCATGC ACGCACGCA GGCACCCAT TGGACTCTAT AGCACCCGT GGAAGCCCAC CCGACACGGG GCATCGCCAA AGCTGCATCT CCATCCGGGA GCACCGGA GCACCGGA GCACCGGA AGCACCAC AGCACCGAA AGCACCGAA AGCACCGTACA AGCACCGTACA AGCACCTCACA AGCAGCTCCCA	60 120 180 240 300 360 420 540 660 720 780 840 900 960
5560657075	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAG TGCCAGAAG CCGTGAGCCG TGCCAGAGCCG CATCCAGTTT GGAAGGCAAG CATCCAGTTT CCAGTTTTGCC GGTGTCCATC CCTTTTTTCA CAAGCAGAAC CTTTGAGCCA CATCAGACCCC CAGACCTGC CAGACCTGC CAGACCTGC AGTGGAGGAG GCTCAAGATC GCTAGAGTG AGTGGAGGAG GCTCAAGATC	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ience: 125-1 11 GTGTGTCTCT GCTGCAGATG TC3GGCCCCA ACCAACGGC GGGAAAGGTA GTGAGTCGCCGT ATGAGGCCG ATGAGGCCG ATGAGGGCG CGCAAGTG CTGCAAGT CTGGAGGCCG ATCTACT CTGCAGGCCG ATCTACT CTGCAAGT CTGCAAGT CTGCAAGT CTGCAAGT CTGCAAGT CTGCAAGT ATCTGCTACC ATCTACTACC ATTGAGGCCG ATTGAGGTTA	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCOTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGGCGGGA GGAGGGCCT ACGGCGGAA ACGCAGGCCT GGGACGACCA ACGCAGGCT CCGGCTCCGA CCTGCTCGGT CCGCTTCCG CCGGTTCCGG CCGGTTCCGA CCGGTTCCGA CCGGTTCCGA CCGGTTCCGA CCGGTTCCGA CCGGTTCCGA CCGGTTCCGA CCGGTTCCGA CCGGTTCCAGA ACGAGGACA ACGAGGACCCA ACGAGGACCCA ACGCAGGACCCA ACGCAGGACCCA ACGCAGGACCCA ACGCAGGACCAA ACGCAGGACCAA ACGCAGGACAA ACGCATGCAAA ACGAGAGAAA ACGAGATGAAAGAAAAAAAAAA	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCTCGAC GCAGCTCGAC GTTCCCAGCTCCAGC GTCCATTTC GCGGAACAGC GTCCATTTC GCGGAACAGC GAGGTGCT GTGCCAGGC CAAGACGAC CAAGACGATC TAAGAAAGTGG	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRICEKTENSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAGAGGCTC AATGAGTGGC TACTTCAGCA GCTGCCAAGA TCGGAGTCCC TACCCCGGG TGCGAGTCCT TCCTTCTGCG CTGCTCAGC GAGCTCTTCT AACAAAGG CAGAAGAGCA	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACCCC CCAGGATGC CCAGGCATGC ACGGCAGCCC GGAGACCCC GGAGACCCAT TGGACTCTAT AGCCACCGT GGAAGCCAC CCGACACGG GCACCGT CCATCGGCA AGCACCGA GCACCGT AGCACCGA AGCACCGA AGCACCCAC AGCACCAC AGGACCCAC AGGACCCAC AGGACCCAC AGGACCCCAC AGGACCCCAC AGGACCCCAC AGGACCCCAC AGGACCCCAC AGGACCCCAC AGGACCCCAC AGGACCCCAC	60 120 180 240 300 420 480 540 660 720 780 840 900 960 1020
55606570	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG CCCTCACAGACCC CCTGAAGCCC GGTGTCCAT GGAAGGCAAG TACCTTTGCC GGTGTCCAT CAAGACCCCAC CTTTGAGGC CCTTTGAGGC CCTTTGAGGC CCTTTGAGGC CAGACCTGC CAGACCTGC AGTGGAGGAG CCTTTGAGGC CCAGACCTGC AGTGGAGGAG CCTAGAGCCCC CCAGACCTGC AGTGGAGGAG CCTAGAGCTC CAAGAGCTTC	PLILIAAQUIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession 11 GTGTGTCTCT GTCACCTATC GCTGCAGATG TCAGGCCCCAACCAGGCCGAAAGGGCAAGTCAAGT	VEGKKKVING VEGKKKVING VEGKKKVING LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGGA GGAGCCCT ACGCGGGGA GGAGCCCT ACGTGCCTCGA CCTGCCTGGT CCGCCTTCCG CCGCTTCCG CCGTGCATGG TTTGCATGTT AGAAGGAGAC AGGAGAGCAC AGGATGAAG AGAAGGAGAC AGGAGGCCAT	LHSKVVSEQK EPSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGCAGACTGAG GTTCGCGGG GAAATCCAAC CCAGCTGAG GTCATTTTC GCGGAACAC GGAGCTGCG GGAGCTGCG GGAGCTGCC AGACCACCAG CCAGCCAGC CCAGCCAGC CCAGCCAG	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAAGAGC AATAGTIGG GGCAAGAGC TACTTCAGCA TGGGAGTCCC TGCCCCGGG TGCCACTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CGGAGACGCC CCAAGCACCC CCAAGGAAGCA CCCCAAGGAAGCA TGGGCAGCCC GGAGACCGCT GGAAGCCCAT TGGACCCGT GGAAGCCCAC CCGACACGGG GCATCGCAA AGCTGCATCT CCATCCGGGA AGCTGCATCT CCATCCGGGA GCCAGCCGT GCACCGTGAC AGCACGGCAA AGCTGCATCAC AGCACCGTGAC AGCACCGTGAC AGCACCTGAC AGCACCGTGAC	120 180 60 120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
5560657075	MKICSLTLLS VTHOQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequ 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG TGCCAGAAAG CATCCAGTTT GGAAGGCAA CATCCAGTTT GGAAGGCAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGACTC CCCAGAACTGC AGTGGAGAGA GGTCAAGATTC CAAGAGCTTC CAACAGACTTC CAACAGACTTC CAACAGCCTGAAG	PLILIAAQUIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession lence: 125-1 11 GTGTGTCTCT GTCACCTATC GCTGAAGTG TCGGGCCCCA ACCAACGGCC GGGAAGGTA GTCGAGTCCG GTGTCAGTCCG GTGTCAGTCCG GTGAAGGCCG GGGAAGGTCA GTCGAGTCCC CGCAAGTCCC CGCAAGTTC CTGGAGGCC GCCAAGTTC CTCGAGTCCC ATCTGAGTCC ATCTGAATGAC ACCAATG ACCACAATG AAGCAAATG AAGCAAAAGG AAGCAAAAGG AAGCAAAAGG AAGCAAAAAGG AAGCAAAAAGG AAGCAAAAAAGG	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGGA GGAGCGCCT ACGTCGCAGAC CCTGCAGGGC CCGGCTCCGG CCGGCTCCGG CCGGCTCCGG CCGGCTCCGG TTGCATGGT AGGAAGGAGAC AGGAAGAGAC AGGAAGAGAC AGGAAGAGAC AGGAAGGA	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGAC GCAAGCCTGAC GCAGCTGAG GTTCCCAGC GCAGCTGAG GTTCCCAGC CCAGCTGAG GTCATTTTC GCGGACAGC CCAGCTGGG GTCCATTTTC GCGGACAGC CAAGACGATC GTGCCAGGC CAAGACGATC CAAGACGATC CCAGGAGCAC GGAGCTGTCA TGAGAAGTGG CCTGGAGCAC GGAGCTGCCT GGAGCAC GGGCTGCGCTG	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCAGGAGGCTCAG ACCAGGAGGCTCAGAGCTCAGCTC	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCAACCA CCGAGAAGCA ACGCAAGCAA	60 120 180 120 180 300 360 420 480 540 660 720 780 840 900 960 1020 1080
5560657075	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCAGAAGCC CCTGAAGCCC CCTGAAGCCAC CATCCAGTTT GCAAGCAGC CCTGTTTTCC CAGGCAGC CAGCCAGC CAGGCCAC CAGGCCAC CAGGCCAC CCAGGACCTGC CAGGACCTGC CAGGACCTGC GGACCTGC TGTGGACCAA	PLILIAAQVIL PALILIAAQVIL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession lence: 125-1 11 GTGTGTCTCT GCTGCACTATC GCTGCAGATG TCGGGCCCCA AGGTCGCAGT GGGGAAGGTA GTCGAGTCGC AGGTCGAGT GCGGAAGTCG CGGAAGTCCAAGT CCGAAGTCCCAT CCGAAGTCCCAT CCCAAGTCT CCCAAGTCT CCCAAGTCT CCCAAGTCT ACCAAGTCT ACCAAGTCT ACCAAGTCT ACCACAATC ACCAATC ACCACAATC ACCACAATC ACCACAATC ACCACAATC ACCACAATC ACCACAATC ACCACAATC ACCACAATC ACCACAATC ATCAACCAATC ATCAACCAATC ATCAACCAATC ATCAAGCAAAACG GTGAAGGTTCA	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KNDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT GGAGCGCCT GGGAGCGCCT GGGAGCCCT GGGAGCCCT CCGCTCCGG CCGGCTCCGA CCTGCTGGT CCGCCTTCCG CCGTCTCGG CCGGCTTCCG CGGTCCTGGT TTTGCATGT AGAAGGAGAC AGGATGAAGC AGGATGAAGC AGGATGAAGC TCATGGATGG TCATGGATGA	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCCTGAC GCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGAG GTCCAGC GCAGCTGAG GTCCAGC CCAGCTGAG CCAGCTGAG CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTAC CCAGGTCCTCCCTGAGCCAC CGAGCTGCCTCCCTGATCAC CCTGGAGCAC CCTGGAGCAC CCTGGACCAC	I DTLGNTQIKQ DTLGNTQIKQ DTLGNTQIKQ TSCLIKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTCAG AGCCAGAAG ACCAAGGCTC TACTCAGCA TCGGAGTCCC TACCCCGGG TGGGACTCCT TACCCCGGG TGCGACTCTCT TACCCCGGG CAGCATCTT TCCTTCTGGG CAGCATCTT ACTCCAGC CAGCATCTCAGC CAGCATCTCAGC CAGCATCTCGGG CAGCATCTCGGG CAGCATCTCGGG CAGCATCCGGG CAGCAGCGGGG AGACCAAGG	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACGCC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAAGCACCC CCAAGCACCCAT TGGACTCTAT AGCACCCAT GGAAGCCCAC CCGACACGGG GCATCGCACA GCACCGTAC AGCACCGA AGCACCTGAC AGCACCTGAC AGGACCCCAT ACCTGGTGCC AGCACGCAT ACCTGGTGCC AGCACGCAT ACCTGGTGCC AGCACGATGC TGCTGCATGA	60 120 180 240 300 420 480 540 660 720 960 1020 1020 1140 1200
5560657075	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG CCGGAGCCCG CCTGAAGCCC CCTGAAGCCC CCTTGAGCCA CATCCAGTTT GGAAGCAAGA TACCTTTGCC CGTTTCACTC CCTTTTTTCA CAAGCAGAGC CTTTGAGGCC CCTGAGCCCAC CTTTGAGGCC CCAGACCTGC AGTGGAGGAG AGTGCAGAGC CCTAGAGCCC CCAGACCTGCAG TACCTGAGGC CCAGACCTGC CCAGACCTGC CCAGACCTGC CCAGACCTGC CCAGACCTGC CCAGACCTGCAG GGTCAAGACCA GGACCAAGCCCAC CGAGCCTAGAGCCC CCAGACCTGCAG CCTAGAGCCCAC CCAGACCTGCAG CGACCTGGAG CGCCCAAGACCAC CGACCCAC CGACCACACCAC CGACCACAC CGACAAGCCAC CGACAAGCCAC CGACAAGCCAC CGACAAGCCAC CGACAAGCCAC CGACAAGCCAC CGACAAGCCAC CGACAAGCCAC CGACAAGCACAC CGACAAGCACAC CGACAAGCACAC CGACAAGCACAC CGACAAGCACAC CGACAAGCACAC CGACACACAC	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession lence: 125-1 GTGTGTCTCT GTCACCTATC GCTGCAGATG ACCAACGGGC GGGGAAGGTA ACCAACGGGC GAGTCCAAGTC GCTGAGGTCC CGGTCCAAGTC GCGAAGGCCC CGCAAGGCCC ACCAAGGCCC ACCAAGGCCC ACCAAGGCCC ACCAAGGCCAAGTC ACCAAGGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCCAAGAGCAAAGAGCAAAAGG ACCCAGGGAGCCAACCCAAGCCAAGCAAG	VEGKKKVKING VEGKKKVKING LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE L#: NM_0121 L891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCTCCA ACGCGGGGGA ACGCAGGCT ACGTGCCTCGC CCGGCTTCCG CCGGCTTCCG TTTGCATGT AGAAGGAGA CCAGGCTTCCA AGGATGAAGC AGGATGCATAG AGCTGCATAG	LHSKVVSEQK EFSCVFAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA GGAGAATGGC GGAGATGGC GGAACTCCAAC CCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGAG GTCCATTTTC GCGGAACAGC GGAGCTGCAG GCAGACCACCA GCAGCCGCAG GCAGCTGCAG CCAGGACCACC GGAGCTGCAG CCAGGACCACC CCAGCTGCAG CCAGGACCACC GGAGCTGCAG CCTGGAGCAC GCAGCTGCAG GCTTGCAGCCAC CCTGGAGCAC CCTGGAGCAC CCTGGAGCAC CCTGGAGCAC CCTGGAGCAC CCTGGATGAG CCATCAGCGAC	DTLGNTQIKQ DTLGNTQIKQ DTLGNTQIKQ PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG AGCCCAGAAG ACCAAGGCTG GGCAAGAGCC AATAGGTGG TCGCACAGA TCGGAGTCCC TCCTTCTAGGC TCGCTCCAGG TCGGACTCTT CTTCAGGC CTGCTCAAAGG GAGCTCTTCT AAGAATCATA CTGCAAAAGG CAGAAGGGAA AACTTCCGGG GAGCAAGGGAG AACTTCCGGG GAGCAAGGG CAGAGGGAGA AACTTCCGGG GAGCCAAGGG TCTGTTGTTGT	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGGACCCC CCAGGAACCC CCAGGAACCA ACGCAAGCA TGGGCAAGCA TGGGCAACCA TGGACCCAT TGGACTCAT AGCCACCGT GGAAGCCCAT CCATCGCGA GCATCGCAA AGCTGCAAC GCAGCACCAA AGCACCGAT ACCTGGTGCA AGGACCGCAT ACCTGGTGCA AGGACCGCAT ACCTGGTGCC AGCAGGATGCC TGCTGCATGA AGCACCGCAT ACCTGGTGCC AGCAGGATGCC TGCTGCATGA TTCTGCAGGA	60 120 180 240 300 420 480 540 660 720 780 840 900 960 1020 1080 1140 1260
556065707580	MKICSLTLLS VYHOQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequ 1 CTCCTCACAG TGCCAGAAAG TGCCAGAAAG TGCCAGAACC CCTGAAGCCC CCTGAAGCCC CCTGAAGCCA CATCCAGTTT CCAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CAAGCAGAAG CCTTAGAGCC CCTTAGAGCC CCTTAGAGCC CCTTAGAGCC CCTTAGAGCC CCAGAGCTTC CCAGAGCTTC CAAGAGCTTC CAAGAGCTC CAAGAGCTTC CAAGAGCTC CAAGAGCTTC CAAGAGCTAC CAAGAGCTTC CAAGA	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession lence: 125-1 11 GTGTGTCTCT GTCACCTATC GCTGCAGATG ACCAACGGCC AGGGCCCCA AGGGCCCCA AGGGCCCCA AGGGCCCCA AGGGCCCG GCGAAGGGC GCGAAGGCCG GCGAAGGCCG CCGACCAAGT CTGGAGGCC GCCAAGGCCG ATTGGAGGCCG ATTGGAGGCCG ATTGGAGGCCG ATTGGAGGCCG ATTGAGAGTTC ACCACCAATG ACCACCAATG AAGCAAAAGG GTGAAGGGCA ACCGCGGAGC TTGATGAGGTCA ACCCCCATTG AAGCAAAAGG GTGAAGGTGA ACCCGCGGAGC TTGATGAGCCA	VEGKKKVKNG VEGKKKVKNG LEVECTQLDH KDFPESSLKL PDMANQRKTA LENCE 1 #: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT ACGGCGGGAA ACGCAGGCCT ACGTGCCTCA CCTGCCTGGT CCGCCTTCCA CCTGCCTGGT CCGCCTTCCA CCTGCCTGGT CCGCCTTCCA CCGCCTCCA CCGCCCCA CCGCCCCA CCGCCCCA CCCCCCCA CCCCCCCC	LHSKVVSEQK EPSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAAGCCTGA CAACGGGTCG GGAGAATGGC GGAGAATGGC GGAGACTGAG GTTCGCTGGG GAACTCCAAG CCAGCTGAG GTCCATTTTC GCGGAACAGC GCAGGAGCGC AGACCACG GCAGGAGCGC AGACCACTGC GCAGGAGCGC CCAGGAGCGAC GCAGGAGCGAC GCAGGAGCGAC GCAGGAGCGAC GCAGGAGCAC GCAGGAGCAC CCTGGAGCAC GCTGCACGC CCTGGATGAC CCTCGGATGAC CCCCCCCCCC	DTLGNTQIKQ DTLGNTQIKQ TSCLKLKDER PRKEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAGAGGCTC AATAGGTCAG GGCAAGAGCC AATAGGTCCC TACTCCCGGG GGTGCCAAGA TCGGAGTCCC TGCTTCTGCG CTGCTTCTGCG CAGCTCTTCT TCCTTCTGCG GAGCTCTTCT AAGAATCATA CTGCAAAAGG CAGAAGGAGG AACATCCGGG GAGCAGGGG AGAGCCAAGG TCTGTGTGTTGT CTGTGCCACCT	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CGGAGACGCC CCAGGATGC CCAAGCACCC CCAGGATGC ACGGCAGGCA TGGGCAGGC GGGACCCAT TGGACCCGT GGAAGCCCAC CCGACACGGG GCATCGCAA AGCTGCATCT CCATCCGGGA AGCTGCATCT CCATCCGGGA AGCACCGT GCACCCGT ACCTGGCAA AGCACCCGT CCATCCGGGA ACCTGCATCA ACCTGCATCAC AGCACCCGT ACCTGCATCAC AGCACCCGT ACCTGCATCA ACCTGCATCAC AGCACCCTTCAC AGCACCCTTCAC AGCACCCTTCAC AGCACCCTTCAC AGCACCCTTCAC AGCACCCTTCAC ATCTGCTGCG AGCACGAT ACCTGGTGCG AGCACGATCA ATCTGCTGCAGAA ATCATCTCCT	120 180 60 120 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1206 1320
5560657075	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequing TGCAGAAAG TGCAGAAAG TGCAGAAAG TGCAGAAAG CCGGAGCCG TGCCAGGACC CCTGAAGCCA CATCCAGTTT GGAAGCAGCAC CCTTTTTGC CAAGCACAC CTTTGAGCC CCAGACCTGC CAAGACCTGC CCAGACCTGC GGACCTGC GGACAAGCAC ATTTGGTGCA AGGACAAGCAC GGACAAGCAC GCTGGAGGGGG	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA sequid Accession ience: 125-1 11 GTGTGTCTCT GCTGCACTATC GCTGCAGATG TCGGGCCCCA AGGTCGCAGT GGGGAAGGTA GTCGAGTCGCG AGGTCGAAGT GCGGAAGTGCCG ATGGAGCCG ATGGAGCCG ATTGAGTCTC ATCTGCTACC GCCAAGGCCC ATTGAGAGTC ATTGAGATTG ACCACCAATG ACCACA	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCCA CCTCCAGGAG GTGGCAGCCT GGAGCGCCCT GGGAGCGCCCT GGGAGCGCCCT GGGAGCGCCCT GGGAGCGCCCT CCGCTCCGG CCGGCTCCGA CCTGCCTGGT CCGCCTTCCG CCGCTTCCG CCGGCTTCCG CCGGTCATGG TTTGCATGT GGAAGGCCAT AGGAAGGCCAT AGGAAGGCCAT AGGAAGTCAC GGACGCTCAC AGCTCACT GGACGTCACCT	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCCTGAC GCAGCTGAG GTTCGCGGGC GAACTCCAAC CCAGCTGAG GTCCAGTCGGC GAACTCCAG CCAGCTGAG CCAGCTGAG CCAGCTGAG CCAGCTGAG CTCGCAGCC CAGACCACT CTGGAGCC CCAGCTCCAC CCAGCTCCAC CCAGCTCCAC CCAGCTCCAC CCAGCTCCAC CCAGCTCCAC CCACCCCCCCCCC	DTLGNTQIKQ DTLGNTQIKQ TSCLIKLKDER PRICEKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCAGAAG ACCAAGGCTCAG AGCCCAGAAG ACCAAGGCTCAG CACTCCAGC TACTCAGCA CCACAGCTCAG CACAGCTCAG CACAGCTCAGC TACCCCAGGG TGGGAACTCCT TACCCCAGGG TGCTCCAGC CAGCACTCCT CTCTCTCGAGC CAGCACTCCT CTCTCCAGC CAGCACGAGGAGAACACTA AACGAACGACGAG AACTTCCGGG AGGACCACC TCCCCACCT CTGCTCAGC CTGCTCGGG CAGCAGGAGGAGA AACTTCCGGG AGGACCAAGG TCTGTTTGT CTGCCCACCT CTGCCCCACCT CTGCCCCCCCC CTGCCCCCCC CTGCCCCCCCC CTGCCCCCCCC	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACGCC CCAGGATGC CCAAGCACCC CCAGGATGC ACGGCAGGA TGGGCAGCGC GGCACCCAT TGGACCCCT GGAAGCCCAC CCGACACGG GCATCGCAT AGCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA TCCATCGGGA AGGACCGA AGGACCGCAT ACCTGGTGCG AGGACGCAT ACCTGGTGCG TGCTGCATGA TTCTGCAGGA ATCATGTCCT TGCTCAATGT	60 120 180 240 300 420 480 540 660 720 840 900 1020 1020 1140 1200 1260 1380
556065707580	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAG TGCCAGAAG CCGAGCCCG TGCCAGAGCCCG TGCCAGAGCCC CCTGAAGCCC CCTGAAGCCC CCTGAGCCAG CATCCAGTTT GGAGCAGCAC CTTTTTCC CAAGCAGCAC CTTTGAGCCA CATCGAGCAGCCTC CAAGCACCAC CTTTGAGGCC CCAGACCTGC GGAGCCTGC GGAGCCTGC GGAGCCTGC AGTGGAGGAG AGTGAAGATC CAAGAGCTTC GGACCTGGAG GGACCTGGAGAC TGTGGACCAA GGACAAGCAG ATTTGGTGCA ATTTGGTGCA ATTTGGTGCA ATTTGGTGCA ATTTGGTGCG ATTCGAGGGG ATTCCATGCGCC	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA Bequid Accession ience: 125-1 11 GTGTGTCTCT GCTGCAGATG TC3GGCCCCA ACCGGGCCCAAGTGCAAGTGCAAGTGCAAGTGCAAGTGCCGAAGTGCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCAAGAGCCGAAGAGCCGAAGAGCAATGAAGAGCCGAAGAGCAATGAAGAGCAAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAAG	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGAGCCCT GGGACGACCA ACGCAGGGCCCT GGGACGACCA ACGCAGGGCCCT CCGGCTCCGA CCTGCCTGGT CCGCCTTCCG CCGTTCCAG CCGGCTTCCA ACGAGGACA ACGCAGGACA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACA ACGCAGGACA ACGCAGGACA ACGCAGGACA AGGAGGACA AGGAGGACA AGGAGGACA AGGAGGACA AGGAGGACA AGCAGCACA AGCAGCACA AGCAGCACA AGCAGCACA AGCAGCACA AGCAGCACA AGGATGCACA AGGATGCACA AGGATGCACA AGGATGCACA	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCCTGAC GGAGATGGC GAACTCCAAC CCAGCTGAG GTTCCCAGCC GAACTCCAC CCAGCTGAG GTCCAGTCCT GCGGACAGC CAGGACTGC GAGCTGCT GTGCCAGGC CAGGACTGC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCCCCCCC	DTLGNTQIKQ DTLGNTQIKQ DTLGNTQIKQ FRICKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAGAGGCTCAG AGCCCAGAAG ACCAGAGGCC TACTCAGCG TTCGAGGTCCC TACCCCGGG TGCGAGTCCC TACCCCGGG TGCGAGTCCC TACCCCAGGA AACATCATCA AGCACTCCT AAGAATCATA AACAATCATA AAGAACCAAGG TCTGCTAGGG GAGCCGCGG TCTGCTTGGGG TCTGCTCAGC AGCACTAGC AGCACAAGG TCTGTTTGT CTGCCCACCT AAGGACCACA AGCCCTAACT AAGGACCACA AGCCGTAACT	KSRPGNKGKP VYWKQVARNIL REHIKGKETT DTSC 51 CCGAGACCCC CCAGGCACCC CCAGGCATGC ACGGCAGCACCC CCAGGCATGC ACGGCACCGT GGAGCCCAT TGGACTCTAT AGCCACCCT CCGACACGG GCATCGCAT CCATCCGGA GCACCTTGAC AGCACCTTAC TCATCCGGA ATCATCTCT TGCTCAATGT TCCATTGAGAG TTCTTGAGAG	60 120 180 240 300 420 480 540 660 720 780 840 900 1020 1080 1140 1260 1320 1440
556065707580	MKICSLTLLS VTKDQANCRW RSQKDICRYS PSSLAVTOTM Seq ID NO: Nucleic Ac: Coding sequence 1 CTCCTCACAG TGCCAGAAG TGCCAGAAG CCGAGCCCG TGCCAGAGCCCG TGCCAGAGCCC CCTGAAGCCC CCTGAAGCCC CCTGAGCCAG CATCCAGTTT GGAGCAGCAC CTTTTTCC CAAGCAGCAC CTTTGAGCCA CATCGAGCAGCCTC CAAGCACCAC CTTTGAGGCC CCAGACCTGC GGAGCCTGC GGAGCCTGC GGAGCCTGC AGTGGAGGAG AGTGAAGATC CAAGAGCTTC GGACCTGGAG GGACCTGGAGAC TGTGGACCAA GGACAAGCAG ATTTGGTGCA ATTTGGTGCA ATTTGGTGCA ATTTGGTGCA ATTTGGTGCG ATTCGAGGGG ATTCCATGCGCC	PLILIAAQVILL AATEQEEGIS KTAVKTRVCR ATKAPECVED 94 DNA Bequid Accession ience: 125-1 11 GTGTGTCTCT GCTGCAGATG TC3GGCCCCA ACCGGGCCCAAGTGCAAGTGCAAGTGCAAGTGCAAGTGCCGAAGTGCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCCAAGTGCAAGAGCCGAAGAGCCGAAGAGCAATGAAGAGCCGAAGAGCAATGAAGAGCAAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAAG	VEGKKKVKNG VEGKKKVKNG LRVECTQLDH KDFPESSLKL PDMANQRKTA Lence L#: NM_0121 891 21 AGTCCTCGTG CTGAACCCA CCTCCAGGAG GTGGCAGCCT ACGCGGGAGCCCT GGGACGACCA ACGCAGGGCCCT GGGACGACCA ACGCAGGGCCCT CCGGCTCCGA CCTGCCTGGT CCGCCTTCCG CCGTTCCAG CCGGCTTCCA ACGAGGACA ACGCAGGACA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACCA ACGCAGGACA ACGCAGGACA ACGCAGGACA ACGCAGGACA AGGAGGACA AGGAGGACA AGGAGGACA AGGAGGACA AGGAGGACA AGCAGCACA AGCAGCACA AGCAGCACA AGCAGCACA AGCAGCACA AGCAGCACA AGGATGCACA AGGATGCACA AGGATGCACA AGGATGCACA	LHSKVVSEQK EFSCVPAGNP VSSTLFGNTK LEPCGETWSS 01 31 GTTGCCTGCC GCAGCCTGAC GCAGCCTGAC GGAGATGGC GAACTCCAAC CCAGCTGAG GTTCCCAGCC GAACTCCAC CCAGCTGAG GTCCAGTCCT GCGGACAGC CAGGACTGC GAGCTGCT GTGCCAGGC CAGGACTGC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCAGGACCAC CCCCCCCC	DTLGNTQIKQ DTLGNTQIKQ DTLGNTQIKQ FRICKTEMSP LCTFFLSIVQ 41 CCACTCCCTG AACAGCTCAG AGCCCAGAAG ACCAGAGGCTCAG AGCCCAGAAG ACCAGAGGCC TACTCAGCG TTCGAGGTCCC TACCCCGGG TGCGAGTCCC TACCCCGGG TGCGAGTCCC TACCCCAGGA AACATCATCA AGCACTCCT AAGAATCATA AACAATCATA AAGAACCAAGG TCTGCTAGGG GAGCCGCGG TCTGCTTGGGG TCTGCTCAGC AGCACTAGC AGCACAAGG TCTGTTTGT CTGCCCACCT AAGGACCACA AGCCCTAACT AAGGACCACA AGCCGTAACT	KSRPGNKGKP VYWKQVARNI, REHIKGKETT DTSC 51 CCGAGACGCC CCAGGATGC CCAAGCACCC CCAGGATGC ACGGCAGGA TGGGCAGCGC GGCACCCAT TGGACCCCT GGAAGCCCAC CCGACACGG GCATCGCAT AGCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA GCACCGGA TCCATCGGGA AGGACCGA AGGACCGCAT ACCTGGTGCG AGGACGCAT ACCTGGTGCG TGCTGCATGA TTCTGCAGGA ATCATGTCCT TGCTCAATGT	60 120 180 240 300 420 480 540 660 720 780 840 900 1020 1080 1140 1260 1320 1440

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                                                                                       1740
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                                                                                       1980
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                                                                                       2040
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PCT/US02/12476

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45			VKWHTAVTYV				240
			PPTCPLPYHL				300
	FLSACNVCLD	PITYFFMCRS	PSRRLFKKSN	IRTRSESIRS	LOSVRRSEVR	IYYDYTDV	
50		153 DNA sec id Accession		. 1			
50		ence: 149-7		•••			
	1	11	21	31	41	51	
55	1	1		1			
22	•		1	1		!	
			GCGGAGGCCG				60
	CGAAAGGAGT	GAGGCGCCGA	GAGCCCAGAT	ACCATTTTGG	CGTGAGAGCT	GGTGGTTGGC	120
	CGAAAGGAGT AAGGCCGCGG	GAGGCGCCGA GAGTGGGAAG	GAGCCCAGAT CGTCCGCCAT	ACCATTTTGG GTTCTGCGAA	CGTGAGAGCT AAAGCCATGG	GGTGGTTGGC AACTGATCCG	
	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT	GAGGCGCCGA GAGTGGGAAG CGCGCGCCCG	GAGCCCAGAT	ACCATTTTGG GTTCTGOGAA GCCTGCCTTC	CGTGAGAGCT AAAGCCATGG AACGAGGATG	GGTGGTTGGC AACTGATCCG GACTCAGACA	120 180
60	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA	GAGGCGCCGA GAGTGGGAAG CGCGCGCCCG GAGATGAAAG CGAAGTGATT	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC	ACCATTTTGG GTTCTGOGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT	GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG	120 180 240 300 360
60	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC	GAGGCGCCGA GAGTGGGAAG CGCGCCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA	ACCATTTIGG GITCTGOGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA	GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG	120 180 240 300 360 420
60	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT	GAGGCGCCGA GAGTGGGAAG CGCGCGCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC	ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG	GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT	120 180 240 300 360 420 480
60	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT	GAGGCGCCGA GAGTGGGAAG CGCGCCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT	ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC	GGTGGTTGGC AACTGATCOG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA	120 180 240 300 360 420 480 540
	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAAGTTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT	GAGGCGCCGA GAGTGGGAAG CGCGCGCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA	ACCATTTGG GTTCTGOGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA	GGTGGTTGGC AACTGATCOG GACTCAGACAA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGGAAAT TGGGAGGAGA TTGAAGTCCG	120 180 240 300 360 420 480
60 65	CGAAAGGAGT AAGGCCGCGG CGAGCCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTTG GTGTCTAAAA	GAGGCGCCGA GAGTGGGAAG GAGATGAAAG CGAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACATTACAC	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT	ACCATTITGG GAT GCTTCCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTACTTACTACTACTACTACTACTACTACTACTACT	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG CACATGGCTG AGCCTATATA ACTTCAGTCC	GGTGGTTGGC AACTGATCOG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAAGACA TTGAAGTCCG TATTAAAAAA	120 180 240 300 360 420 480 540
	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTG TGTTCTAAAA AAATAGCCAG GGAGCACATC	GAGGCGCCGA GAGTGGAAG CGCGCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGGAG CACTTTTTAC CACTTTTTAC CACTTTTTAC CACTTTTTAC CTGTCATGAC CTGTCATGAC	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CATGGCCCGA	ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGATGAG ATGATGAGGG ATGTGAGCAG GGCACTTCCA	CGTGAGAGCT AAAGCCATGG AACGAGGTG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCCTATATA ACTTCAGTCC CTGATCAGGAC GGCTTCACTC GGCTTCACTC	GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA	120 180 240 300 360 420 480 540 660 720 780
	CGAAAGGAGT AAGGCCGCG CGAGCTGCAG AGTCTCTGGAG GTCAGGTGGA AAATCGACAGC ATGGGAATAT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTG GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA	GAGGCGCCGA GAGTGGAAG CGCGCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGGAG CACTTTTTAC CACTTTTTAC CTGTCATGAC CTGTCATGAC CTCACTCTCT	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTACA CCATACCTGTA TGCCAAATGC AAGGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CCACCACTCC	ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACACTTT ATTACGATTT ACCACCAAAA TGATGATGACAG ATGTGACAG GGCACTTCCA CTTCACCTCC	CSTGAGAGCT AAAGCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATCAGGCTG AGCCTATATA ACTTCAGTCC CTGATCAGCC GGCTTCACTC CTCTTTGATT	GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA TTAGAAGCTA TTAGAAGCTA	120 180 240 300 360 420 480 540 600 720 780 840
65	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TCAAAGGTTTT TCAAAGGTTTC GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT	GAGGGGCGA GAGTGGAAAG GCGAGGTGATT TGCACTGTAG GGTAGGGTCT AATAATTATA GACATTATAG GACTATAGAG CACTTTTAC CTGTCATGAC CTCACTCTCT TTAAGATAAC	GAGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCTAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGA CATGCGCCGA CACACTCC TAAGAATACT	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGATGGC ATGTGAGCAG GGCACTTCCA CTTCACCTCC TGGCTAAGAA	CGTGAGAGCT AAAGCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA CACATGGCTG ATGAGGTCAC CTGATCAGCC CTGATCAGCC CTGATCAGTC CTCTTTGATT GTATAATTTG	GGTGGTTGGC AACTGATCACA ATGAAGCAAA ATGAAGCAAA CTCTGTTTAAG GAGCACTCAG CTGAAGRAAT TGGGAGGAG TTGAAGTCAG TATTAAAAAAA AAGGAGTCCT AACTCATTGAA CTTAGAATTCAT	120 180 240 300 360 420 480 540 600 660 720 780 840 900
	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGT TGAAAGGTTT TGAAAGGTTT GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA AGGACTTCT AGGACTTCT AGGACTTCT AGGACTTCT AGGACTTCT AGGACTTCT AGGACTTCT AGGACTTCT AGGACTTCT	GAGGCGCCGA GAGTGGAAG CGAGGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGAC CACTTTTAC CACTTTTAC CTGTCATCAC TTAAGATAAC TTAAGATAAC TTAAGATAAC TTAAGATAAC TTTAAGATAAC TTTATAAC TTTAAGATAAC TTTATAAT TTTATATG	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTGTA TGATACCTGTA TGACACATCT AAGATCTCT AAGATCTCT AAGATCTCT ACGATATGAA AATTTGAAGT CTCGATGGAA CATGCGCCGA CCACCACTCC TAAGAATACT TTGTACACTA	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACAATTT TGCTACTTAT ACCACCAAAA ATTGTAGTGATTAT ACCACCAAAA TGTGACTTCCA CTTCACCTCC TGGCTAAGAA TTCTTCCTAC	CSTGAGAGCT AAAGCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA AGCTTAGTCC CTGATCAGTCC CTGATCAGCC CTGATCAGACC CTCTTTGATTC CTCTTTTGATTC CTCTTTTGATT CTTTTTTTTTT	GGTGGTTGGC AACTGATCGG GACTCAGCAAA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA TTAGAAGCTA CTAACTATTA CTAACTATTA TTTTGGTTTT	120 180 240 300 360 420 480 540 660 720 780 840 900
65	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTC TGTTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT TAGACATTGT TAGACATTGT TTTGTAGA	GAGGCGCCGA GAGTGGAAAG CGAGGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTTTTAC CACTTTTAC CACTTTTAC CTGTCATGAC CTTCATGAC CTTCATGAC CTTCATGAC CTTCATGAC CTTCATTAC GACTGTCTCATGAC GACTGTCTCATGAC GACTGTCTCA	GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CATGGCCGA CCACCACTCC TAAGAATACC TTGTACACTA CTATGTTGCC	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACAATTT TGCTACTTAT ACCACCAAAA TGATGATGGG GGCACTTCCA CTTCACCTCC TTGCTAAGAA CAAGCTGTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCTCCACCCCCC	CSTGAGAGCT AAAGCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTGGGATCA ACCTATATA ACTTCAGTCC CTGATCAGAC GGCTTCACTC CTCTTTGATT GTATAATTTG TCTTTTTTGG TCAAACTCCT	GGTGGTTGGC AACTGATCGG GATCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA CTAACTATTA TTTTGGTTTT GGCCTCAAGC	120 180 240 300 360 420 480 540 600 660 720 780 840 900 900 960 1020
65	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTC AGATCACACAC CCTCCTCTGTA TAGACATTGT AGGACATTTCT GTTTTGTAGA AGTCCTCCCA	GAGGGGCGA GAGTGGAAAG GCGAGGTGATT TGCACTGTAG GGTAGGGTCT AATAATTATA GACATTATAG GACTATTAGC CACTTTTAC CTGTCATTAGC CTCACTCTCT TTAAGATAAC TTTTTTAATA GACTGTCTCA GACTGTCTCA CTGTCTTCA	GAGCCCAGAT CGTCCGCCAT AGGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATCTCA AGGATATGA AATTTGAAGT CTCGATGGACGA CATGCGCCGA CCACCACCTCC TAAGAATACT TTGTACACTA CTAAGTGTTCCC TCAAGAGTGTT	ACCATTTIGE GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGATCATTAT ACCACCAAAA TGATGATGGC ATGTGAGCAG CTTCCACCTCC TGGCTAAGAA TTCTTCCTAC CAAGCTGGTC CAAGCTGGTC CAAGCTGCTAC	CSTGAGACCT AAAGCATGA AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCCTATATA AGCTTCAGTCC CTGATCAGAC CGCTTTAGATT GTATAATTTG TCTATTTTTTGG TCAAACTCCT GCGTGAGCCA GCCTGAGCCC GCCTGAGCCC GCCTGAGCCC GCGTGAGCCC	GGTGGTTGGC AACTGATCGG GACTCAGCAAA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA TTAGAAGCTA CTAACTATTA CTAACTATTA TTTTGGTTTT	120 180 240 300 360 420 480 540 660 720 840 900 960 1020 1080
65 70	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GCAGTGGTTT GCAAGGTTTT GTAAGGTTTG GTGTTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT AGGACTTTCT GTTTTGTAGA AGTCCTCCCC GTGTGTTTTT GTGTTTTTT	GAGGCGCCGA GAGTGGAAAG CGAGGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC CACTTTACA CACTTTACA CACTTTACAC TTAAGATAAC TTAAGATAAT GACTTTTAC CTGTCATCTT TTAAGATAAT GACTGTCTCA TTTTTTAAT GACTGTCTCA TTTTTTCTAAT TTAAATGAAAA TAAATGAAAA	GAGCCCAGAT CGTCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTATA TGATACCTATA AGATACCTATA AGATTTCAATGA AATTTGAAGT CTCATAGAAG CCACCACTCC TAAGAATACC TATGTTCC TCAAAGTGTT AGGCTGTACC TCAAAGTGTT TGAACCTAC TCAAAGTGTT TAAACATGGT	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACAATTT TGCTACTTAT ACCACCAAAA TGATGATGGCG GGCACTTCCA CTTCACCTCC TGGCTAAGAA TTCTTCCTAC CAAGCTGGTC GAGATCACAG TGTAATCACA TGAAACAATTCAAA TATCATTTGAA	CSTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTGGATCA AGCCTATATA AGCCTATATA AGCCTATATA AGCCTATATA CTTCAGTCC CTGATCAGTCC CTGTTCAGTCC CTCTTTGATT CTTTTTTTGG TCTAAATTG CCTTTTTTTGG TCAAACTCCT GCGTGAGCCA CTCTTCTAAAT	GGTGGTTGGC AACTGATCAG ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA CTTAGAAGTTCCT AACTCATGGA CTTAGTTTTTTTTTGGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGGAGTCCC	120 180 240 300 360 420 540 660 660 720 780 840 900 1020 1030 1140
65	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAAATCGACGC ATGGGAATAT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT AGACATTGT AGGACACATTGT AGGACTTTCT AGGACTTTCT AGGACTTTCT AGGACTTCCCA CCCCTACTCC GTGTGTTTTT TTGGCTGGAC	GAGGGGCCGA GAGTGGGAAG CGGAGGCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGGAG CACTTTTAC CTGTCATGGAG CTCACTCTC TTAAGATAAC TTTTTTAATG CACTTGCTCA CCTTAGCTCC TTAAGATAAC CTTTTTTTTTT	GAGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAC CACACTCC TAAGAATACT TTGTACACTA CTATGTACCTT AGGATTGCC TAAGAATACT TTGTACACTA CTATGTACCT TAAGAATACT TTGTACACTA CTAAGTGTT AAGCTGTATC TAAAACATGGT TAAAACATGGT TAGATCCTGT	ACCATTTIGE GTTCTGGGAA GCCTGCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ACTACCAAATA ACCACCAAAA TGATGATGAT ACCACCAAAA TGATGATGAG GGCATTCCA CTTCCACCTCC TGGCTAGAA TTCTTCCTAC CAAGCTGGTC GAGATCACAG TGTAATCACA TGTAATCACA TGTAATCACA GTGTCTTGTT	CSTGAGAGCT AAAGCATGG ACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGGATCA CACATGGCTG ATCAGGTCA ACCTTCAGTCC CTGATCAGAC GGCTTCACTC CTCTTTGATT GTATAATTTG TCTAATCTTTTTTGG GCATTCCATC GCGTGAGCCA GCATTCTTAAAT TTCTGGTCAT TCTGGTCAT TCTGGTCAT	GGTGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTTAAG GAGCACTTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA CTAACTATTA TTTTGGTTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGTA	120 180 240 300 360 420 480 540 660 720 780 840 900 1020 1080 1140 1200 1260
65 70	CGAAAGGAGT AAGGCCGCGG CGAGCTGGA AATTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTC CTCTCTAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACATTGT AGGACTTCT GTTTTTGTAGA AGTCCTCCCA CCCCTACTCC GTGGTTTTT TTGGCTGGAC CAAGCTAGAG	GAGGCGCCGA GAGTGGAAG CGCAGCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC CTGTCATTGCAC CTCACTCTCT TTAAGATAAC TTTTTTAATG GACTGTCTCT TTAAGATAAC TTTTTTAATG GACTGTCTCT TTTTTTTTTAATG GACTGTCTCT TTTTTTTTTT	GAGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGACAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGACCAC CCACCACTCC TAGGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT AAGCTGTATC TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAACTGGT TAGAATACCAC TCTGAAGATACCAC TCTAAGAATACCAC C TCTAAGAATACCAC CACACACACACACACACACACACAC	ACCATTTGG GTTTTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGCTACTTAT ACCACAAAA ACCACAAAA ACCACAAAA ACCACAAAA ACCACAAAA ACCACAAAA TCTTCCTAC CGCTAAGAA TTCTCCTAC CAGCTGGCTAAGAA TTCTTCCTAC CAGCTGGTC TGGCTAACAA TCTTCACTC CAGCTGTTC TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA TACATTTGAA CATTTTCAAA	CSTGAGAGCT AAAGCCATGA AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA CACATGGCTG ATGAGTCAC CTGATCAGAC CTCTTTTGATT CTTTTTTTGG TCTTTTTTTTG CTTTTTTTTG CTTTTTTTT	GGTGGTTGGC AACTGATCAC ATGAAGCAAA ATGAAGCAAA ATGAAGAAAT TGGGAGGAGA TTGAAGTCAT TATTAAAAAAA AAGGAGTCCT AACTCATGAA TTTTGGTTTT GGCCTCAAGC TTTTTTGGTTTT GGCCTCAAGC AGTGTTTACA AAGCAGTCAC GTGTATTTACA AAGCAGTCAC GTGTATTGTA GTGAAGAGCA	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1200 1200
65 70	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AATTCTGGAG GTCAGGTGGA AAATCGACCG ATGGGAATAT GGAGTGGTTT TGAAGGTTTG GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA AAGACATTGT AGGACTTCT GTTTTGTAGA AGTCCTCCCA CCCTACTCC GTGTGTTTT TTGGCTGGAC CAGCTAGAG TGGTCTTTAG	GAGGCGCCGA GAGTGGAAG CGAGGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGAC CACTTTTAC CACTCTTC TTAAGATAAC TTTATAATAAC CTCACTCTCT TTAAGATAAC CTTAGCTTCA CCTTAGCTTCA CCTTAGCTTCA TAAATGAAAC AGGAAGAAGA AGGAAGAAGA AGCTGAATTT	GAGCCCAGAT GGTCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTATA TGATACCTATA TGATACCTATA TGACAACTGCT AAGGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CATGCGCCGA CCACCACTCC TAAGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT TAGACATGCT TAGACATCAT TAGATACATATATATATAT	ACCATTTGG GTTCTGGGAA GCCTGCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGATGGCAG GGCACTTCCA CTTCACCTCC TGGCTAAGAA TTCTTCCTAC CAAGCTGGTC GAGATCACAG TGTAATCACA TACATTTGAA GTGTCTTTCAA GTGTCTTTCAA	CGTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA ACTTCAGTCC CTGATCAGAC GGCTTCACTC CTCTTTGATT TCTTTTTTGG TCAAACTCCT GCGTGAGCCA TCTCTTTAAT TCACATGCAA ATACTAATTT	GGTGGTTGGC AACTGATCGG GACTCAGCAAA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA TTAGAAGCTA CTAACTAATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGAT GTGAAGATGA AAGCAGTCAC GTGTATTGA	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020 1020 1140 1200 1250 1320
65 70	CGAAAGGAGT AAGGCCGCGG CGAGCTGCA AGTTCTGGAG GTCAGGTGGA AAAATCGACGC ATGGGAATAT TGAAGGTTT TGATTTGAA AAATAGCCAG GGAGCACATC TCTCCTCTGTA TAGACATTGT AGGACTTCCCA CCCCTACTCC GTGTGTTTTT TTGGCTGGAC CAAGCTAGAG TGGTCTGTAG TATTTGGGAA	GAGGGGCCGA GAGTGGAAG CGGAGGTGAT GCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGGAG CACTTTTAC CTGTCATGAG CTCATCATCAT TTAAGATAAC TTTTTTAATG GACTGTCTC TTAAGATAAC CTTTTTTTTTT	GAGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAC CACACTCC TAAGAATACT TTGTACACTA CTATGTACACTA CTATGTACCTT AGGATTGCC TCAAAGTGTT AAGCTGTATC TAAACATGGT TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGAATACTAATAATAATAATAATAATAATAATAATAATAATA	ACCACTATTGE GTTCTGGGAA GCCTGCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ACTACCAAATA ACCACCAAAA ACCACCAAAA ACACCACAAAA ACACCAC	CSTGAGAGCT AAAGCATGG ACGAGCATGT TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATCAGGTCA ACCTTCAGTCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTCTTTTAGTT GTATAATTTG TCTATTTTTTGG CCATTCATAC GCGTTCACTC CCGTGAGCCA GCATTCCTAC TCAAACTCCT TCACACTCCAA TTCTGGTCAT TCACATGCAA TTCTGGTCAT TCACATGCAA TTCAGGTCAT TCACATGCAA TTCACATGCAA TTCACATGCAA TACCATGGTA	GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTTAAG GAGCACTTCAG CTGAAGAAAT TGGGAGGAG TATGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA CTAACTATTA TTTTGGTTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGTA GTGAAGAGA ATCATCGG GCTGGTTGTG GGCGCTGACCCGG GGTGTTTGTA GTGAAGATGA ATCATCTGG GCTGGTTGTGG GCTGGTTGTGG	120 180 240 360 420 480 540 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1340
65 70 75	CGAAAGGAGT AAGGCCGCGG CGAGCTGGAA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAACATTGT AGACATTGT AGACATTGT AGACATTGT TGTTTTGTAGA AATTGTCCCA CCCTACTCC GTGTGTTTTTTTTGTAT TTGGCTGGA TGTTTTGTAG TTTTGTAGA TTTTGGGAG TATTTGGAGA TTTTTGGAGA TTTTTGGAGA TTTTTGGAGA TTTTTGGGTA	GAGGGGCCGA GAGTGGAAG CGAGGTGATA TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTATAG GACTATTAGAG CACTTTTAC CTGTCATTGAC CTTATAGAGATAAAC TTTTTAATG GACTGTCTC TTAAGATAAC TTTTTTAATG GACTGTCTC TTTTTCTAAT TAAATGAAAG AGGAAGAAAG AGCTGATTT AAATTTCAG GGAAGGACAC TTGGGTGATT CAGGGTGATT CAGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGGTGAT CTGGGTGAT CTGGGGTGAT CTGGGTGAT CTGGGGTGAT CTGGGTGAT CTGGGGTGAT CTGGGTGAT CTGGGGTGAT CTGGGG	GAGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCTAC CATACCTGTA TGACACTCC AAGGATCTCA AGGATATCA AGGATATGA CATGCGCCGA CCACCACTCC TAGGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT AAGCTGTATC TAGAACATGCT TTGAACATAC TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAACATGCT TAGAATACAT TAGAATACAT TAGAATACAT TAGAATACAT TAGAATACAT TACATGGATTCA	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGATCATTAT ACCACCAAAA ACCACCAAAA TGATGATGGC ATGTGAGCAC TGACTACTCC TGGCTAAGAA TTCTCCTAC CAGCTGGTC CAGATTTCAA TACATTGAA TACATTGAA TACATTTGAA GTTTAATGAC TGCACATTTCAA GTTTAATGAC TGCACATTTCC CACTTTGGA	CSTGAGAGCT AAAGCATGA AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTGA AGCCTATATA AGCTTCAGTCC CTGATCAGAC GGGTTCACTC CTCTTTGATT GTATAATTTG TCTTTTTTGG TCTTTTTTTGG TCTTTTTTTGG TCTTTTTTTG TCTTTTTTTG TCTTTTTTTG TCTTTTTTTG TCTTTTTTTG TCTTTTTTTG TCTTTTTTTT	GGTGGTTGGC AACTGATCAC ATGAAGCAAA ATGAAGCAAA ATGAAGCACA ATGAAGCACA ATGAAGCACA TGGGGGGGGA TTGAAGTCCT AACTCATGAA ATGAAGTCCT AACTCATGAA TTTGGGTTTA GGCCTCAAGC AGGAGCAC AG	120 180 240 360 420 540 660 720 780 960 1020 1020 1140 1260 1320 1340 1440 1500
65 70	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTG GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTT AGGACTTCT GTTTTTGTAGA AGTCCTCCCA CCCCTACTCC GTGTGTTTT TTGGCTGGAC TGGTCTGAG TGGTCTGTAG TATTTGGGAA CTTGTGGCTA CTTAGAGAAGG	GAGGCGCCGA GAGTGGAAG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGGAG CACTTTTTAC CTGTCATGAC CTCACTCTCT TTAAGATAAC TTTTTTAATG GACTGTCTCA CCTTAGCTTC TTAATGAAAG AGGAAGAAGA AGGAAGAAGA GGAAGAAGAC GGAAGGACAC TGGGGTGAC CTGGGGTGAC CTGGGGTGAC CTGGGGTGAC CTGGGGGGACAC CTGGGGTGAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGTGAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGGGACAC CTGGGGGGACAC	GAGCCAGAT CGTCGCCAT AGGGCAACT CTTTGTATGA TGATACCAGA TGATACCAGA TGATACCAGA TGACAGAT AGAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGA CATGCGCGA CCACCACTCC TAGGAATACCT TTGTACACTA CTATGTTGCC TCAAAGTGTT AGAGTGTT AGAGTGTT AGAGTGTT AGAGTGTT AGATCAGTAT ACATGGATACA TATATATAT ACATGGATTC AGGTTTACACTA AGTTTTCCCT	ACCATTTGG GTTCTGGGAA GCCTGCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGACTTTT TGCTACTTAT ACCACAAAA ACCACAAAA ACCACAAAA TTCTTCCACTCC CTTCACCTCC CAACCTGGCTAAGAA TTCTTCCTAC CAACTGGTC GAGATCACAG TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA TGTTAATCACA GTTTAATGAA GTTTAATGAC GTTTAATGAC GCACTTTCCAA GTTTAATGAC GTTTAATGAC GAGATTCCACACTTTCCAC GAGATTCAGA GAGATTCAGA GAGATTCAGA	CSTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA ACTTCAGCTG ATGAGSTCAC CTGATCAGAC GGCTTCACTC CTGTTCAGAC GGCTTCACTC TCTTTTTTGG TCTATTTTTTGG TCTATTTTTTGG TCTATTTTTTGG TCTTTTATT TCTCTTAATT TCTCTTAATT TCTCTTAATT TCTCTTAATT TCACATGCAA ATACTAATTT CACCATGCAA ATACTAATTT CACCATGCAG ATACTAATT CACCATGCAG ATACTAATTT CACCATGCAG ATACTAATTT CACCATGCAG ATACTAATT CACCATGCAG ATACTAATTT CACCATGCAG ATACTAATT CACCATGCAG	GGTGGTTGGC AACTGATCGA ATGAGCAAA ATGAGCACA ATGAGCACA ATGAGCACACA CTCTGTTTAG GAGCACTCAG CTGAAGGAAT TGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGGA CTAACTATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGTA ATCATCTGC GCTGATTGTA	120 180 240 360 420 540 660 720 780 840 960 1020 1080 1140 1260 1320 1380 1440 1560
65 70 75	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAA AAATCGACGC ATCGGAATAT GGAGTGTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGACATC GTGTCTAAAA AAATAGCCAG GGAGCACATC GTCTCTGTA TAGACATTGT AGCACTTCC GTGTGTTTT TTGGCTAGA CAAGCTAGAG TGGTCTGTAG TATTGGGCTA CTTGGGCTA CTTGGGCTA CTTGGGCTA CTTGGAGAAGG TGGTTGTT TCCAGGTTAGT TCCAGTTTAT	GAGGGGCGA GAGTGGAAG GCGAGGTGAT TGCACTGTAG GGTAGGGTCT AATAATTATA GACATTATAG GACTATTAGC CTGTCATTGAC CTGTCATTGAC TTTAAGATAAC TTTTTTAAT GACTGTTC TTAAGATAAC TTTTTTAAT TAAATGAAAG AGCTGACTTC TTAAGAGAAGAAGG AGCTGAATTT AAATTTTCAG TGAGGGACAC TGGGGTGAT CACTTTTTAAT TAAATTTTCAG TGAGGGACAC TGGGGTGATC AACTTTGTAC TTGTTTTTTTTTT	GAGCCCAGAT CGTCCGCCAT AGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGACAAATGC AAGGATATGA AAGTTGAAGA CATGCGCCGA CCACCACTCC TAAGAATACT TTGTACACTA CTATGTTGCC TAAGAATACT TTGTACACTA CTATGTTGCC TAAGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT AAGCTGTATC TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT TAGATCCTGT CTGAGATACA TATATATATA ACTAGGATTC AGTATGTTTCCTT GGTATGTTTT TTTTATGCTT	ACCATTTGG GTTCTGGGAA GCCTGCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACCACTATA ACCACCAAAA TGATGATGGC ATGTGAGCAG CTTCCACCTCC TGGCTAAGAA TTCTTCCTAC CAAGCTTGCA GAGATCACA TACATTTGAA TACATTTGAA GTTTAATGAC TGCACATTTC CACTTTGTA GGTTATTAATGAC TGCACATTTC CACTTTTGA GAGATCAGA AGACAGCTGA AAACAGCTGA TGGGTGTTTGC	COTGAGACCT ANAGCATGA ACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCCTATATA AGCTCATCA GGCTTAATA GTATCAGTC CTGATCAGC CTCTTTGAT GTATAATTTG TCTATTTTTGG TCAAACTCCT TCCTTAAAT TCTCTTAAAT TCTCTTAAAT TCTCTAAAT TCTCTAAAT TCTCTAAAT TCTCTAAAT TCACATGCAA ATACTAATTT CACCATGCAA ATACTAATTT ACCCAGGTG AGGGGACAGT TTGACTGAAA CATTTTAAAT ATCCGAGAAA	GGTGGTTGGC AACTGATCAG ATGAAGCAAA ATGAAGCAAA ATGAAGCAAA TTGAGAGGAGA TTGAAGTACG TATTAAAAAA AAGGAGTCCT AACTCATGAG TTGAAGTCCG TATTAAAAAA AAGGAGTCCT AACTCATGAG CTGAACCTATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTTACA AAGCAGTCAC GTGTATTGTA GTGAAGATGA ATCATCTGGC GCTGGTGGG GAAATTGGGG AGTCACATGA TTTGATGAAA TCTTTTCCCA	120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500 1560 1620 1680
65 70 75	CGAAAGGAGT AAGCCGCGG CGAGCTGCAA AATCGACGG AAATCGACGG ATCGGATTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTCT CTCCTCTGTA AGACATTCT TTGACATTCT TTGTTTTTTTGAGA AGTCTTCCCA CCCTACTCC TTTTTTTTTT	GAGGCGCGA GAGTGGAAG CGCAGCCGG GAGATGAAAG CGAAGTGATT TGCACTGTAG GATATACAC CACTTTTAC CACTTTTAC CACTTTTAC CACTTTTAC CTGTCATGAC CTCACTCTCT TTAAGATAAC TTTTTTAATG GACTGTCTCA TTTTTCTAAT TAAATGAAG AGGAAGAAGA AGGAAGAAGA CGGAAGGACTC TGGGGTGATT AAATTTTCAG GGAAGGACAC TGGGGTGATC AACTTTGTAC CTCTTTTTAAT CACATTTTTAAC CGCTAATTTTAAC CGCTTTTTAAC CGCTTCTTTAAC CGCTTCTTTAAC CGCTTCTTTAAC CGCTTTTTAAC CGCTTTTTAC CGCTTTTTAC CGCTTTTTAC CGCTTTTTTT CACATTTTTT CACATTTTT CACATTTT CACATTTT CACATTTT CACATTTT CACATTTT CACATTTT CACATTTT CACATTT CACATTT CACATTT CACATTT CACATTT CACATTT CACATTT CACATTT CACATT CACATTT CACATTT CACATTT CACATTT CACATT CACA	GAGCCCAGAT GGTCGCCAT AGGGGCACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAC CACACTCC TAGGAATACCT TTGTACACTA CTATGTTGCC TAAGAATACT TAGATGTTGCC TCAAAGTGTT AAGCTGTATC TAGATACATGA TAGATACAT ACATGGATTC ACAGTATCA AGTTTTCCCT GGTATGTTTT TTTTTATGCTT TTCCTTTTTA	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGCTACTTAT ACCACCAAAA ACCACAAAA TGGTGAGCAG GGCACTTCCA CTTCACCTCC CTGGCTAGCA TTCTCCTAC CAACTGGT GAGATTCAACTCC CAACTTGGA TCTTCACTCC TGAATACAA TCTTCACAC TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA TGTAATTGAA GTTTAATGAC TGCACTTTGGA GAGATTCAGA AAACAGCTGA AAACAGCTGA TGGGTGTTGC CTTCTAGAAG CTTTCTAGAAG CTTTTTTTTTT	CSTGAGAGCT AAAGCCATGA AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA ACTTCAGTCC CTGATCAGAC CCTGATCAGAC GGCTTCACTC CTCTTTGATT GTATATATTG TCTTTTTTGG TCAAACTCCT TCCTCTTAAAT TCTCTGATCA ATACTAATT CACATGGAC ATACTAATT CACATGCA ATACTAATT CACATGCA ATACTAATT CACATGCA ATACTAATT CACATGCA ATACTAATT CACATGGAAA CATTTTAAAT TTGACTGAAA CATTTTAAAT ATCCAGAGAAA TCTTATAATT	GGTGGTTGGC AACTGATCCG AACTGATCCA ATGAAGCAAA ATGAAGCACA ATGAAGCACA ATGAAGCACA ATGAAGCACA TTGGAAGCACA TTGGAAGTCCT AACTCATGGA ATTAGAAGTCAT TTTTGGTTTT GGCCTCAAGC AGCACCCG AGTTGTTACA AAGCAGTCAC GTGAACTCAC GTGTATTGTA GTGAAGCACTA ATCATCAGA TTTGATCAAA TCTTTTCCCA TTTAGACTTA	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1260 1320 1380 1440 1500 1500 1620 1680 1740
65 70 75 80	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AATTCTGGAG GTCAGGTGGA AAATCGACGG ATGGGATAT GGAGTGGTTT TGAAGGTTTG GTGTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA AGGACTTCT GTTTTTGTAGA AGTCCTCCCA GTGTTTTT TGGCTGGAC CAGCTAGTCC CAGCTAGTCC CAGCTAGTC CAGGTTGTTT TTGGCTGAA CTTGTGGCTA CTTGTGGCTA CTTGTGGCTA CTTGTGGCTA CTAGAGAAGG AGAGTTGATT TCCCAAGTTGAT TCCCAAGTTTAT TCCCAAGTTT	GAGGCGCCGA GAGTGGAAG CGCGCGC GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGAC CACTTTTTAC CTGCACTCTCT TTAAGATAAAC CTTACTCTCT TTAAGATAAC CTTAGCTTCTAAT TAAATGAAAG AGGAAGAAGAG AGCTGACTTCTTAAT TAAATGAAAG AGCAGGACAC CTGGGTGAT AAATTTTCAG GGAAGGACAC TGGGGTGATT CACATTTTTTAC CTCTTTTTAAT TAGATGAAAT TAGATGAAAT TAGATGAAAT TAGATGATTCAC CTCTTTTTAAT TAGATGATAAT TAGATGTTC ACAATTTTTT TATGACCGT	GAGCCAGAT GGTCGCCAGAT GGTCGCCAGAT GATACCTGTATGA TGATACCAGAC CATACCTGTAT TGATACCAGAC AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAA CATGCGCCGA CCACCACTCC TAAGAGATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT CTAAAGTGTT CTAAACATGT CTGAGATACA TAGATACAT ACATGGATTA ACATGGATTA ACATGGATTA ACATGGATTT ACCAGTATCA AGTTTTCCCT GGTATGTTT TTTTATGCTT TTTTATGCTT TTTTTTTTTT	ACCATTTGG GTTCTGGGAA GCCTGCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA TGATGATGGC GGCACTTCCA CTTCACCTCC CTTCACCTCC CAGGTTACACTC CAGGTTACACT CAGGTTACACT CAGGTTACACT CAGGTTACACT CAGGTTACACT CAGGTTCTAC TGCTAATCACA TGTTAATCACA TGTTAATCACA TGCACTTTCAA GTTTAATGAC TGCACTTTCC CACTTTTGAA GTTTAATGAC TGCACTTTCC CACTTTTGGA AAACAGCTGA TGGGTGTTGC CTTCTAGAAG CTTTTAGAAG CTTTTTAGATTTT	CSTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA ACTTCAGCT AGCTATATA ACTTCAGCT GTATAGAC GGCTTCACTC CTCTTTGATT TCTTTTTTGG TCTATATTTG TCTTTTTTTG TCTTTTTTTG TCTCTTAATT TCTCGTCAT TCACATGGAC ATACTAATT ACCATGGTG AGGGGACAGT TTGACTGAAA CATTTTAAAT ATCGAGAAAA CATTTTAAAT ATCGAGAAAA CATTTTAAAT ATCGAGAAAA CATTTTAAAT GTTTTTTAATT GTTTTTTAATT GTTTTTTAAAT ATCGAGAAAA CATTTTAAAT GTTTTTTTATATT GTTTTTTTTTT	GGTGGTTGGC AACTGATCGA ATGAGCAAA ATGAGCAAA ATGAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCT AACTCATGGA ATGAAGAAT TTAGAGCTCT AACTCATGGA CTAACTATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGTA ATCATCTGGC GCTGGTATGGA ATCATCTGGC GCTGGTATGGA ATCATCTGGC GCTGGTATGA ATCATCTGGC GTTGTATTGAT ATTTGATGAAA TCTTTTCCCA TTAGAGCTTTA TTTGATGAAA TCTTTTCCCTT	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740
65 70 75	CGAAAGGAGT AAGGCCGCGG CGAGCTGCAT AGTTCTGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAACATTGT AGGACATTCT GTTTTGTAGA AGTCCTCCCA CCCTACTCC GTGTGTTTT TTGGCTGGAC CAAGCTAGAG TGTTCTGAGA CTTTGGGAA CTTGTGGCTA CTAGAGAAGG ACAGTTCAT TCCAGGTTAT TCCCAGGTTAT TCCCAAGATC TACTTTGGTC TACTTTGGTC TCCAAGATC TACTTTGGTC TACTTTGGTC TCCAAGATC TACTTTGGTC TTTTGGGTA	GAGGGGCGA GAGTGGAAA CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTATAG GACTTTTAC CTGTCATTGAGAG CACTTTTAC CTGTCATTGAG CACTTTTAAT TAAGATAAC TTTTTTATAT GACTTTTAAT TAAATGAAA AGGAAGAAG AGGAAGAAG AGGAAGAAG AGGAAGAA	GAGCCCAGAT CGTCCGCCAT CGTCCGCCAT AGGGCAACT CATACCTGTA TGATACCAC CATACCTGTA TGCCAAATGC AAGGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAC CACACCTCC TAAGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT AAGCTGTT CTCAAAGTGTT CTCAAAGTTTC CTTCAACTTTTT CTCTTTTTT TTCTTTTTTTTT	ACCATTTIGE GTYTIGGGAA GCCTGCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACCGCTTG ATTACGATTT TGACCGCTTG ATTACGATTT TGACACATAA TCATCACATAA TCATCACATAA TCATCACACA TGATGATGAC GGCACTTCCA CAGACTGCTC CAGCTGGTC CAAGCTGGTC CAAGCTGGTC CAAGCTGTTC CATTTTCAAA GTTTAATGAC TGCACATTTCCAA GAGATTCAGA AGAGTTCAGA AGAGTTCAGA AGAGTTCAGA TGCACTTTTGA AGGCTGGTC TTTGTAGAG TTTGGTAGTTGC CTTTTGGAA TGGGTGTTGC TTTTGAGAG TTTTGTTTT AGGCTGGGGTT AGGCTGGAGG TTTTGTTTT AGGCTGGGGGTT AGGCTGGGGGT AGCACACAC AGAACAGCTGA AGCAGGGGGGAG AGGCTGGGGGT AGGCTGGGGGGT AGGCTGGGGGT AGGCTGGGGGGGT AGGCTGGGGGT AGGCTGGGGGT AGGCTGGGGGT AGGCTGGGGGT AGGCTGGGGGT AGGCTGGGGGT AGGCTGGGGGGT AGGCTGGGGGGT AGGCTGGGGGGT AGGCTGGGGGGT AGGCTGGGGGGT AGGCTGGGGGGGT AGGCTGGGGGGT AGGCTGGGGGGT AGGCTGGGGGGGGGG	COTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTGA AGCTTATATA AGCTTCAGTCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTCTTTTAGT GTATAATTTG TCAAACTCCT GCGTGAGCCA GCATTCCTAC TCCCTTAAAT TCCTGGTCAT TCACATGCAA ATACTAATTT CACCATGGTA AGGGGACAGT TTGACTGAAA ATACTAATTT AGGGGACAGT TTGACTGAAA ATACTAATTT TCTGGTTAAAT ATCCGAGAAA TGTTATAAATT GTTTTTTCTGG GCAGTGGGGG GCAGTGGGGG GCAGTGGGGGG AGGT TGACTGAAA TGTTATAAATT GTTTTTTTCTG GCAGTGGGGG GCAGTGGGGG GCAGTGGGGG GCAGTGGGGGG GCAGTGGGGG GCAGTGGGGGG GCAGTGGGGGG GCAGTGGGGGG GCAGTGGGGGG TGCACTGGGGGGGGGG	GGTGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TAATAAAAAA AAGGAGTCCT AACTCATGGA CTAACTATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGTA GTGAAGAGA ATCATTGGG GTAATTGTA ATCATCAGG GTGTATTGTA GTGAAGCATGA ATCATCTGGC GAAATTGGG GAAATTGGG AATTCAGC TTAAGCTTTA TTTTCCCA TTAAGCTTTT GATCTTTTCCCA TTAAGCTTTT GATCTTGCCT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1020 1140 1260 1380 1340 1560 1560 1680 1740 1800
65 70 75 80	CGAAAGGAGT AAGGCCGGGGA AAGTCGAGGGGA AAATCGACGG ATCGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGACACATTCT TGTTTTTTTTT AGGACTTCT TTTTTTTTTT	GAGGGGCGA GAGTGGAAA CGAAGTGATT TGCACTGTAG GGTAGGGTCT AATAATTATA GACATTAGAG CACTTTTAC CTGTCATGAC CTCACTCTT TTAAGATAAC TTTTTAATG GACTATGAC TTTTTAATG GACTATTCTAAT TAAATGAAA AGGAAGAAGA AGCTGATTC AACTTTCAAT TAAATGAAG AGCTGATTC TTTTCTAAT TAAATGAAG AGCTGATTT AAATTTCAG GGAAGGACAC TTGTGTC ACTTTGTC ACTTTTTTAAT TGGGTGATTT AAATTTCAG GGAAGGACAC TGGGGTGATT AACTTTGTAC TGGAGTCTTGT CACAATTTTT TATGACCGT GGAGTCTTGT TCTATCCCCT	GAGCCCAGAT CGTCCGCCAT CGTCCGCCAT AGGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGATACCAAC AGGATATCA AGGATATCA AGGATATCA AGGATATGA CCACCACTCC TAGGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT AGGCTGTATC TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGATCATT ACCAGTATCA TATATATATA ACTATGTTTCCT TGTAACATT ACCAGTATCA TATATATATA TTTTTATCCT TTTTTTTTTT	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACACTATAT ACCACCAAAA ACCACAAAA ACCACAAAA TCTTCCTCC CTTGACTCCC CTTGACTCCC TGGCTAAGAA TTCTCCTAC CAAGTGTACACA TGATATCACA TGATATCACA TGATATCACA TGATATCACA TGATATCACA TGATATCACA TGTAATCACA TGTAATCACA TGCACATTTGAA GTTTAATGAC TGCACATTTGAA AAACAGCTGA AAACAGCTGA AAACAGCTGA AAACAGCTGA CTCTTGGA CTCTTAGAA GTTTTGTTTT	CSTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA AGCTTCAGTCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTCTTTGATT GTATATTTG TCTTTTTTGG TCTTTTTTTGG TCTCTTCACT CCCTGATCACC GCATCCCTAC GCATCCCTAC CACATGCAG ATACTAATTT CACCATGCAG ATACTGATG TTGACTGAAA CGTTTTTAAAT GTTTTTTTTTT	GGTGGTTGGC AACTGATCAC ATGAAGCAAA ATGAAGCAAA ATGAAGCACA ATGAAGCACA ATGAAGCACA TGGGGGGGGA TTGAAGTCCT AACTCATGAA ATGAAGTCCT AACTCATGAA TTGAGTTCCT GGCCTCAAGC ATGACTATA ATTGAGTTAC GCTGAACTATA ATTGAGTTAC AAGCAGTCAC GTGATTTGAT GTGAAGATGA ATCATTGGG ATTGTTACA AGCAGTCAC GTGATTTGTA GTGAAGATGA ATCATTTGGT ATCATTTGGT ATCATTTGGT TTGATGAAGA TTTAAGCTTTA TTGTTTCCCA TTAAGCTTTA TTGTTTCTTT GATCTTGGCT CCAAGTAGCT CCAAGTAGCT CCAAGTAGCT ATGATGACCT CCAAGTAGCT CC	120 180 240 360 420 540 660 720 780 840 960 1020 1020 1320 1320 1340 1560 1560 1620 1740 1860 1860 1860
65 70 75 80	CGAAAGGAGT AAGGCCGGGGA AAGTCGAGGGGA AAATCGACGG ATCGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGAAGGTTTT TGACACATTCT TGTTTTTTTTT AGGACTTCT TTTTTTTTTT	GAGGGGCGA GAGTGGAAA CGAAGTGATT TGCACTGTAG GGTAGGGTCT AATAATTATA GACATTAGAG CACTTTTAC CTGTCATGAC CTCACTCTT TTAAGATAAC TTTTTAATG GACTATGAC TTTTTAATG GACTATTCTAAT TAAATGAAA AGGAAGAAGA AGCTGATTC AACTTTCAAT TAAATGAAG AGCTGATTC TTTTCTAAT TAAATGAAG AGCTGATTT AAATTTCAG GGAAGGACAC TTGTGTC ACTTTGTC ACTTTTTTAAT TGGGTGATTT AAATTTCAG GGAAGGACAC TGGGGTGATT AACTTTGTAC TGGAGTCTTGT CACAATTTTT TATGACCGT GGAGTCTTGT TCTATCCCCT	GAGCCCAGAT CGTCCGCCAT CGTCCGCCAT AGGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGATACCAAC AGGATATCA AGGATATCA AGGATATCA AGGATATGA CCACCACTCC TAGGAATACT TTGTACACTA CTATGTTGCC TCAAAGTGTT AGGCTGTATC TAGAACATGGT TAGAACATGGT TAGAACATGGT TAGATCATT ACCAGTATCA TATATATATA ACTATGTTTCCT TGTAACATT ACCAGTATCA TATATATATA TTTTTATCCT TTTTTTTTTT	ACCATTTGG GTTCTGGGAA GCCTGCCTTC ACAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACACTATAT ACCACCAAAA ACCACAAAA ACCACAAAA TCTTCCTCC CTTGACTCCC CTTGACTCCC TGGCTAAGAA TTCTCCTAC CAAGTGTACACA TGATATCACA TGATATCACA TGATATCACA TGATATCACA TGATATCACA TGATATCACA TGTAATCACA TGTAATCACA TGCACATTTGAA GTTTAATGAC TGCACATTTGAA AAACAGCTGA AAACAGCTGA AAACAGCTGA AAACAGCTGA CTCTTGGA CTCTTAGAA GTTTTGTTTT	CSTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA AGCCTATATA AGCTTCAGTCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTGATCAGCC CTCTTTGATT GTATATTTG TCTTTTTTGG TCTTTTTTTGG TCTCTTCACT CCCTGATCACC GCATCCCTAC GCATCCCTAC CACATGCAG ATACTAATTT CACCATGCAG ATACTGATG TTGACTGAAA CGTTTTTAAAT GTTTTTTTTTT	GGTGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCG TAATAAAAAA AAGGAGTCCT AACTCATGGA CTAACTATTA TTTTGGTTTT GGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCAGTCAC GTGTATTGTA GTGAAGAGA ATCATTGGG GTAATTGTA ATCATCAGG GTGTATTGTA GTGAAGCATGA ATCATCTGGC GAAATTGGG GAAATTGGG AATTCAGC TTAAGCTTTA TTTTCCCA TTAAGCTTTT GATCTTTTCCCA TTAAGCTTTT GATCTTGCCT	120 180 240 360 420 540 660 720 780 840 960 1020 1020 1320 1320 1340 1560 1560 1560 1680 1740 1860 1860

	TTTTACCATG	TIGGCCAGGC	TGGTTTCAAA	CTCCTGACCT	CAAGTGACCC	ACCTTGGCCT	2040
						CATTTTGAAT	2100
						AATATAGATA	2160
5						CCTTTGCATT	2220 2280
,		TITTCTCTCC					2340
	TCTAATAATT	CTTGAAACAG	ATAGTATTAA	TGTGTCATAT	TTTTGCTGTT	GITTGTATTT	2400
		TGGGGTTTCA					2460
10		CTCGTCCTCC					2520
10		CATTTCTTTT					2580 2640
		GGTGGATCAC					2700
	AACTCCGTCT	CTACAAAAAA	TAGAAAAAAT	TAGCCAGGTG	TGGTGGTGCA	TGCCTGTAGT	2760
1.5						CAAGACTGCA	2820
15						TCTATCTCAA CCCTGTTGGG	2880 2940
						ACATCTTAAT	3000
		CTTCTGGCCT					3060
						GTCAGCATTT	3120
20						GTTGCTAGTA	3180
						GTGAGTTCTC	3240
	ATGGTGTTTT	TGTAAATTAC	ATCAACAGTC	ATGTGTTCTA	TGAATAAAGA	GTTTTACTCC	3300
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	1	11	21	31	41	51	
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40	1	11	21	31	41	51	
40		AAAGCGCGGA	0000300000	PCCCC PCPCC		ACCACTACAA	60
		GAGGCGCCGA					120
		GAGTGGGAAG					180
15		CGCCCCCCG	AAGGGCAACT	GCCTGCCTTC	AACGAGGATG	GACTCAGACA	240
45	AGTTCTGGAG	GAGATGAAAG	AAGGGCAACT CTTTGTATGA	GCCTGCCTTC ACAAAACCAG	AACGAGGATG TCTGATGTGA	GACTCAGACA ATGAAGCAAA	300
45	AGTTCTGGAG GTCAGGTGGA	GAGATGAAAG CGAAGTGATT	AAGGGCAACT CTTTGTATGA TGATACCAAC	GCCTGCCTTC ACAAAACCAG TATCAAATTT	AACGAGGATG TCTGATGTGA CGACACTGTT	GACTCAGACA ATGAAGCAAA CTCTGTTAAG	300 360
45	AGTTCTGGAG GTCAGGTGGA AAATCGACGC	GAGATGAAAG CGAAGTGATT TGCACTGTAG	AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG	AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG	300
-	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT	GAGATGAAAG CGAAGTGATT	AAGGCCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT	AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT	300 360 420
45 50	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTG	GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC	AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA	AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG	300 360 420 480 540 600
-	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTG ATGCAGTGGC	GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG	AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC	AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA TCCCAGGTTC	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAAGGAGA TTGAAGCTGG ACCTCAACTG	300 360 420 480 540 600 660
-	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTG ATGCAGTGGC CAACCTCCAC	GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC	AAGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACCTAATA ACCACCAAAA AACCTCCACC AAGACTATGG	AACGAGGATG TCTGATGTA CGACACTGTT CTTCGGATCA CACATGCTG ATGAGGTCAC AGCCTATATA TCCCAGGTTC AGAATTTGAA	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG	300 360 420 480 540 600 660 720
50	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTTC ATGCAGTGGC CAACCTCCAC GCACTTCAGT	GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG	AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC	GCCTGCCTTC ACAAAACAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AGACTATTG AGCACTTTTT	AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGC	300 360 420 480 540 600 660
-	AGTTCTGGAG GTCAGGTGGA AAATCGACGA ATGGGATAT GGAGTGGTTT TGAAGGTTTC ATGCAGTGGC CAACCTCCAG GCACTTCAGT AGCTGATCAG	GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA	AAGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AGGACTATTG AGCACTTTTT TCCTGTCATG	AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA TCCCAGGTTCA AGCATTGAA ACCTCGATGG ACCATGGCCC	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGC GAGGCACTTC	300 360 420 480 540 600 660 720 780
50	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT GGAGTGGTTT TCAAGGTTTC CAACCTCCAC GCACTTCAGT AGCTGATCAG CCAGCTTCAC CCCCTCTTTGA	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC	AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACC TGGAGCACT TATAGACATT	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AAGACTATGG AGCACTTTTT TCCTGTCATC TACTCACTCT TCTTCACTCT TCTTTAAGATA	AACGAGGATG TCTCATGTGA CGCACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG CCTCCACCACT ACTAAGAATA	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGAGGAGAA ACCTCAACTG GTTGATGATG GAGGCACTTC CCCTTCACCT CTTGGCTAAG	300 360 420 480 540 600 660 720 780 840 900
50	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT GGAGTGGTTT TGAAGGTTTG ATGCAGTGGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAG CCCCTCTTGA AAGTATAATT	GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTTAGAAGC TTGCTAACTTAT	AAGGGCAACT CTTTGTATGA TGATACCAGT TGACCAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TAAGGACTTT TAAGGACTTT	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGACTTA ACCACCAAAA AACCTCCACC AAGACTATTG AGCACTATTG TCCTGTCATG TACTCACTCT GTTTAAGATA CTTTTAAGATA CTTTTAAGATA CTTTTAAGATA CTTTTTAAGATA CTTTTTTTTAA	AACGAGGATG TCTGATTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATTATA TCCCAGGTTC AGAATTGAA ACCTCGATGG ACCATGCCC CTCCACCACT TCTTGATGATATA TCTTGTACAC	GACTCAGACA ATGAAGCAAA CTCTGTTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG GAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT	300 360 420 480 540 600 660 720 780 840 900 960
50	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC AGTGATAATT AAGTATAATT ACTCTTTTTT	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATAA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATATGAA CTCAACCTGC CGGTGTCTAA AAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TAAGGACTTT TAAGGACTTT	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AAGACTATCG ACCACTTTTG TCCTGTCATG TACTCACTCT GTTTAAGATA CTTTTTTTAA CAGACTGTCT	AACGAGGATG TCTGATTIGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCATATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCATGGGCC CTCCACCACT ACTAAGAATA TGTTGTACAC CACTATGTTG	GACTCAGACA ATGAAGCAAA CTCTGTTTAAG GAGCACTCAG CTGAAGAAAT TGGAGGATGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGC GAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCT CCCAAGCTGG	300 360 420 480 540 600 720 780 840 900 960 1020
50	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT GGAGTGGTT TCAAGGTTTC CACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CAGACTTCAC CAGACTTCAC CAGACTTCAC CAGACTTCAC CAGACTCACAC CAGACTCACAC CAGACTCACAC CAGACTCACAC CACACACAC C CACACACAC C CACACACAC C CACACACACAC CACACACAC CACACACACAC CACACACACAC CACACACACAC CACACACACACAC CACACACACACACAC CACACACACACACAC CACACACACACACACACACACACACACACACACACACACA	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT CTGGCCTCAA	AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACC CTGGAGCACT TATAGACATT TATAGACATT TTGTTTTGTA GCAGTCCTCC	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AAGACTATGG AGCACTTTTT TCCTGTCATG TACTCACTCT GTTTAAGATA CTTTTTTTAA GAGACTGTCT GACCTTAGCT CACCTTAGCT CACCTTAGCT	AACGAGGATG TCTGAATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA ACCCCAGGTTC AGAATTTGAA ACCCTGATGG CCCTCCACCACT ACTAAGAATA TGTTGTACAC CACTATGTTG TCTCAAAGTT TCTCAAAGTG	GACTCAGACA ATGAAGCAAA CTCTGTTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG GAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT	300 360 420 480 540 600 660 720 780 840 900 960
50 55	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT TGAAGGTTTT TGAAGGTTGGC CAACCTCCAGC GCACTTCAGC GCACTTCAGC CCCTCTTTGA AAGTATAAATT ACTCTTTTTT TCTCAAACTC CAGGCGTGAGG CAGCGTTGAG CAGCGTGAGGC CAGCATTCTTTTT CCTCAAACTC CAGGCGTGAGC CAGCATTCCT	GAGATGAAG GGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT CTGGCCTCAA CACTGCACCC ACAGTGTTTA	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTAAGCACTT TTAGTTTTGTA GCAGTCCTCC GCCCCTACT CAGTGTGTTT	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTATT ACCACCAAAA AACCTCCACC AAGACTATGG AGCACTTTT TCCTGTCATG TACTCACTCT GTTTAAGATA CTTTTTTTAAA GAGACTGTCT CCTTTTTCTA CTTTTTCTA	AACGAGGATG TCTGATTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCATGGGCC CTCCACCACT ACTAAGAATA TCTCAAGGT TCTCAAGGT TCTCAAGGT ACTAAGATT AGTAAACATG ATAAGATAA AGTAAACATG	GACTCAGACA ATGAAGCAAA CTCTGTTTAG GAGCACTCAG CTGAAGAAAT TGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGC GAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TCTGAATCA CTTAGATTAC GTTACATTTG	300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1260
50 55	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT GGAGTGGTT TCAAAGGTTTC CACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CACCTCTTTGA AAGTATAATT ACTCTTTTT ACTCTTTTTT ACGCGTGACC CAGCATTCCT AAGCATTCCT AAGCATTCCT AATCTCTTAAA	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTTGGTT CTGGCCTCAA CACTGCACCC ACAGTTGTTA	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACC TATAGACATT TAAGACATT TTGTTTTGTA GCAGTCCTCC GGCCCTACT CAGTGTGTGTG ACTTGGCTGG	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AAGACTATGG AGCACTTTT TCCTGTCATG TACTCACTCT GTTTAAGATA CTTTTTTTTAAGCT CCTTTTCTA TTTAAATGA ACAGGAAGAA	AACGAGGATG TCTGAATGTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCCTATATA ACCCAGGTTC AGAATTTGAA ACCTCGATGG CCTCCACCACT ACTAAGAATA TGTTGTACAC CACTATGTTG TCTCAAAGTG ATAAGCTTA AAGAATA AAGAATA GGTAAAACATG GGTAGATCCT	GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA ATGAAGCTGG ACCTCAACTG GTTGATGATG ANATGTGAGC CAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC CTTGAGATCAC CTTGAGATCAC CTTGAGATCAC TTGTAATCA GTTACATTTG GTGTGTCTTG	300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1250
50 55	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATTT TGAAGGTTTT TGAAGGTTCAC GCACTTCAGT AGCTGATCAC CCCTCTTTGA AAGTATATT ACTCTTTTT TCTCAAACTC AGGCGTGACC AGGCGTGACC AGGCGTGACC AGGCGTGACC AGGCGTGACC AGGCGTGACC AGGCGTGACC ATTTCTCGGTC	GAGATGAAAG GAAAGTGATT TGCACATGTAG GGTAGCGTCT AATAATTATA GACATTACAC CTCCAGGTC CCTATTAAAA ACAAGGAGT TCTAACTCATG TTTTAGAAGC TGCTAACTATT GGTTATTTTGGTT CTGGCCTCAA CACTGCACC ACAGTTGTTA ATAAGCAGTC ATGTGTATTTG	AAGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGAACATT TATAGTACTTTTTTTTT GCAGTCCTCC CGGCCCCTACT CAGTGTGTTT ACTTGGCTAG TACAAGCTAG	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGACTTA TGACCACAAA AACCTCCACC AAGACTATTG TCCTGTCATG TACTACTTTT TCCTGTCATG TACTCACTCT TACTTCATCTTTTTTTAAATGAA ACACTTTTTCTAATTGAT TTTAAATGAA ACAGGAAGAA ACAGGAAGAA AGAGCTGATA	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCCTATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCACACT ACTAAGAAT TGTTGTACAC CACTATGTTACAC CACTATGTACAC CACTATACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATGTACAC CACTATA	GACTCAGACA ATGAAGCAAA ATGAAGCAGA CTCTAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGG CACTTCACCTTCACCTT CCCTTCACCTT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TTGTAATCA GTTACATTTG GTGTGTTTCCT GCACATTTTCC CACATTTTCC	300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320
50 55 60	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTGGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CCCTCTTTGA AAGTATAATT ACTCTTTTT TCTCAAACTC CAGCGTGAGC CAGCATCCCT AATCACTC AATCACTTC AATCACTTC AATCACTTC AATCACATGC CAGCATTCCT AATCACATGC CATCACATGC CATCACATGC CATCACATGC CATCACATGC CATCACATGC CATCACATGC CATCACATGC	GAGATGAAG GGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCTACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT CTGGCCTCAA ACACGCC ACAGTTGTTA ATAAGCAGTC ATGGAAGTT AAGTGAAGATT AAGTGAAGATT AAGTGAAGATT	AAGGGCAACT CTITGTATGA TGATACCACAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGAGGCACA GACTCCTCTG TATAGACATT TTGTTTTGTA GCAGTCCTCC CGGCCCCTACT CAGTGTGTTT ACTTGGCTGG TACAAGCTAG TACAAGCTAG GACGCTAGT ACTTGGCTGG TACAAGCTAG TACAAGCTAG GATGGTTGT TGACTAGG TACAAGCTAG TACAAGCTAG TACAAGCTAG GATGGTTGT TACTTGGCTGG TACAAGCTAG GATGGTCTGT	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AAGACTATGG TCCTGTCATG TCCTGTCATG TTTAAATGAA CAGCATTGT CACCTTAGCT TCTTTAAATGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA AGAAATTTTC	AACGAGGATG TCTGATTGA CGACACTGTT CTTCGGATCA CACATGGCTG AGCATATATA TCCCAGGTTCA AGCATATATA TCCCAGGTTC AGAATTGAA ACCTCGATGGCC CTCCACCACT TCTAGAGATG ACTAGAGATA AGTAGATGAA AGTAGAGTTACA CACTATGTG CCACTATGTG CCACTATGTTG CTCAAAGTT AGTAGAACTA AGTAAACTT AGTAGATCT AGTAGATCT AGTAGATCT AGTAGATCT AGTAGATCT AGTATATATA	GACTCAGACA ATGARGCANA CTCTGTTTAG GAGCACTCAG CTGAAGANAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ANATGTGAGG CGCTCACTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TTGAGATCAC GTTGAGATCAC GTTACATTTG GTGTGTCTTG CACATTTTC ATGTTTAATG ATGTTTAATG	300 360 420 480 540 600 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1340
50 55	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT GGAGTGGTT TGAAGGTTT TGAAGGTTG CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC CAGCTTCAC AAGTATAATT TCTCAAACTC AGGCGTGAGC CAGCATTCCT AATCTCTTAA TTTTCTGGTC AATCACATGC CACATACTAA TCCACCATGG	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT CTTGGCTCAA CACTGCACCC ACAGTTGTTA ATAAGCAGTC ATGGTATTT AATTATT TATCATCTG TTGGCTGTGT TTATCATCTG TTGGCTGGTGT TTATCATCTG TGGCTGGTGTT TGGCTGGTGTT	AAGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TAAGGACTTT TAAGGACTT TAGTTTTGTA GCAGTCCTCC GGCCCTACT CAGTGTGTTT ACTTGGCTGG TACAAGCTAG GATGGTCTGT GCTATTTGGG GGCTTGTGGG GCTATTTGGG	GCCTGCCTTC ACAAAACCAG TATCAAATT TGACCGCTTG ATTACGACTT ACCACCAAAA AACCTCCACC AAGACTATTG TCCTGTCATG AGCACTTTT TCCTGTCATG TTTTAAGATA CTTTTTTAA CAGCTTTTTTTAA CAGCATTTT TCACCTTAGCT CCCTTTTTCTA TTTAAATGAA ACAGGAAGAA AGAGCTGAAT AGAAATTTTC AAGGAAGAA AGAGCTGAAT AGAAATTTTC AAGGAAGAA AGAGCTGAAT AGAAATTTTC AAGGAAGAA AAGAGCAC AAGGAAGAA TATGGGGTGA	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCCTATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACTAGAGAT TCTCAAAGTG ATAAGCATGA AGTAAACATG GTAGATCCT TTCTGAGATA AGTATATTAA AGTATATATA AGTATATATA	GACTCAGACA ATGAAGCAAA ATGAAGCAGA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGC CCCTTCACCTT CCCTTCACCTT CCCTAGCTGG TTGAGATCAC TCTGGCTAAG TTTACATTTC TCTGTAATCA GTTACATTTC CACACTTTC ATGTTTAATC ATGTTTAATC TTTGCACATT CACCACTTTG CACACTTTTG ACACCTTTTT	300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1260 1320 1380 1440 1500
50 55 60	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT TGAAGGTTTT TGAAGGTTGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CCCTCTTTGA AAGTATAT ACTCTTTTT TCTCAAACTC CAGCATTCCT AATCTCTTAA TTTTCTGGTC AATCACTTGA TTTCAGGTC AATCACATGC AATCACATGC ACACATGC ACACATGG CAACGGGACA CAGAGGGACA CAGCATTCACATGC AATCACATGC ACACATGC ACACATGG CAAGGGGACA	GAGATGAAG GGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCAACTCATG TTTTAGAAGC TCTAACTATG GGTTTTTGGATC TGGCTCAA CACAGGACT ACAGGACT ACAGGACT ATAAGCAGT ATAAGCAGT TTTTGAACT ATAAGCAGT TTTTGAACT ATAAGCAGT TTTTTAGAACG TTTTTTT AAGTAACT TTTTTT AAGTAACT TTTTTT TGGCTGTT	AAGGGCAACT CTITGTATGA TGATACCAGT TGACCAACT TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTGTTTTGTA GCAGTCCTCC GGCCCCTACT CAGTGTGTTT ACTTGGCTGG GATGGTCTGG GATGGTCTGG GATGGTCTGG GATGGTCTGG GGTTTTTGGCAGG GGCTTGTTGGCG GGCTTGTTGGCG GGCTTGTGGC	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGACTTA ACCACCAAAA AACCTCCACC AAGACTATTG TCCTGTCATG TACTCACTCT GTTTAAGATTT TCCTGTCATG TACTCACTCT GTTTAAGATA CAGGACTATGCT CCCTTTTTCTA TTTAAATGAA ACAGGAAGAA AGAGCTGAT AGAAATTTTC AAGGAAGGAC TATGGGGTGA AGAACTTTC TATGGGGTGA AGAACTTTGT GGGAACTTTGT GGGAACTTTGT GGGAACTTTGT GGGAACTTTGT	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTG AGCATATATA TCCCAGGTTCA AGCATATATA TCCCAGGTTC AGAATTGAA ACCTCGATGG ACCATGCCC CTCCACCACT TCTCACCACT TCTCACACT ATAAGATA AGTATATATA AGTAAACTG ATAAACTG ACCACTAT ACCACAGTAT TCACCAGTAT TCACCAGTAT ACACTTTTCC	GACTCAGACA ATGAAGCANA CTCTGTTTAG GAGCACTCAG CTGAAGANAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG CCCTTCACCT CTTGGCTAAC CTTGGCTAAC CTTGGCTAAC CTTGGCTAAC CTTGGCTAAC CTTGGTAAT CTTGCTTGATCAT CTTGTGTTCTT CTTGGTTAAT CACATTTTC CACATTTTC CACATTTTC ATGTTTAATG TTTGCACATT CACCACTTTG CTGAGATTCA CTGAGATTCA CTGAGATTCA CTGAGATTCA CTGAGATTCA	300 360 420 480 540 600 720 780 840 900 960 1020 1080 1140 1200 1200 1320 1380 1440 1500 1560
50 55 60	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT TGAAGGTTT TGAAGGTTGT TGAAGGTTGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CCCTCTTTGA ACTCTTTTT TCTCAAACTC AGGCGTGAGC CAGCATTCCT AATCTCTTAA TTTTCTGGTC AATCTCTTAA TTTTCTGGTC AATCACATGG ACATACTAAT TCCACACTGG GAAGGGGACA GAAGGGGACA GAATGACTGA	GAGATGAAG GAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTAATAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT CTGGCCTCAA CACTGCACCC ACAGTTGTTA ATAAGCAGTC ATGTGTTATTATA ATAAGCAGTC TTATCATCTG TGGCTGGTGT TGGCTGGTGT TGGCTGGTGT TGGCTGGAATTGG AAAGTGAAATTGG AAAGTGAAATTGG AAAGTGAAATTGG AAAGTGAAATTGG	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTGTTTTGTA GCAGTCCTCC GGCCCCTACT CAGTGTGTTT ACTTGGCTGG TACAAGCTAG GATGCTCTG GCTATTTGGG GCTTGTTGGG GCTATTTGGG GCTTGTGGG GCTAGTGGAA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTATT ACCACCAAAA AACCTCCACC AAGACTATGG TACTCATCT TCCTGTCATG TACTCACTCT GTTTAAGATA CTTTTTTTAA GAGACTGTCT CCCTTTTCTCA TTTTAAATGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA TTTAAATTTC AAGGAAGGAC TATGGGTTGA TATGAGTTTTTTTTTT	AACGAGGATG TCTGATTGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATATATA TCCCAGGTTC AGAATTTGAA ACCTCATGGGC CTCCACCACT TGTTGTACAC CACTATGTTG TCTCAAAGTT AGTAAACATG GGTAGATCCT TTCTGAGATA AGTAAACATG AGTAATATATA ACCATGGGT TCCACATTTTCC ATGAGATT ACCATGTTT CCCACATTTTCC ATGATTTTC ATGAGATT ACCATGTTT TCACAGTTT TCACAGTTT TCACAGTTT TCACAGTTT TCACAGTTT TCACAGTTT TCACAGTTT TCACAGTTT TCACAGTTTTCC ATGGTATGTT	GACTCAGACA ATGAAGCAAA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGG GAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TCTGTAATCA GTTACATTTG GTTACATTTG GTTACATTTG GTTACATTTG CACATTTTTG CACATTTTTG CACATTTTTG CACATTTTTC CTGGGATTCA TTGCACATT CACCACTTTG CTGAGATTCA CTGAGATTCA CTGAGATTCA CTGAGATTCA CTGAGATTCA CTTAAACAGCT	300 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1320 1320 1340 1560 1560 1620
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT TGAAGGTTT TGAAGGTTT TGAAGGTTGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CAGGCTTTTGA AAGTATATTT TCTCAAACTC AGGGGTGAGC CAGCATTCCT AATCTCTTAA TTTTCTGGTC AATCACATGC CAACATGC CAACATGC CAACATGC CAACATGC CAACATGC CATGCTAACTCAACTC	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG GCTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT CGTTTTGGTT CTGGCCTCAA CACTGCACCC ACAGTTGTTA AATAGCAGTC TTATGATTT AAGTGAACTT TTATCATTT TATCATCTT TAGACTCT AAGTGAACTA ATAGCAGTG TTATCATATTATACATT TGGCTGGTGT TTATCATCTG TGGCTGGTGT GTGAAATTGG AAAGTCACAA AAATTCACAG AATTTTGATGA	AAGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TAAGGACTT TAAGGACTT TAGGACTT TAGGACTT TAGGACTT TAGTTTTGTA ACTTGCTCC GGCCCTACT CAGTGTGTTT ACTTGCTGG GATTGTTTGCTG GATTGGTTG GCTATTTGGG GGCTAGAGAA GAAGAGTTGA GAAGAGTTGA AAACCAGTTT	GCCTGCCTTC ACAAAACCAG TATCAAATT TGACCGCTTG ATTACGACTT ACCACCAAAA AACCTCCACC AAGACTATTG ACCACCTACT ACCACCTACT ACCACTACT ACCACTACT TCCTGTCATG TACTTATTAAGATA CTTTTTTTAA GAGACTGTCT CCTTTTTCTA TTTAAATGAA ACAGGAAGAA AGAGCTGAAT AGAAATTTTC AAGGAAGAC TATGGGTTGA TATGGGTTGA TATGGGTTGA TATGGGTTGA TTTGTCTTTTT TTTGTTTTTT TTTTAATTTTAATTTTAATTTTAATTTTAATTTTTT	AACGAGGATG TCTGATTIGA GGACACTIGTT CTTCGGATCA CACATGGCTG AGCACTATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACCATGATGG ACTAGAGAT ACTAGAGT AGTAGATAGT AGTAGACAT AGTAGATCT TCTCGAGATA AGTATATTA AGTATATTA AGTATATTA AGTATATTATA ACACATGAT TCACCAGTAT ACACAGTAT ACACTGTT TCACCAGTAT ACAGTTTTCC ATGGTATATTCC ATGGTATATTCC ATGGTATATTTC	GACTCAGACA ATGAAGCAAA ATGAAGCAGA CTCAGCTCAG	300 360 420 480 540 660 720 780 840 900 960 1020 1140 1260 1320 1380 1440 1560 1620 1620 1620
50 55 60	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATTT TGAAGGTTTT TGAAGGTTGGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CACTCTTTA ACTCTTTTT TCTCAAACTC CAGCATTCCT AATCTCTTAA ATTTCTCAAACTC CAGCATTCCT AATCTCTTAA TTTCTGGTC AATCACTGGAC ACATTCACAGG CAGCATTCACAGG CAGCATTCACAGG CAGCATTCACAGG CAATGACTGA GAAGGGACA GATTGACTGA GACATTTTAA GCATCCGAGA	GAGATGAAG GGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTATT GGTTTTGGTT CTGGCCTCAA ACAGGACCC ACAGTTGTTA ATAAGCAGTC ATAGGAGTC ATGGTATTG AAGTGATCG TGGCTGGTGT TTATCATCTG TGGCTGGTGT TGGCTGGTGT TGGCTGGTGT TGGCTGTGT TGGCTGTGT TGGCTGTGT TGGCTGTGTATCATCTG TGGCTGTGT TTATCATCTG AAGTCACAC AATCTTTTCATA	AAGGGCAACT CTTTGTATGA TGATACCACT CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTATTTTGTA ACTGCTCTCC CGGCCCCTACT CAGTGTTTT ACTTGGCTGC GATGGTCTG GATGGTCTG GATGGTCTG GATGGTCTG GCTTATTTGG GATGGTCTG GCTTATTTGG GATGGTTGGC GGCTTAGTGGA AAACAGTTT CATCCCAAGA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGACTTA ACCACCAAAA AACCTCCACC AAGACTATGG AGCACTITT TCCTGTCATG TATTAAGATT TCCTGTCATG TATTAAGATA CACCTCACC CTTTTTTTAA ACAGCAGAGAA ACAGGAAGAA ACAGGAAGAA TATAGGAAGACT TATGAATTTT TAAATGAA ACAGGAAGAAC TATGGGAGAAT AGAAATTTT TAGGAAGGAC GGAACTTTGT TTGTCTTTTT TTGTCTTTTTT TTACATTTTTTTTTT	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATATATA TCCCAGGTTC AGAATTGAAA ACCTCGATGG ACCATGCCC TCCACCACT TCTCACACAT TGTTGTACAC ACTATATTG ACTACAGGTT AGTAAACTA AGTAAACTG ATAAACATG AGTAAACATA AGTATATATA ACACATGAT TCCTCAAAGTG TCCCAAGTAT ACACATGAT ACACATGAT TCACCAGTAT ACACATGAT TCACCAGTAT ACAGTTTTCA	GACTCAGACA ATGAAGCAAA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG CCCTTCACCT CCCTACCTC CCCAAGCTGG TTGATGATC TCTTGCTACT CCCAAGCTGG TTGAGATCAC TTACATTTC GTGTGTCTTG CACACTTTG CACACTTTG CACACTTTG CACACTTTG CACACTTTG CACACTTTG CACACTTTG TTACACTTG TTACACTTG TTACACTTG TTGAGATTCA TTAAACAGCT TTAAACAGCT TTAGAGTTCA TTAGGTTTT TTTTGGGTTT TACTTCTAGA	300 360 420 480 540 660 720 780 840 900 960 1020 1140 1200 1250 1380 1440 1500 1620 1680 1620 1680
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTT TGAAGGTTGGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CCGCTTTGA AAGTATAAT ACTCTTTTT TCTCAAACTC AGGCGTGACC CAGCATCCTTAA TTTTTCTGGTC AATCACATGG AAATCACATGG ACATTCACATGG GCAGCATTCAC TTTCAGGTC AATCACATGG AACATTCACATGG GCAGCATTTTAA TCCACCATGG GCACTTTTAA TTCACATGG ACATTTTAA GCATTCGAGA AGTTGACTGA ACTTCTTAA TTGTTTTTT TCCACCATGG AACTCCGAGA ACTTTTAA TCTCCAGGA ACTTTTAA TTGTTTTTTT TTTTTTTTTT	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTAATTAAAA ACAAGGAGTC TCAACTCATG TTTAGAAGC TGCTAACTAAC CACTGCACCC ACAGTTGTTA ATAAGCAGTC ATGTGATATTA ATTAGAAGTA TTATCATCTG TGGCTGGTGT TGGCTGGTGT TTATCATCTG TGGCTGGTGT TTATCATCTG TGGCTGGTGT ATTTTTTTTTT	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTGTTTTGTA GCAGTCCTCC GGCCCCTACT CAGTGTGTTT ACTTGCTGG GATGTCTTG GATGTTTTGCG GCTATTTGGG GCTATTTGGG GGCTTGTGGC AAAGCTAG AATCCAGGT AATCCCAAGA TATACCTTGG TGTTTTGAG TATCCCAAGA TATACTTTGG	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACCGCTTG ACTACTTATT ACCACCAAAA AACCTCCACC AAGACTATGG TACTCACTT TCCTGTCATG TACTCACTCT CTTTTAAGATA CTTTTTTTAA GAGACTGTCT CCTTTTTCTA TTTAAATGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA TATGGGTGAT TTGTCTTTTT TCATATGATTT TCACAATTTT TCACAATTTT TCACAATTTT TCACAATTTT TCACAATTTT TCACAAGTTTT TCACAATTTT TCACAAGTTTT TCACAATTTT TCACAAGTTTT TCACAAGTCTT TCACAAGTCTT TCACAAGTCTT TCACAAGTCTT TCACAAGTCTT TCACAACTTTT TCACAAGTCTT TCACAAGTCTT TCACAAGTCTT TCACAACTTTT TCACAACTTTT TCACAACTTTT TCACAAGTCTT TCACAAGTCT TCACAAGTCTT TCACAAGTCTT TCACAAGTCTT TCACAAGTCT TCACAACTT TCACAACT TC	AACGAGGATG TCTGATTIGA CGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATATATA TCCCAGGTTC AGAATTIGAA ACCTCGATGG ACCATGGGCC CTCCACCACT ACTAAGAATA TCTCAAAGTG ATAAGAATA AGTAAACATG GGTAGATCCT TTCTGAGATA AGTAAACATG AGTAAACATG AGTAATATAA ACACATGGAT TCACAGTTTC ACGATTTTC ACGATTTTC CTTTTTATGC TTTTTTTTTT	GACTCAGACA ATGAAGCAAA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAAG TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGG GAGGCACTTC CCCTTCACCT CTTGGCTAAGT CTAGTTAGT CTTGGCTAGG TTGAGATTACA GTTACATTTCCT CCCAAGCTGG TTGAGATTCA CTTGTAATCA GTTACATTTG GTGTGTCTTG CACACTTTTG CTGAGATTTCA TTGGACATT CACCACTTTG CTGAGATTCA TTAGACAGGT TTTGGGTGTT TACTTCAGAT TTTGGGTGTT TACTTCAGAT TTTGGGTGTT TACTTCTAGA TTGTTTTGGTT CCAGGCTGGG	300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1290 1380 1440 1500 1560 1680 1740 1860 1860
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGATAT GGAGTGGTT TGAAGGTTT TGAAGGTTG CAACCTCCAC GCACTTCAGT AGCTGATCAG CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC CAGGCTTCAC CAGCTTCAC AAGTATATTT TCTCAAACTC AAGCATTCCT AATCACATGC CAGCATTCCT AATCACATGC CAGCATTCCTAA TTTTCTGGTC AATCACATGC GAAGGGGACA GATTGACTAA GCATTCGAGA GACATTTTAA GCATCCGAGA AGTGTTATAA TGTTTTTTC GTGCAGTGGC	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG GCTACCAGGTC CCCAAGGTC CCTATTAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT CTTTTAGATC CACTGCACCC ACAGTTGTTA AATAAGAGTC ATAGTATTG TTATCATCTG TGGCTGAA TATACATCTG TTAACATCTG TTTAAGTTTCC TTTTAAGCTTT GTTTTTTTCT GTTGTTTTCT GTGATCTTTG TGTTTTTTTTTT	AAGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGAACATT TAAGGACTTT TAAGGACTTT TAAGGACTTT ACTTGGTTTTTGTA ACTTGGCTCC CGGCCCCTACT CAGTGTGTTT ACTTGGCTGG GCTTATTTGGA GATGGTCTGG GGCTTATTTGGG GGCTTAGTTGGC GGCTAGTGGC GGCTAGTGGC TACAAGATTGGC TACAAGATTGGC TATACTTTGG TATTTTTGGA TATTCCAAGA TATACTTTGG TTGTTTTTGGG TTGTTTTTGGG TTGTTTTTGGG	GCCTGCCTTC ACAAAACAG TATCAAATT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCACC AAGACTATGA AGCACTATT TCCTGTCATG TACTCATCT TCTTTATAGATT TCCTGTCATG TACTCACTCT CACCTTATC CACCTTAGCT TAGAAATTTT CAGAAATTTT TCACAAATTTT TCACAAATTTT TCTATGACCC ATGAGACTT	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCATGCGCC CTCCACCACT TCTCACCACT TCTCACACT TCTCAAAGTG AATAAGATA AGTATATTGA AGTATATTGA GGTAGATCA AGTATATTGA AGTATATTTG TCTCCAAGATA ACACATGAT TCACCAGTAT ACACATGAT TCACCAGTAT ACACATGAT TCACCAGTAT ACAGTTTCC ATGGTATGTTC TTTTTTTTTT	GACTCAGACA ATGAAGCAAA ATGAAGCAGA CTCAGCTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG ATGATGATG ATGATGATG ATGATGATG CCTTCACCTTC CCCTTCACCTT CCCAAGCTGG TTGAGATCAC TTTACATTTC CCCAAGCTGG GTGTGTCTTC CTGTAATCA GTTTACATTTC ATGTTTAATCA ATGTTTAATG TTTGCACATT TTACACTTTG CTGAGATTCA TTAAACAGCT TTTAGGGTGTT TTTGGGTGTTT TTTGGGTGTT TACTTCTAGA TTGTTTTTTT CCAGGCTGGG GTGATTCCT CCAGGCTGGG GTGATTCCT CCAGGCTGGG GTGATTCCT	300 360 420 480 540 660 720 780 840 900 960 1020 1020 1140 1250 1320 1320 1340 1550 1620 1620 1620 1630 1740 1860 1920
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTGG CAACCTCAGC GCACTTCAGC CACCTCAGT AGCTGATCAG CAGGCTTCAC CCCTCTTTGA AAGTAAATT ACTCTTTTT TCTCAAACTC AGGCGTGAGC CAGCATTCCT AATCTCTTAA TTTTCTGGTC AATCACATGC ACATCACATGG CAACATTCACA GAAGGGACA GATGACTGA GAAGGGACA GATGACTGA GAATTCTAAA TTCCACATTGA GAACTTTAAA TTCCACATTGA GAACTTTTAA GCATCCGAGA AGTGTTATAA TTGTTTTTTC GTGCAGTGGC TGTCTCAGCC TGTCTCAGCC TGTCTCAGCC TTGCAGTGCC TTTCAGCC TTGCAGTGCC TTTCAGCCT TTGCAGTGCC TTTCAGCC TTGCAGTGCC TTGCAGTGCC TTGCAGTGCC TTTCAGCC TTGCAGTGCC TTTCAGCC TTGCAGTGCC TTTCAGCC TTTCAGCC TTTCAGCC TTTCAGCC TTCAGCC TTCAGCC TTCAGCC TTTCAGCC TTCAGCC TTTCAGCC TTCAGCC TTC	GAGATGAAG GAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCTATGAAGC TCTAGCTCATG TTTTAGAAGC GGTTTTGGTT CTGGCCTCAA ACACTGCACCC ACAGTTGTTA ATAAGCAGTC ATGGTATTTA ATAGCAGTC ATGGTATTTA TTACATCTG TGGCTGGTGT TTATCATCTG TGGAGTAGT ATTTTTGATGA AATTTTTGATGA AATTTTTTCC TTGTATTTC TTTTTAAGCTT GTTTTTTC GTTTTTTC GTTTTTTC GTTTTTTC TCCCAAGTTG TCCCAAGTTG T	AAGGGCAACT CTITGTATGA TGATACCACAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATGGAGCACT TAAGGACTTT TTGTTTTGTA CTGGTGGTGTTA ACTTGGCTGG GCCCCTACT CAGTGTGTTT ACTTGGCTGG GGCTGCTGG GGCTGCTGG GGCTGTTGGCTGG GGCTGTTGGC GGCTGTTGGCTGG TACAAGCTTG CTCATTGGCTGG TACAAGCTTG TACAAGCTTG CTCACTGCAAC TTGTTTTGAG CTCACTGCAAC CTCACTGCAA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCCACC AAGACTATGG TCCTGTCATG TCCTGTCATG TTCTGTCATG TTTAAGATA CAGCACTATGT CCTTTTTTTAAATGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA TTTAAATGAA ACAGGAAGAA TTTAAATTTT AAGGAAGGTTTT TCTATTTTTTTAATTGTTTTTTAATTGTTTTTTAATTGTTTTTT	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTGA AGCATATATA TCCCAGGTTCA AGCATTATAA TCCCAGGTTC AGAATTGGAA ACCATGGCCC CTCCACCACT ACTATGGTGC CACTATGTGG ACTATGTTG TCTCAAAGTT AGTAGATATAA AGTAAACAT AGTAGATATATA ACACATGGT TCACAGTTT CACCAGTAT TCACCAGTAT TCACCAGTAT TCACCAGTAT TCACCAGTAT TCTTTTTTTT GTTCTGTCAC CTGGGTTCAA CGCCAGCCT CTGGGTTCAA CGCCAGCCT CTGGGTTCAA CGCCAGCCT CTGGGTTCAA CGCCACGCCT	GACTCAGACA ATGAAGCAAA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATCATG CTGATCATG CTGATCATC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAT GTGTGTATTG GTGTATTTG GTGTATTTG CACATTTTG ATGTTTTAATG TTTGCACATT CACCACTTTG CTGAGATTCA TTAACAGCT TTTGAGTTCAT TTTGCACATT CACCACTTTTG CTGAGATTCA TTAACAGCT TTTGGGTTTT TACTCTCAGA TTAATCAGCT TTTGGGTTTT TACTCTCAGA TTACTTTTATT CCAGGCTGGG GTGATTCTT GCGTAATTTT CCGGGTTGGG GTGATTCTT GCCTAATTTT	300 360 420 480 540 660 720 780 840 900 960 1020 1250 1380 1140 1250 1380 1560 1560 1560 1580 1740 1880 1740 1860 1920 1980
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT TGAAGGTTT TGAAGGTTG CAACCTCCAC GCACTTCAGT GCAGTTGGC CAGCTTCAGT AGTGGATAAT ACTCTTTTT TCTCAAACTC AGGCGTGAGC CAGCATCCTTTTA TTTTCTGGTC AATCTCTTAA TTTTCTGGTC AATCACATGG AAGGGGACA GAATCCATGG GAAGGGGGAC GATTGACTTTA TCCACCATGG GAAGGGGAC GATTGACTGA GAATTCTAA TTCCACCATGG CAGCATTCTAA TTCCACCATGG CAGCATTCTAA TTCCACCATGG CAGTCGAGC GATTGACTGA GAATTCTAA TTCCACCATGG GAATTCTAA TTCCACCATGG CATTCCAGGA GACTTTTTA GCATTCGAGGA TTGTTTTTTT GTGCAGTGGC TGTACTTTTTTA	GAGATGAAG GAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTAATAAAA ACAAGGAGT TCTAACTCATG TCTAACTCATG TCTAACTCATG GGTTTAGAAGC ACATGCACCC ACAGTTGTTA ATAAGCAGTC ATATGATTA ATAAGCAGTC ATGTGATTA TTATCATCTG TGGCTGAATTGG TGGAATTGG AAGTCACTA ATTTTGATGA AATCTTTTCC TTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TTTTAAGCTT TCCCAAGTAG CCCAAGTAG CCCAAGTAG CGTAGAGACAG	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTGTTTTGTA GCAGTCCTCC GGCCCTACT CAGTGTGTTT ACTTGGCTGG GATGTCTTG GCTATTTGGG GCTATTTGGG GCTATTTGGG GCTAGTGGAA AATACCAGGTTG TATACCAAGCTAG TATACCAAGCTAG TATACCAAGCTAG TATACCAAGCTAG CTCATTTGGG TGGTTGTGGC TTGTTTTGGG TTGTTTTGAG CTCACTGCAA CTGGGATTAC CAGTGGTATAC CTGGGATTAC CAGTGTTTCACCAAGC CTGGGATTAC CAGTGTTTCACACTGCAA CTGGGATTAC CAGTGTTTCCAA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTATT ACCACCAAAA AACCTCCACC AAGACTATGT TCCTGTCATG TACTACTTAT CTCTTTTTTAAGTAT CTTTTTTTAAATGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA TTTTAAATTTC AAGGAAGGAC TATGGTTTTT TCATGGTTTTT TCATATGACC ATGGAGTCT TCTTATACCC ATGGAGTCT TCTTTTCTATCCC ATGGAGTCTT TCTTATACCC ATGGAGTCTT TCTTTTACCC ATGGAGTCTAT CCTCTTATCCC ATGGAGTCTACCC ATGGAGTCTACCC ATGGAGTCAGGC ATGGACACGC ATGGAGCACAGCC ATGGAGCCAGGC ATGTATCCC ATGGAGCCAGGC ATGTATCCC ATGGAGCCAGGC ATGTATCCC ATGGAGCCAGGC ATGTATCCC ATGGAGCCAGGC ATGGACCAGC ATGTATCCC ATGGAGCCAGGC ATGTATCCC ATGGACCACGC ATGTATCCC ATGGACCACGC ATGTATCCC ATGTATCCC ATGGACCACGC ATGTATCCC ATGTATCC ATGTATC ATG	AACGAGGATG TCTGATTGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCATATATA TCCCAGGTTC AGAATTTGAA ACCTCAGGGCC CTCCACCACT TGTTGTACAC CACTATGTG ATAAGATTA AGTAAACATG GGTAGATCT TCTCAAAGTT AGTAAACATG GGTAGATCT TCTGAGATA AGTAAACATG AGTATATATA ACACATGGT TCTTTATATT TCTTTTATGC TTTTTATGC TTTTTTTTT GTTTCTTCA CTGGGTTCAA CTGGGTTCAA CTGGGTTCAA CTGGTTCAC CTGGGTTCAA CTGCACCCCT CTGGTTTCA	GACTCAGACA ATGAAGCANA CTCAGTTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGG GAGGCACTTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TCTGTAATCA GTTACATTTG GTTACATTTG CACATTTTG ATGTTTAATG TTTGCACATT CACCACTTTG CTGAGATTCA TTTGGGTGTT TACTTCTAGA TTTTGGGTGTT TACTTCTTGC TTAGACTTG CTGAGATTCA TTTTGGGTGTT TACTTCTTGA TTTTGGGTGTT TCCAGGCTGGG GTGATTTTTTTTTT	300 360 420 480 540 660 720 780 960 1020 1140 1250 1320 1320 1340 1560 1560 1740 1860 1920 1980 2040 2040 2010
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTC ATGCAGTGGC CAACCTCACC GCACTTCAGC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCATTCAC CAGCATCCT AATCTCTTAT TCTCAAACTC AATCTCTTAA TTTCTGGAC AATCACATGC AATCACATGC GAAGGGACA GATTGACTGA GAAGTTTAAA TTGTTTTTT CTCAGAGTGC GACATTCTAA TTGTTTTTTC GCAGTGGC TGTCTCAGCC TGTCTCAGCC TGTCTCAGCC TGTCTCAGCC TGTCTCAGCC TGTCTCAGCC TGTCTCAGCC TCTAAGTTGA CCAGCCTATGA	GAGATGAAG GAAGTGATT TGCACTGTAG GGTAGOGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCTACACT TTTTAGAAGC TCCAAGTTCTTAGATT CTGGCCTCAA CACTGCTCAA CACTGCTCAA ATAAGCAGTC ACAGGTGTTA ATAAGCAGTC ACAGGTGTTA ATAAGCAGTC TTATCAATCG TGGAAATTG TGGACTGTTT AATACATCTG TGGATGTTT TTTTACATCTG AAAGTCACAT ATTTTGATGA AATCTTTTCC TTTTAAGCTT GTTTTTTTCT TTTTTTTTCT TTTTTTTTTC TTTTTTTT	AAGGGCAACT CTITGTATGA TGATACCAGT TGATACCAGT TGACCAGTA TGCCAAATGC AAAGATCTCT AAGATATCAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TTGTTTTGTA CCAGTCCTCC GGCCCCTACT CAGTGTCTCC CAGTGTCTTC CAGTGTCTTC CAGTGTCTTC CAGTGTCTTT CATTTTGGC GGCTCATTTGGC GGCTTGTGGC GGCTTGTGGC GGCTTGTGGC TATACAGT TATACCAGTT TATCCCAAGA TATACTTTGG CTCACTGCAA CTCCCAAGT CTCACTGCAA CTCCCAAGT CTCACTGCAA CTCCCAAGT ATGATTTACCA AGTTTTACCA AGTTTTACCA AGTTTTACCA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACCGCTTA ACCACCAAAA AACCTCCACC AAGACTATTG TCCTGTCATG TTACTGATTT TCCTGTCATG TTTTAAGATA CTTTTTTTAAATGAA ACAGGAAGAA ACAGGAAGAA ACAGGAAGAA TTTTAAATGAA ACAGGAAGAA AGAGCTGTTT TCTAAGGTACAATTTT TCAGGAGTCTT TCACAATTTT TCACAATTTT TCATAACCC ATGGAGTCTT TCTCTAACCC ATGGAGTCTT TCTCTAACCC ATGGAGTCTT TCTCTAACCC AGGCACAGG TTTGGCATTA TTTGGCATA	AACGAGGATG TCTGATTIGA GGACACTGTT CTTCGGATCA CACATGGCTG AGCATTATA TCCCAGGTTCA AGCATTATA TCCCAGGTTC AGAATTIGAA ACCTCGATGG ACCATGCCC TCCACCACT ACTAAGATG ATTAGAAGTG ATTAGAAGTG ATTAGAAGTG ATTAGAACTG TTCTCAGAGT TCCACAGTAT TCACCAGTAT TCACCAGTAT TCTTTTATTG TTTTTTTTT GTTTTTTTTT GTTTTTTTTT	GACTCAGACA ATGAAGCAAA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG CCTCACTT CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TTGTGATCAT GTGTGTATCA GTTACATTTG GTGTGTCTTG CACATTTTCA ATGTTTAATG TTTGCACATT CACACATTTC CTGAGATTCA TTAAACAGCT TTAGGTGTT TTTGGGTGTT TTTGGGTGTT TTTGGTTCTTC CCACGCTGGG GTGATTCTTTCACT CCACGCTGGG GTGATTTT AACTCCTTAC CCACCGCGGGC TCCACCTTCC	300 360 420 480 540 600 660 720 780 960 1020 1080 1140 1220 1380 1320 1380 1440 1560 1560 1620 1680 1740 1860 1920 1980 2040 2100 2100 2220
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT TGAAGGTTTT TGAAGGTTGG CAACCTCCAC GCACTTCAGT AGCTGATCAG CCCTCTTTGA AAGTTATAT ACTCTTTTT TCTCAAACTC AGCGGTGGC CAGCATTCCT AATCTCTTAA TTTTCTGGTC AATCTCTTAA TTTTCTGGTC AACACTCGACATGG GAAGGGGACA GAAGTCCAAATTTAA GCATTCGACATGG GAAGGGGACA GAATTCTAAA TTGTTTTTTCTGTTC TTCACCTTGA CTCACATGGC CACATTCAGA CACATTCTAA TTGTTTTTTC TGCAGTGGC TGTATTTTTA CTCAAGTGAC CTCTAAGTGAC CTCAAGTGAC CTCAAGTGAC CTCAAGTGAC CTCTATTTTTTTTTT	GAGATGAAG GAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTAATAAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT GGTTTTGGTT CTGGCTCAAC CACTGCACCC ACAGTTGTTA ATAGCAGTC TTATCATTTA ATAGCAGTC TTATCATCTG TGGAAATTG GAGAATTG GTGAACTTTC TTTTAGACT TTTTTAGTTA AATCTTTTC TTTTTTTCT TTTTTTCT TTTTTTTCT TTTTTT	AAGGGCAACT CTITGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG GATGCTTT TTGTTTTGTA GCAGTCCTCC CAGTGTGTTT ACTGGCTGG TACAAGCTGC CAGTGTGTTT ACTGGCTGG GCTCTTGGCTGG GCTATTTGGG GGCTGGTGGCA GAAGAGTTGA AATCCAGTTT CATCCCAAGG TATACTTTGGG TGTTTTCAC CTCACTGCAA CTGGCAAGT ATGACTTTCCAAAGT ATGACTTTACCA CTCCCAAAGT ATGACTTTACCA CTCCCAAAGT ATGAATTTT TATCCAGCTG	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGACCGCTTG ACCACCAAAA AACCTCCACC AAGACTATGG TACTCACTTT TCCTGTCATG TACTCACTCT TTTATAGATTT TCCTGTCATG TACTCACTCT TTTTATAGATCA CACCTTAGCT CCTTTTTCTA TTTAAATGAA ACAGGAAGAA AGAGCTGAAT AGAAATTTT AGAAATTTT TCTATGGGTTA ATTCGTTTTT TCTATGACCC ATGGAGTTT TCTATAGACCC ATGGAGTTT TCTATAGACCC ATGGAGTCT TCTCTATCCC TCTTTTGGATTA TATATGGTGC TTTGGGATTA TATATGGTGC TTTTGGGATTA TATATGGTGC TTTTGGGATTA TATATGGTGC TTTTGCACTACC	AACGAGGATG TCTGATTIGA GGACACTGTT CTTGGGATCA CACATGGCTCA AGCATATATA TCCCAGGTTCA AGCATATATA TCCCAGGTTC AGAATTIGAA ACCATGGCCC CTCCACCACT ACTATGTGC ACCATGCCC CTCCACCACT ACTATGTTG TCTCAAAGTT AGTATATATA ACACATGGAT AGTATATATA ACACATGGAT TCACCAGTAT TCACCAGTAT TCTTTTTATGT TCTTTTTATGT TCTTTTTTTTT GTTCTGTCAC CGCGGTTCA CAGGGTTCA CAGGTTCAA ATTTTTTATA	GACTCAGACA ATGAAGCAAA CTCAGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG AAATGTGAGG ACCTCACTC CCCTTCACCT CTTGGCTAAG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TTGGATAATCA GTTACATTTG GTGTGTCTTG CACATTTTCA ATGTTTAATG TTTGCACATT TACACCACTTTG CTAGATTCA TTAGACTAGT TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACTTCA TTAGACACTT CCAGGCTGGG GTGATTCA TGCTTTTAGT CCAGCCTGGC GCCAACTTTCA ACCCCTTCA AGGACTGCC CCACCCTTCA AGGACTGCCC	300 360 420 480 540 660 720 780 960 1020 1080 1140 1250 1320 1380 1440 1500 1560 1680 1740 1800 1980 2040 2100 2160 2220
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTGT CAACCTCAC GCACTTCAGT AGCTGATCAG CCAGCTTTAA TACTCTTTT TCTCAAACTC AGGCGTGAGC CAGCATTCTT TCTCAAACTC AGTCATCT AGTCATTTT TCTCAAACTC AGTCATCT AATCACATGG CAACATCCT AATCACATGG CAACATCTAA TTTCTGGTC ACATCCAGA ACATTTAA TCCACCATGG GAACATTTAA GCATCCGAGA ACTTTTTTT GTCCAGGG CTCTCCAGC TTTTCTTCCTCAGC CTCAATTTTT CTCAAGTGC CTCAATTTT CTCAAGTGAC CAGCCTATGA CTTTTTCTTT CTTTTCTTTT	GAGATGAAAG GAAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAG GCGATCTCGG CTCCCAGGTC CCTAATAAAA ACAAGGAGTC TCAACTCATG TTTTAGAAGC TGCTAACTAT CTGGCCTCAA CACTGCACCC ACAGTTGTTA ATAAGCAGTC TTATAGAGT ATTAGATGT ATTAGATGT AGGATGTACT TTATCATCTG TGGCTGGTGT TGGCTGGTGT TTATCATCTG TGGCTGGTGT TTATCATCTG TGGCTGGTGT TTTTTAAGCTT TTTTTAAGCTT TTTTTAAGCTT TTTTTAAGCTT TTTTTAAGCTT TTTTTAAGCTTC TTTTTTC TTGTTTTC TTGTTTTC TTGTTTTC TTGATCTTC TCCAATTTGG CACATTTTGG GGAATATAGA CACCTTTGCA	AAGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC CATACCTGTA TGCCAAATGC CAGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TAAGGACTT TAAGGACTT TAGTTTTGTA TACTTGCTCC CGCCCCTACT CAGTGTGTTT ACTTGCTGG GACTAGTAGACATG TACAAGCTAG GATGGTCTGT CATACTTGGGC GGCTAGAGAA CAAGGTTAG CTAATTTGG GCTAGTAGA CATACTTTGG CTCCCAAGA TATACTTTGG CTCCCAAGA TATACTTTGAC CTCCCAAAGT ATGATTTT CATCCACGCT TTTTTGTTAA	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCACCC AAGACTATTG ACCACCATG AGCACTTTT TCCTGTCATG TACTACTTT TCCTGTCATG TTTTAAGATA CTTTTTTTAA GAGACTGTCT CCTTTTTCTA TTTAAATGAA ACAGGAAGAA AGAGCTGATT TCACACTTTT TCACAATTTT TCACAATTTT TCACAATTTT TCACAATTTT TCTATGCCC AGGCACAGGC TTTGGGTTA TTTGGGTTA TCTTTTTCATAGCCC TTTTCTTATCCC AGGCACAGGC TTTGGGTTA TTTTGGGTTT TCTTATCCC AGGCACAGGC TTTGGGGTTA TATATGGTGC TTTTCACTACC AAAGTAGTTG TTTACACTACC AAAGTAGTTG TTTACCTACC AAAGTAGTTG TTTACCTACC AAAGTAGTTG TTTACCTACC	AACGAGGATG TCTGATTIGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCA AGCCTATATA TCCCAGGTTC AGAATTTGAA ACCTCGATGG ACCATGGCGC CTCCACCACT TCTGAGATA ACTAGAGAT ACTAGAGAT ACTAGAGAT ACTAGAGAT ACTAGAGAT ACTAGAGAT ACTAGAGT ATTAGACAC GTTCAGAGTA AGTATATTA AGTATATTA AGTATATTA ACACTGAT TCACCAGTAT TCACCAGTAT TCACCAGTAT TCATTTTGT GTTTTTTTTTT	GACTCAGACA ATGAAGCAA ATGAAGCAAA ATGAAGCAGA CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG ATGATGATG ATTCTTCCT CCCTAACTG TTGAGGTAG TATTCTTCCT CCCAAGCTGG TTGAAGTAATCA TTTACATTTC TTTGGCTAATCA TTTTCAATTTC CACACTTTG CTGAGATTCA TTTTGCACATT TTTGGCGTTT TACTTCTAGA TTTTTGTT TACTTCTAGA TTGTTTTTTT CCAGGCTGGG GTGATTCT GGCTAATTTT CAGGCGTGT GGCTAATTTT ACTCCTGCC GCCTAATTTT ACTCCTGAC TCACCTCTG CCACCTTCA AGGCTCCC CCACCTTCA AGGACTGCCC TCACCTCCA TGGGGGTTTA	300 360 420 480 540 660 720 780 840 960 1020 1080 1140 1290 1380 1440 1500 1560 1680 1740 1860 1920 1980 2040 2040 2160 2220 2220 2340
50 55 60 65	AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTTC ATGCAGTGGC CAACCTCACC GCACTTCAGC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCTTCAC CAGCATTCAC CAGCATTCAT ACTCTTTTT TCTCAAACTC AATCTCTTAA TTTTCTAAACTC AATCTCTTAA TTTTCTGGTC AATCACATGG CAACATTTCA GAACGGGACA GATTGACTGA GAACTGTTAA TTGTTTTTTT CTCAGGAC TGTCTAGGT TGTCTCAGCC TGTCAGTGGC TGTCTCAGCC TGTATTTTTTC CAGCTATGA CTTTTCTTGT TTTCTTGT TTTCTTGT TTTCTTGT TTTCTTGT TTTCTTGT TTTCTTGT TTTCAGGACT	GAGATGAAG GAAGTGATT TGCACTGTAG GGTAGOGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTATTAAAA ACAAGGAGTC TCTACACT TTTTAGAAGC TCTAACTAT GGTTTTGGTT CTGGCCTCAA ACATGACTCA ACATGACTCA ACATGACAC ACAGTGTTA ATAAGCAGTC ACAGTGTTA ATAAGCAGT TTATCATCTG TGGCTGTA ATATCATCTG TGGCTGTGT ATATCATCTG TGGAGACC TTTTTGATTG TGGAGTGTTT TTTTGATTG TTTTGTTTC TTTTTGTTTC TTTTAGAGTC TCCCAAGTAG CCACCTTGGC CCACTTTTGA GGAATATAGA CACCTTTTGA CTTTTTTTTTT	AAGGGCAACT CTITGTATGA TGATACCACT CATACCAGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CTCAACCTGC CGGTGTCTAA AAAAATAGCC CTGGAGCACA GACTCCTCTG TATAGACATT TAAGGACTTT TAAGGACTTT TAAGTCTCTCC GGCCCCTACT CAGTGTTTTGA ACTTGGCTGG GATGGTCTG GATGGTCTG GATGGTCTG GCTTATTTGGG GGCTTAGTAGA AAACAGTTT CATCCCAAGA TATACTTGG TTGTTTTTGG CTGCCCAAGA TATACTTTGG CTCCCCAAGA TATACTTTGG CTCCCAAGA TATACTTTGG CTCCCAAGA TATACTTTGG CTCACTGCAA CTGGGATTAC AGTTTTACAGCT ATGAATTTT TATCCAGCTG TTTTTTTTTT	GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT ACCACCAAAA AACCTCACCC AAGACTATGA AGCACTATGT TCCTGTCATG TTTTAAGATTT TCCTGTCATG TTTTAAGATA CCTTTTTTTAA ACAGCAGAGA ACAGTAGTGCT CACCTTAGCT CCTTTTTCTA TTTAAATGAA ACAGGAAGAAC TATGGGTGCT TAGGGAGCTGATTT TCACTAGCT CACAATTTT TCACTAGCT CACAATTTT TCTATGACCC AGGAGCACCAGC TTTGGGCTGA TTTGGCTTAACCC AGGAGCAGC TTTGGCCTAACCC AGGCACAGCC TTTGGCCTACC AGGCACAGCC TTTGGCCTACC AGGCACAGCC TTTGGCCTACC AGGCACAGCC TTTGGCCTACC AGGCACAGCC TTTGGCCTACC AAGATTTC TTTCACTACC AGGCACAGCC TTTGGCCTACC AGGCACAGCC TTTGGCCTACC AAGATTTC TTTCACTACC AAGATTTC TTTTCACTACC AAGATATTC AAGAGTAGTTC AAGATAGTTC AAGAGTACT CTTTTTCACTACC AAGATATTC AAGAGTACT TTTCACTACC AAGATATTC AAGAGTACT AAGAGTACT AATATGGTTC AAGATACT AAGAGTACT AATATGGTTC AAGATACT AATATGGTTC AAGATATTC AAGATACT AATATGGTTC AAGATATTC A	AACGAGGATG TCTGATTIGA GGACACTGTT CTTCGGATCA CACATGGCTG ATGAGGTCAC AGCATTATA TCCCAGGTTC AGAATTGAAA ACCTCGATGG ACCATGCCC TCCACCACT TCTCACACAT TGTTGTACAC CACTATGTTA AGTAAACTA AGTATATTA AGTAAACTG ATTAAAGTT ACACATGATT TCTCAAAGTA ACACATGATT TCTCAGAGTA ACACATGATT CACCAGTAT TCACCAGTAT TCACCAGTAT TCACCAGTAT CCTGATTCTT GTTTTTTTTT GTTTTTTTTT GTTTTTTTTT GTTTTTT	GACTCAGACA ATGAAGCAAA ATGAAGCAAA CTCTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGCTGG ACCTCAACTG GTTGATGATG ATGATGATG CCCTTCACCT CCCTAACTG GTTGATGATG TATTCTTCCT CCCAAGCTGG TTGAGATCAC TTGATCAT GTGTGTTTCT CCCAAGCTGG TTGAGATCAC TTACATTTG CACACTTTG CACACTTTG CACACTTTG CACACTTTG CTGAGATTCA TTAAACAGCT TTAGAGCTTGG TTGGGTGTT TACTTCTAGA TTGTTTTGT CCAGGCTTGGG TGGGTTTGT CCAGGCTGGG TCCACCTCCA AGGACTGCCC CCCACCGCGC TCCACCTTCA AGGACTGCCC TTCACCCTTCA AGGACTCCCT CTGTGGGTTT AACTCCTTCA AGGACTGCCC TCCACCTTCCA AGGACTGCCC TCTGGGGTTTA AATACCCATAT	300 360 420 480 540 600 660 720 780 900 960 1020 1080 1140 1200 1200 1200 1380 1380 1500 1560 1580 1590 1620 1680 1740 1860 1920 1980 2040 2160 2210 2280 2340 2400
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50 55 60 65 70 75	AGTTCTGGAG GTCAGGTGGA AAATCGAGGTGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTGC CAACCTCCAC GCACTTCAGT AGCTGATCAG CCGCTTTGA AAGTTTAT TCTCAAACTC AGGCGTTAGT CAGCGTTAGT ACTCTTTTT TCTCAAACTC AATCTCTTAA TTTTCTGGTC AATCTCTTAA TTTCTGGTC AATCACATGG GAAGGGGACA GATTCTAA TTGTTTTTTC GTGAGTGGC TGTTCAGGC TGTTTTTTTCTGGTC TTTCAGGTGAC TTTTCTTGTTTTTTTCTTGTTC TTTCAGGACTTTTA TTTCAGGACT TTTTCTTGTTTTTTTTCTTG TTTTCTGTTCTTTTTTTCTTGTTCTTG TTTTCAGGACT TTTTTAGTAGCT TTTTTTTTTT	GAGATGAAG GAGATGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GCGATCTCGG CTCCCAGGTC CCTAATTAAAA ACAAGGAGTC TCAACTCATG TTTAGAAGC TCCACTGAC CACTGCACC ACAGTGACAC ACATGCACC ACAGTGATAT ATAAGCAGTC TTATGATAT ATAAGCAGTC ATGTGATAT ATAAGCAGTC TTATCATCTG TGGCTGAAATTTG TGGCTGGTGT TTATCATCTG TGGCTGGTGT TTATCATCTG TGGCTGGTGT TTATCATCTG TCCAAGTAGA AATCTTTTCC TTTTAAGCTT GTTGTTTTCT TCTATTTGTTTCT TCTATTTGTTTTCT TGGATTTTGTTTTTTTTTT	AAGGGCAACT CTTTGTATGA TGATACCACC CATACCTGTA TGCCAAATGC CATACCTGTA TGCCAAATGC CAGGATATCAACTGTA AGGATATGAA 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Seq ID NO: 181 DNA sequence Nucleic Acid Accession #: Eos sequence

WO 02/086443 Coding sequence: 148-4518

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	CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG	CACGCACGAT ATTICCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TTCATAACAC GAGTTTCAGA	CTCACTTCGA CTCCCCCTCC TCTGGAATGG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT	TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAG ATCTCACTAA AGATAACTTT	ACCARACARA AGGAGCCGCA CGCTTGCATT ACAGAGARARA TTGGGGARAG AGATCTTACA ATCATTGGA TGACTACCGT TCACTGGGA	120 180 240 300 360 420 480 540
50	CACACATACG CAAAAAAAAC CAGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AAATATCCAA AACACATTCA GTCAGCGGAG AAATGCAATA	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TTCATAACAC GAGTTTCAGA TGTCATCTGA	CTCACTTCGA CTCCCCTCC TCTGGAAATG CTCTGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA	TCTATACACT TCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG	GGAGGATTAA TGAGAAGCA AGCGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT	120 180 240 300 360 420 480
50	CACACATACG CAAAAAAAAC CGGGGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAAAA GGAAAAGGGA	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC	CTCACTTCGA CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACA GGAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAC TGATGCAGAC TTTATCCATT	TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GCAGGACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG TGGTTTGAGG TTTTCAGG	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAACA ATCTCACTAA AGATAACTTT AAGGACAAAA ATTTTGAGGA TTGGGACAGA	ACCARACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCACTT AGCAGTCAAA AGAAATTTG	120 180 240 300 360 420 480 540 600 660 720
50	CACACATACG CAACATACG CAACACGGGGGGGCAGCTCCTCT CTTGTTGAAG ANATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GGAAAAGGGA GGATTCAAAG	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TGTCATCTGA TGTTAAGAGC CGATTATTGA	CTCACTTCGA CTCGCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA GAAACTTAAA TGGGAAAACA TGGATCAGAG TGATGCAGAC TTTATCCATT TGGAGTCGAA	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAG GATTTTCAG ATGTTTCAG AGTGTTTAGTC	GGAGGATTIAA TGAGAAGCAG AGCGTTTCCT ACTICAGGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTACTIAA AGGATAACTIT AAGGACAAAA GTITTGAGGA GTITTGAGGA GTITTTGAGGA	AACAAACAAA AAGAGCGCCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAATTTG GCAGGCTGCT	120 180 240 300 360 420 480 540 600 660 720 780
50	CACACATACG CAAAAAAAAC CAGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAAA GGAAAAGGGA CATTCAAAG TTAGATCCAT	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGAT TCTACTCTTA AGTTAAGAGC CGATTAATTGA TCATACTGTT	CTCACTTCGA CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACA GGAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAC TGATGCAGAC TTTATCCATT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTCAG TGTTTCAG GGTTTTCAG TGTTTTCAG TGTTTTCAG TGTTTTCAG TGTTTTCAG TGTTTTCAG TGTTTTCAG TGTTTCAG TCTAACTCAA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGGGACAGA CTTGACAAGTA	AACAAACAAA AAGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TGACTACCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC	120 180 240 300 360 420 480 540 600 660 720
50	CACACATACG CACACATACG CACACACACC CAGCTCCTCT CTTGTTGAAG ANATATCCAA CAAGTAAATG ACACATTCA GTCAGCGGAG ANATGCAATA GAGATGCAATA GGAAAGGGA GATTTCAAAG TTAGATCCAT ACAGTTCAT ACAGTTCATCA CACACTCAT ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA ACAGTTAGCA	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TCATAACAC GAGTTTCAGA TGTCATCTGA TGTCATCTGTA TGGTTAAGAGC CGATTATTGA TCATACTGCTT TGACATCTCTT TGACATCTCT TCTCTGAAAG	CTCACTTCGA CTCGCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAACA TGGGAAACA TGGATGCAGA TTTATCCATT TGGATCCAT TGGAGTCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTCAG GATTTCAG GATTTTCAG GATTTTCAG AGTGTTAGT CCAAACTCAA GACACAGTTG GTTTTTTTTG	GGAGGATTIA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACT ATCTCACTAA AGATAACTIT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGAAGTA ACTACAAGTA ACTACAAGTA	AACAAACAAA AAGAAGCGCAC CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCACTGGGA ATTTCCACTT AGCAGTCAAA AGGAAATTTG GCAGGCTAAA AGGAAATTTG GCAGGCTGCT TTACATTTAC TTACATTTAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960
50 55 60	CACACATACG CAAAAAAAAC CAGCAGAGGG CAGCTCCTCT CTTGTTGAAG AAATATCAA CAAGTAAATG AACACATTCA GTCAGCAGAG AAATAGCAAAA GGAAAAGGGA GATTCAAAG GTTTCAAAG GTTTGAAAG TTTGATCAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG TTTCTAGAC	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TCAATAACAC GAGTTTCAGA TGTCATCTGA TCTACTCTTA AGTTAAGAGC CCGATTATAGAGC TCATACTGT TGACATCTCT TGACATCTCC TCTTGAAAG TCTATGCTGAT AGTTGTTTCAAAG TCTATGCTGAT AGGTGTTTTC	CTCACTTOGA CTCACTTOGA CTCCCCTCC CTCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA TGGGATCAGAG TGATGCAGAC TTTATCCATT TGGATCAGAG GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACTTA GCACTACACT CTCATACACT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GCAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGTA CGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTTCAG GACACGTTG GTTTTTTTTTT	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACCTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA CTGACAAGTA ACTGGATTGGAAA CTGACAAGTA ACTGGATTGT AAGTGTTTTAGAAA ACTGGATTGT AAGTGATAACTTT AAGAACAAAAA ACTGGATTGT AAGTACATAA	AACAAACAAA AAGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATCATTGGAA ATTCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTACACTT AGCAGTCAAA AGAAAATTTG ACAGTCAAA AAGACAACAA AACAGTACAACA AACAGTACAAG AGCAGTTTGT	120 180 240 300 420 480 540 600 660 720 780 840 900 960 960
50	CACACATACG CACACATACG CACACACACC CAGCGAGGGG CAGCTCCTCT CTTGTTGAAG ANATATCCAA CAAGTAAATG ACACATTCA GTCAGCGGAG ANATGCAATA GAGATGCAATA GAGATGCAATA ACAGTTCAAAG TTAGATCCAT ACAGTTAGCA TCTGGTTATGCA TCTGGTTATGC TCTCTAGAC ACTTCTAGAC	CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TCATAACAC GAGTTTCAGA TGTCATCTGA TGTCATCTGTA TCATACTGCTT TGACATCTGTT TGACATCTCTC TCTCTGAAAG TCATGCTGAT TGACATCTCC TCTCTGAAAG TCATGCTGAT TGACATCTCC TCTCTGAAAG TCATGCTGAT TGGCGTTTTTC CAGAAAATGT CAGAAAATGT	I CTCACTTCGA CTCGCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA TGGGAAACA TGGATGCAGA TTTATCCATT TGGATCAGAG GAACCTTCTG GAACCTTCTG GACTACTTC GGACTACTTA TCCAGTTGGCT TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAG GATTTTCAGG AGTGTTAGT CCAAACTCAA GACACAGTT GAAACAATT GGAAACAATT GGAAACAATT GGAAACAATT GGAAACAATT GGAAAGAAAT CCAGAGAAT	GGAGGATTIA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGAAGTA ACTGACAGTA ACTGACAGTA ACTGGACTTAC TTCGAGAGCAGA ATACCAGCAGAAAAA ATACCAGCAGAAAAAAAAAA	AACAAACAAA AAGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCACTGGGA ATTTCCACTT AGCAGTCAAA AGGAAATTTG GCAGGCTCAAA AGGAAATTTG GCAGGCTGCT TTACATTTAACATTTAA ACAGTACAACA ACAGTACAACA ACAGTACAACA ACAGTACAACA ACAGTACAACA ACAGTACAACA ACAGTACAACA ACAGTACAACA TCTTGTTACA	120 180 240 300 420 480 540 660 720 780 960 1020 1020 1140
50 55 60	CACACATACG CAAAAAAAAC CAGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAAT AATGCTCAT AATGGCTCAT ACAGTTAGAC TCTGGTTATG TCTCTAGAC CAGTTCAGAAC CAGTTCAGAAC CAGTTCAGAAC CAGTTCAGAAC CAGTTCAGAAC CAGTTCAGAAC CAGTTCAGAAT CAGTTCAGAAC CAGTTCAGAAT CAGTTCAGAAC CAGTTCAGAAT CAGGTTCAGAAC CAGTTCAGAAT CAGTTCAGAAT CAGTTCAGAAC CAGTTCAGAATC	CACGCACGAT CACGCACGAT CCGCAGACCC GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGAT AGTTAACTGCTT AGTTAACTGCTT AGTTAACTGCTT TGACATCTCT TCATACTGTT TGACATCTCT TCTCTGAAA TCATGCTGAT AGGTGTTTTC CAGAAAATGT CTCAGAGTCCCA GAGAGAGCCCA	CTCACTTOGA CTCACTTOGA CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGATAACAA GATCCATT TGGATCAGAG TGATGCAGA CTATATCCATT TGGATCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT CCAGTTGGCT TCAGGCTGACT TCAGGCTGAC TCAGGCTGAC CAGTTAGCATTA CTCATACACT TCAGGCTGAC TCAGGCTGAC AACCAAGCAT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAG GGTTTTCAG GGTTTTCAG GCAACTCAA GACACAGTTG GTTTTTTTGTG CCAAACTACA GCTAACAATT GGAAGGAATT ATGATGGAAGGAAT ATGATTGAGA GCAATTGAGA CCAGAGAATT ATGATTGAGA GAATTTTTAG GAAATTTAGAGA GAATTTTTAGAGA GAATTTTTTAGAGA GAATTTTTTAGAGA GAATTTTTTAGAGA GAATTTTTTAGAGA GAATTTTTTAA	GGAGGATTIA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA ACTGACAAGTA ACTGGATGT ACTGGATGT ACTGGATGT ACTGGATGT ACTGACAGCA AGATTCATGA AGATTCATGA ATACCAGCCT AGGATGCTA	ANCARACARA ARGAGCOGCA CGCTTGCATT ACAGAGRARA TTGGGGAARG AGATCTTACA ATCATTGGAA TGACTACCGT TGACTACCGT AGCAGTCAAA AGARATTTG GCAGGCTAAA AGARATTTG TTTAARATT AATGCAACAA ACAGTACAAG ACAGTTTACA TTTTTAARAT TATGCAACAA ACAGTTACAAG ACAGTTTGT TCTTGTTACA TCTTGTTACAG TCAACACTTG	120 180 240 360 420 480 600 660 720 780 840 900 900 900 1020 1080 1140 1200 1200
50 55 60	CACACATACG CACACATACG CACACACACC CAGCACGGGG CAGCTCCTCT CTTGTTGAAG ANATATCCAA ANATATCCAA CAGTANATG ACACATTCA GTCAGCGGAG ANATGCAATA GAGATGCAATA GAGATGCAAT ACAGTTCAAAG TTTGATCCAT ACAGTTAGCA TCTGGTTATCA TCTGGTTATCA TCTCTAGAC TCTGGAAAC TGGGAAAAC TGGGAAAAC TGGGAAAC TGGGAAAC TGGGAAAC TGGGAAAC TGGGAAAC TGGGAAAC TGGGAAAC TGGGAAC TGGGAATC GGTGCTATTC	CACGCACGAT CACGCACGAT CCGCAGACCC CCGCAGACCC GTGTTTGCCG AGATTGCCG CCATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TCTATATGAT TCATACTGTT TGACATCTCT TCATACTGCT TCATACTGCT TCATACTGTT TGACATCTCC TCTCTGAAAG TCATGCTGAT TCAGTGTTT CCAGAAAATGT CCAGAGAAATGT CAGAGGACCA TCAATAATTT	CTCACTTCGA CTCACTTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAACA TGGGATGCAGG TTTATCCATT TGGATCCAGT TGGACTCTGG GAACCTTCTG GGACTACTTA CCAGTTGGCT TCAGGCTGAC TCAGGCTGAC ACCAAGCAT CAACCAAGCAT GCTACCAAT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAG GATTTTCAGG AGTGTTAGT CCAAACTCAA GACACTCAA GACACAGTT GGAAAGGAAT ACGAGAATT ATGATTGAGA GAATTTTTGAG AAATTATTGAGA ACATTTTGAGA ACATTTTTGAG AAATTTTTGAG AAATTTTTGAA AAATTTTTGAA AAATTTTTGAA AAATTTTTGAA AATGAGTTATG	GGAGGATTIAA TGAGAACAA ATCAAAAAAA ATATGATGA GGGATAAACA ATCACACAA AGATAACTIT AAGGACAAAAA AGTITTGAGGA GTITTGAGGA GTITTGAGGA GTITTGAGGA GTITTGAGGA GTITTGAGAA GTITTGAGAA GTITTGAGAA GTITTGAGAA GTITTGAGAA GTITTGAGAA GTITTGAGAA GTITTCAGAA ACTGAATTGT AAGTTCTTAC TTGAGAGCA ATACCAGCT AGTTTGAGAT ATACCAGCT AGTTTGAGT CAGATGGCTA ATTTCATGA TTCTTCAGAT	AACAAACAAA AAGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG ATCATTGGAA ATCATTGGAA ATCATTGGAA ATTTCCACTT AGCAGTCAAA AGGAATTTGCACTT AGCAGTCAAA AGGAAATTTG GCAGGCTGCT TTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTATTGT TCCTTGTTACA TTTGTACCAG TCCAGACATTGT TCCAGACATTA	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1260 1260
50 55 60	CACACATACG CAACATACG CAACACACCCCTCT CTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA AGGATACAAT ATTGATCAT AATGGCTCAT AATGGCTCAT ACTGGTTAGGA TCTCTTCAGAC TCTCTTAGAC TCTCTTAGAC TCTCGTTAGAC TCTGGTTAGAC TCTGGTTAGAC TCTGGTTAGAC TCTGGAAGAC CAGTTCGAAC TCTGGTTATT GCTCATATT	CACGCACGAT CACGCACGAC CCGCAGACCC CCGCAGACCC CGGTTTCCCC CAGTTACTAC TGAATCTTAA TTCATAACAC GAGTTTCACAC TGTCATCTGA TCTACTGCTT TGACATCTCT TCACACTCTC TCTCTGAAAG TCATGCTGT TCACACTCTC TCTCTGAAAG TCATGCTGT CAGAAAATGT CAGAAAATGT CAGAGGACCA TCAGAGAGACCT TCACTACTCT CAGAAAATTT CAGATAATTT GCTTATATTG	CTCACTTCGA CTCACTTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA GAAACTTAAA TGGGAAAACA TGGGATGCGAG TGATGCAGAG TGATGCAGAG TTAATCCATT TGGAGTCGAA GAACCTTCTG GCACTCTCGCAC TCAGCCCAT TCAGCCCAC TTATGATACC TTATGATACC TTATGATACC TTATGATACC AACCAAGCAT GCTACCAAT AAAATACAGC	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTCAG GATTTTCAG GATTTTCAG GATTTTCAG GATTTTCAG AGCACTCAA GACACTTAG CCAAACTCAA GACACACTT GGAAACGAAT ATGATTAGAG AGATTTTTTTTTT	GGAGGATTIAA TGAGAACACA AGCGTTTCCT ACTICAGACA ATCIAAAAAA ATATTGATGA GGGATAAACTT AAGGACAAAA AGTTTTGAGGA CTGACAGGA CTGACAGGT AACTTTTAGGA CTGACAGGT AACTTTAGAGA CTGACAGGT AACTTCATAA AGATTACTTAC TTCGAGAGCA AGATTCATGA AGATTCATGA AGATTCATGA TTCTTAGAGT TTCTTAGAT TTCTCAGAT TTCTTCAGAT TTCTTCAGAT	ANCARACARA ARGAGCOGCA CGCTTGCATT ACAGAGRARA TTGGGGAARG AGATCTTACA ATCATTGGAA TGACTACCGT TGACTACCGT AGCAGTCAAA AGARATTTG GCAGGCTAAA AGARATTTG TTTAARATT AATGCAACAA ACAGTACAAG ACAGTTTACA TTTTTAARAT TATGCAACAA ACAGTTACAAG ACAGTTTGT TCTTGTTACA TCTTGTTACAG TCAACACTTG	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1020 1140 1200 1320 1380
50 55 60 65	CACACATACG CAACATACG CAACACACCC CACACACCCCCCCCCC	CACGCACGAT CACGCACGAT CATTCCTTCG CCGCAGACCCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TCAATACACC GAGTTTCAGA TCTACTCTTA AGTTAACACC CGATTATATGA TCTACTGCTT AGTTAACAGT TCATACTGTT TGACATCTCC TCTCTGAAAA AGGTGTTTTC CAGAAAATGT CTGAGTCGT CTGAGTCGT CTGAGTCGT CTGAGTCGT CTGAGTCGT CTGAGTCGT CTGAGTCGT CTGAGTCGT TCAATAATTT GCTTATATGG TTGATCTTTT AAGACATTGA	CTCACTTOGA CTCACTTOGA CTCCCCTCC TCTGGAAATG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGATACAGA TGGATCAGAG TGATGCAGAC TTTATCCATT TCGAGTCGAA CCAGTTGGCT GGACTACTTA CTCATACACT TCAGGCTGAC TTATGATACA TCAGGCTGAC TTATGATACA CAGCTTAGC TCATACACT TCAGGCTGAC TATAGATAC CTCATACACT TCAGGCTGAC TATAGATAC GCTACCCAAT AAAATACAGC CCCTGAAATTA AGAAGGCGCT	TCTATACACT TCTATACACT TCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTGAGG AGTTTTCAG GGATTTTCAG GGATTTTCAG GACACGTA GCAAACCAAT GGAAACGAA TCAAACAAT ATGGAACGAAT ATGGAAGGAAT ATGGAAGGAAT ATGGAATTAGA AATTGTAGA AATGGAACTGA ATGGAACTGA ATTGGAACTGA ATTGGAACTGA ATTGGAACTGA ATTGGAACTGA ATTGGAACTGA ATTGGAACTG	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGAGGA CTGACAAGTA ACTGGATGT AAGTTCTTAC TTGAGGACTG AAGTTCTTAC TTGAGAGCA AGATTCATGA ATTCATGA ATTCATGA ATTCATGA TTCGACAGT TTGAGAGCA AGATTCATGA TTCGACAGT TTCTCACGT TTCTCACGT TTCTCACAT TTCTCACAT TTCTCACAT TTCTCACAT TTCTCACAT TTCTCACAT TTCTCACAT TTCTCACAT TTCTTCACAT TTCTTCACAT TTGTTCACAT TTGTTCACAT TTGTTCACAT TTGTTCACAT TTGTTCACAT TTGTTAGAGA	ANCARACARA ARGAGCOCCA CGCTTGCATT ACAGAGARARA TTGGGGARAGA ATCATTGGAR ATCATTGGAR ATCATTGGAR ATCATTGGAR AGACATTACA ATTCACTT AGCAGTCAAA AGARAATTTG GCAGGCTGCT TTACATTTACA ATTCACTT ARTCARCAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG ACAGTACAG CAAGAGCTTG TCTAGACAT AGTAGCATT AGTAGCATT CTAGAGACTTG CCAAGAGCTTG CAAGGAGCT CAAGGAGAC CAAGGAGAC CAGTGCTACA	120 180 240 360 420 540 660 720 780 840 960 1140 1200 1320 1320 1340 1450
50 55 60 65	CACACATACG CAACACACAC CACACACACAC CAGCACGGGG CAGCTCCTCT CTTGTTGAAG ANATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA AAGGTACCAT AATGCTCAT AATGCTCAT ACAGTTAGCA TCTCAGAAC TCTCAATT AATCCTGAAC GAAGAGGGAA AACCAAATCA	CACGCACGAT CACGCACGAC CCGCAGACCC CCGCAGACCC CCGCAGACCC CCGCAGACCC CCGCAGACCC CCGCAGACCC CCATGTACTACC CCATGTAATAG TCATACACAC CGATTATTCA TCATACTCTTA TCATACTCTTT TGACATCTCT TCATACTCT TCATACTCT TCATACTCT TCATACTCT TCATACTCT TCATCACT TCATCTCC TCAGAAAATGT CAGAAAATGT CAGAAAATTT CCTTATATCG TCAGTAACTT TCATTATTCG TCAGTACTTTT AGGACATTTGA GGAAAAAGGA	CTCACTTCGA CTCACTTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA GAAACTTAAA TGGGAAAACA TGGATGCAGA TGATGCAGA TTTATCCATT TGGAGTCGAA GAACTTCTG GCACTCTGCAC CCAGTTGGCT GGACTACTTA CTCATGCACA CTCATGCACA CTCATGCACA CTCATGCACA CTCAGCACT TAGGATACACA CTCAGCATT AAAATACAGC CCTGAATTA AGAAGGCGCT ACCCCAGATT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTCAG GATTTCAG GATTTTCAG GATTTTCAG GAGTTTTAGT CCAAACTCAA GACACACTTG GGAAACTAG CCAGAGAAT ATGATTGAG GAATTTTTTTG CAAAACAATT ATGATTGAG AATTTTTGA GAATTTTTGA GAAACAATT ATGATTGAG AATTTTGA AATGATTATG GAAACTAT ATGATTATG AATGATTATG AATGGAACTG ATTGGAACT TCTACCACAA	GGAGGATTIAA TGAGAACACA AGCGTTTCCT ACTICACGACA AGCGTTTCCT ACTICACGACA ATCAAAAAAA ATATTGATGA GGGATAAACT AGGACAAAAA AGGATAACTIT AAGGACAAAA AGTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAGCA AGATTCATGA AGATTCATGA AGATTCATGA TTGTCAGAT AAGAAATAAT CTGGTAGAGA CACCTACAA	AACAAACAAA AAGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATTACACTT AGCAGTCAAA AGGAGTCAAA AGGAGTCAAA AGGAGTCAAA AGGAGTCAAA AGGAGTCAAA ACAGTACAAG TTTTAAAGAT TTTTAAAGAT TTTTTAAAGAT TTTTTTAAAGAT TTTTTTAAAGAT ACAGTACAAG ACAGTACAAG TCTAGTTACA TTTTTTACA TTTTTTACA TTTTTTACA TCTTTTTACA TCTTTTTACA TCTTGTACCAG TCAAGACTTG AGTAGCCATA GCCTACTGAT CAAGGAGGAG CAGTGCTACA CAGTACAGG	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020 1080 1140 1260 1320 1320 1340 1500
50 55 60 65 70	CACACATACG CAAAAAAAAC CAGCAGAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AAATATCCAA GTCAGCGGAG AAATGCAATACA GAAATACAAT GAGATGCAAT GAGATGCAAT AATGCATCAT AATGCTCAT AATGGCTCAT ACAGTTCAGAC TTCTCTAGAC AGTTCAGAAC CAGTTCAGAAC AACCAAATACA AACCAAATACA AAGGGTGATG	CACGCACGAT CACGCACGAT CATTCCTTCG CCGCAGACCC GTGTTTGCCG AGATTGGCTG CATGTAATAG TCATAACAC GAGTTTCAGA TCTACTCTA TCTACTGCTT AGTTAAGAGC CCGATTATGA TCATACTGTT TGACATCTCT TCATACTGTT TGACATCTCT CAGAAAATTTC CAGAAAAATTT CCTAATAATTT GCTTATATAG TCATACTGTT TGATCTTT AAGACATCTTT AAGACATCTTT AAGACATTTT AAGACATTTT AAGACATTTT AAGACATTTT AAGACATTCA TCATAATTT AAGACATTCA TCATAATCA TTATATTG GGAAAAATTT AAGACATTCA ATGAACCCAA TTCCCAATAC	CTCACTTCGA CTCACTTCGA CTCGCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA GAAACTTAAA TGGGAAAACA GAAACTTAAA TGGGATCAGAG TGATGCAGAG TGATGCAGAG TGATGCAGAG CCAGTTGGAT CCCTGCACA CCAGTTGGCT GGACTACTTA CTCATACACT TCAGGCTCGA CTTATCACTT CAGGCTCACA CACCAAGCAT GCTACCCAAT GAAATACAGC CCCTGGAATTA AGAAGGCGCT ACCCCAGATT ACCTACACCGA ATCTTTAAAT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAG GGTTTTCAG GGTTTTCAG GGATTTTCAG GCAACTCAA GACACAGTTG GTTTTTTTGTG CCAAACTATA GGAAGGAAT ATGATTAGA AGATTTTTGA AGATTTTTGA AGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATGATTTTTGA ATTGAACTC ATTGTGAACT TCTACCACAA TCCCCAACAA TCCCCAACAA	GGAGGATTIA TGAGAAGCA AGCGTTTCCT ACTICAGGACA ATCAAAAAAA ATCATATGAGG GGGATAAACT AGGACAAAA GTTTTGAGGA TTGGGACAGA CTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT TTCGACAGCA AGATTCATGA ATACAGCCT TTCTTCAGT TTCTTCAGT TTCTTCAGT TTCTTCAGT TTCTTCAGT TTCTTCAGT TTCTTCAGT TTCTTCAGAT AGGAAATAAT CTGGTAGAGA ACCACTACAA AGAAATAAT	ANCARACANA ANGAGCOGCA CGCTTGCATT ACAGAGANAA ATGGGGAANG AGATCTTACA ATCATTGGAA ATCATTGGAA ATCATTGGAA ATTCACTGT AGCAGTCANA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTANAGAT AATGCAACAA ACAGTACAAG ACAGACATTG AGTAGCCATA AGCACATAGAG CAAGACTTG AGTAGCCATA AGCATAGAG AGTCTACAA TCAAGAGAGAG ATCATTGAA ATTCTTGAA ATTCTTGAA ATAAATTAGCC	120 180 240 360 420 480 540 660 720 780 960 1080 1140 1260 1320 1380 1440 1500 1560 1620 1680
50 55 60 65	CACACATACG CACACATACG CACACACACC CACACACACC CAGCGCGGGG CAGCCCCTCT CTTGTTGAAG ANATATCCAA CAAGTAAATG AACACATTCA GAGATGCAATA GAGATGCAATA GAGATGCAATA ACAGTTCAAG TTAGATCCAT ACAGTTAGAC TTAGATCCAT ACAGTTAGAC TCTGGTTATG TTCTTAGAC TCTGGTTATG TTCTTAGAC CAGTTCGATC TGGCACAATCA ACTCAATC AATCCTGAAC CAGTTGGAT CGGACAGGGA AACCAAATCA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAAATACA ACGAAAATACA ACGAAAAAGG	CACGCACGAT CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCCG CCATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TGTCATCTGT TGACATCTGT TGACATCTGT TGACATCTCT TCATACTGCT TCATGCTGT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGGAGACCA TCAATAATTT GCTTATATGG TCAATAATTT GCTTATATGG TTGACTTTT AAGACATTCA GGAAAAAGGA ATGAAGCCAA ATGAAGCCAATAC ATATTTCCTT	CTCACTTCGA CTCACTTCGA CTCGCACTTCG TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAACA TGGGATGCAGA TTTATCCATT TGGATCAGAG GAACCTTCTG GACTACTTCT GGACTACTTA TCAGGCTGAC TCAGGCTGAC TATGATACC TATGATACC TATGATACC AACCAAGCAT AAAATACAGC CCCTGAATT AAAATACAGC CCCTGAATT AAAATACAGC CCCTGAATT AACGCAGCTT GCTACCCAAT AACGAGCAT ACCCCAGATT GACTAACCGA ACCCAGATT GACTAACCGA ACCCCAGATT GACTACCCAA ACCTTAAAAT GACTTCACAG	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAG GATTTTCAGG AGTGTTAGT CCAAACTCAA GACACAGTTG GAAACAATT AGAAACAATT AGAAACAATT AGAAACAATT AGGATTTTGAG AAATTTTTGAG CAAAGGAAG ATTGTTGAGA GAATTTTTTG GACAACTGA ATTGGAATC TCTACCACAA TCCACCTACCA ACCGACTTCC ACTGTGACTG	GGAGGATTIA TGAGAAGCA AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACT AGCACAAAAA AGATACTTT AAGGACAAAA AGTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGAT ACTACAAGTA ACTACAAGTA ACTACAAGTA ACTACAGAGTA ATACCAGCT AGTTTGCAGAT TTGTCAGAT CAGATGACT AGATACAAGAT AAGAAATAAT CTGGTAGAGA CACACTACAA GAGGAAGTGA AACCAGTCAC AACTGCCCACC	AACAAACAAA AAGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG ATCATTGGAA ATCATTGGAA ATCATTGGAA ATTTCCACTT AGCAGTCAAA AGGAATTTAC AGTACATT AGCAGTCAAA AGAAAATTTG GCAGCTGCT TTTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACCAAC TCTTTTTAACATTTGT TCTTGTTACATTTGT TCTTGTTACATTTGT CCTTGTTACATTTGT CCTTGTACAGATTTGT CCAGTGCTACAT CCAGTGCTACAT CCAGTGCTACAT TCGCATAGGG ATTCTCTGGA ATTATTCTTGGA TCACACTGTG TCACACTGTT TCACACTGTACTT TCACACTGTACTT TCACACTGTACACTG TCACACTGTACT TCACA	120 180 240 300 360 420 540 660 720 780 840 960 1020 1140 1260 1320 1340 1440 1560 1560 1620 1680 1740
50 55 60 65 70	CACACATACG CAACATACG CAACACACCC CACACACCCC CTGTTGAAG CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAACACTATA GAACACTATA GAACACATTCA ACAGTAAAG GAATACCAT AATGCAATA AATGCAATA AATGCATAAAG TTAGATCCAT AATGGCTCAT ACAGTTAGAC CAGTTCAGAC AGTTCAGAC AGTTCAGAC GAGTAGTATC GGTGCTATTC GGTGCTATTC GGTGCTATC GAACCAAATCA AACGAAATACA AAGGAAATACA AAGGAATACA AAGGAAAAAG CAAGTACTT ACAGAAAAAG CAAGGTACTT ACAGAAAAAG CAAGGTACTT ACAGAAAAAG CAAGGTACTT ACAGAAAAAG CAAGGTACTT ACAGAAAAAG CAAGGTACTT ACTGCACCT ACTGCACC	CACGCACGAT CACGCACGAT CACGCAGACCG GGTTTGCCG AGATTGCCTG AGATTGCTA TGAATCATAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TGTCATCTGA TCATACTGCTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCT TCATACTGTT TGACATCTCT CAGAAAATTT CAGAAAAATTT GCTTATATAG GGAAAAATGA TCATACTGTT AAGACATCAT TCATATTTT AAGACATTCA TCATATTTT AAGACATTCA ATATTTTCTT AAGACACCA ATATTTCCTT CAGCCTCTTT CAGCTCTT CAGCCTCTTT CAGCCTCTTT CAGCCTCTT CAGCCTCTT CAGCCTCTT CAGCTCTT CAGCCTCTT CAGCCTCTT CAGCCTCTT CAGCCTCTT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTCT CAGCCTC CAGCCTC CAGCCTC CAGCCT CAGCCT CAGCCTC CAGCCT CAGCCT CAGCCT CAGCCT CAGCCT CAGCCT CAGCC CAGC CAGCC CAGC CAGCC CAGC CAGCC CAGC	CTCACTTOGA CTCACTTOGA CTCACCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA GAAACTTAAA TGGGAAAACA GAAACTTAAA TGGGATCAGAG TGATGCAGAG TGATGCAGAG TGATGCAGAG CCTCTGTACCATT TCGAGTCGAC ACCAAGCAT TCATACACT TCAGGCTGAC TATACACT TCAGGCTGAC ACCAAGCAT GCTACCCAAT CCCTGCAATTA AGAAGGOGCT ACCCCAGATTA AGAAGGOGCT ACCCCAGATTA AGAAGGOCT ACCCCAGATTA AGAAGGOCT ACCCCAGATTA AGAATACACGA ATCTTTAAAT GACTTCTCAG AACTTCTCAG AACTTCTCAG AACTTCTCAG AACTTCTCAG AACTTCTCAG AACTTCTCAG AACTTCTAAAT GACTTAAAT GACTTAAAT GACTTAAAT GACTTAAAT	TCTATACACT TCTATACACT CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTCAG GGTTTTCAG GGTTTTCAG GCAACTCAA GCAACACATG GCAAACAATT GGAAAGGAAG CCAGAGAATT ATGATTTTGA ATGATTTTGA ATGATTAGA ATGATTAGA ATGATTAGA ATGATTAGA ATGAGAATT GACACACTG ATTGTGAATC TCCCAACAA TCCCCAACAA TCCCCTACCA CTGTGACTG ACTGTGACTG ACTGTGACTG ACAGTTCCC ACTGTGACTG ACAGTTTCTA	GGAGGATTIA TGAGAAGCA AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTT AAGGACAAAA GTTTTGAGGA CTGACAAGA CTGACAAGTA ACTGGACAGTA ACTGGACAGTA ACTGGATGT TCGACAGCA AGATTCATGA ATTCATGAG TTTCTACGAT TTCTTCAGT TTCTTCAGT TTCTTCAGT CAGATGCTA AGATTCATGA ATACCACCT TTGTTCAGAT TTCTTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTCAGAT AGGAATAAT CTGGTAGAGA ACCACTTCCAA ACCACTTCCA AACTGCCAC TTCTTAGATC TTCTTAGATC TTCTTAGATC TTCTTAGATC TTCTTAGATC TTCTTAGATC TTCTTAGATC TTCTTAGATC	AACAAACAAA AAGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG ATCATTGGAA TTGACTGGGA ATTTCACTT AGCAGTCAAT AGCAGTCAAA AGAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA AGAAATTTG CTATTTACATTTAC TTTTTTACAG TCAAGACTTG AGTAGCCATA AGCACTTG AGTAGCCATA AGCATACTGAT CCACAGAGGG CAGTGCTACA TCAAGAAGAGGG ATTCTTTGGA TCAAGAAGAGGG TCAAGAGGG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAAGACTTG TCAACTTGAG TCAACTTGAG TCAACTTGAG TCAACTTGAG TCAACTTGAG TCACACTTGT TCACACTTTACACT TCACACTTTACACT TCACACTTTACACT TCACACTTTACACT TCACACTTTACACT TCACACTTTACACT TCACACTTTACACT TCACACTTTACACT TCACACTTACACT TCACACTTACACT TCACACTTACACT TCACACT TC	120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1380 1340 1560 1560 1620 1680 1740 1800
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75
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        AEDEFVYWPN KDEPINCESF KVTLMAEEHK CLSNEEKLII QDFILEATQD DYVLEVRHPQ
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        CPKWPNPDSP ISKTFELISV IKEEAANRDG PMIVHDEHGG VTAGTPCALT TLMHQLEKEN
        SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAALPDGNI 1440
80
        AESLESLV
        Seq ID NO: 185 DNA sequence
        Nucleic Acid Accession #: EOS sequence
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AGATTCAAC TROCTCACA GACCHAAGGA TCCTTCTATG GAGGARGAG GCTTTCTCCA GACTAATTAC ACTGAGATAC GTGTGATAC ATTGAGAAG ACACCAAG GCTTTCTCCA GACCAACTAC GACCTAACAG GTGTGATACA ATTGAGAAG ACACCAAG ATTATCTACA CTTTGCCTAC TTCCCAACTA ACTGAGATAC CTCATGCTTAT TACAGATCA GACCAACCA TATATCATACA GACCAACTA AGTGAGATAC ACCGAGTAT ACAGCACCA ACCCAACCA TATACAATGA GACCACTAT AGTAGCACTA AGTGCTATA TCCGCAGACA ACCCAACCA AATTACCAACGA GACACTACA TACAGCACTA AGTCCTATAT TACAGACTA ACCCAACCA TATGAGAGA GACGACATA AGTACCACCA GACCTGATAT TACAGACTA ACCCAACCA TATGAGAGA CAGTACACTC CTCAGAGTA TATCCACACC TCCAGACCT TTTACCACAC ACTTGCAGACA TCGGACTAC CTCAGAGTA TATCCACACC TCCAGACCT ATCTTCCA ACTGCAGAGA TGGGATTACA GAGACATTTCA AAAGCACTTTC GAGACATTTC GAGACATTTC GAGACATTT GAGACACTCAC AAAGCACCTA ACCCACCACACACACACACACACACACACACAC	25	~ · · · · · · · · · · · · · · · · · · ·	WATER KIND WITH THE	ADA:MANAL A	ACATATCCCA	AGGGTATATA	TTTTCCTCC	1980 2040
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GCTTTCTCC GACTANTTAC ACTGAGATAC GTGTTGATGA ATCTGAGAMG ACAACLASA CCTTTTCTCC AGGCCAGGA ATTGCAGG GTCCCTCAGT TACGACTTG GAAATGCCA ATTATCTAGC CTTTGCCTAC TTCCCAACTG AGGTAACACC TCATGCTTTT ACCCCATACG TATACCAAGGA GAAGGCAGTT ACCCCATGAGTTA ACCCCATACG AATCCAGGAG GAAGGCAGTT ATCCCCTTG TGATCGTGTT CTCCCAACCG AATCCAGGAG GAAGGCAGTT ATCCCCTTG TGATCGTGTT AGGCCTGACT TTTATCTAGT TAGTGGTTCT TGTGGGAGCA ATTCCAATAA AGCACCATCCT ACTTAGAGGA CAGTACATCC CCTAGAGTTA AGCACCACCC TCCCAACCCG TCCCAACCACCT ATTCAGAGGA CAGTACATCC CCTAGAGTTA TATCCACCC TCCAACCACCT ATCTTCCA ACTAGAGGAG CAGTACATCA CCTAGAGTTA AGCACCTTCAACACC TCCAACCACCT ATCTTCCA ACGAGATCG TGTGACTTA GGTATTACAG CAGCACCACCA ACCACCCA ACCACCAC ACAGCCAAA AGCTTATATT GCTGACCACA AGCACCACCA ACCACCCA ACCACCCA ACAGCCAAA AGCTTATATT GCTCCCCAAG CCCCACGAA ATCCACCACAC AAAATGAATA ATGGGAACA AATTGGAGAG TTATGTCAT GACGACAGACACACACACACACACACACACACACACACA		AAGATTCAAC	TTCATCAGGT	TCAGAAGAAT	CACTAMAGGA	TOTTGGATCA	GGCAGAGAGA	2160
40 ATTATTCIAC AGGOCCAGTG ATGTCACAGG GTCCCTCAGT TACAGATCH GAAGTCACT CCAGACAACA GGATTIGGTC TATACAATGA GGATTIGGTC TATACAATGA GGATTIGGTC TATACAACA GGATTIGGTC TATACAACA GGATTIGGTC TATACAACA GGATTIGGTC TATACAACA GGAGTAAT AGTIGGCATG AGTGTGTATA CCCCAGCC TATACAACACA GGAGTAAT AGTGCCATG AGTGTGTATA CCCCAGCC TATACAACACA GAAGGCATT AGTCACCCTTG TATACTGTT AGCCCATCC TAGAGGAA GAAGGCAGTA ATACCCTTG TATACTGTATACACCC TCAACACCT AGCCCTAGAGTTA TATCCACACC TCCAACACCT ATCTTTCA ATCAAGTAG TGGGGTATACT CCATAGATTA AGCCCATTCC AAGCCTTAC TTTTCAATAAA AGCCACTTC CAACACCTACC AACACCACCA ACAAGAATCG ATACATAAAT ATCGTTACAG AGCACACTCC AACACCACCA GACAACAGA ACAGAACAG ATACATAAAT ATCGTTACAG AGCACACTCC AACACCACCA GACAACAGA ACAGAACAG ATACATAAAT ATCGTTACAG AGCACACTCC AACACACCAC AACACACACA ACAGAACAAA AGCTTATATT GCTGCCCAGA GCCCACTGAA AGCTTATATT GCTGCCAGA CCAAGACAAAA AGCTTATATT GCTGCCCAGA GCCCACTGAA ACAGTTAATT GAGACACAGA ACAGAACAAA AACATATATT GCTGCCCAGA GCCCACTGAA ATCCACACCT ACAGACCAAA AACATATATT GCTGCCCCAGA GCCCACTGAA ATCCACACT CCACAGTACA CTACACACCA GAGACTCCC AGAAAGGAAA ACCCAATGTTA CCATACACCCA TCCACAGTACA CTACACACCA GGACCTCCCAGAGA TTCCCCAGAGAC AACACAACAC AAAAATAAAA AAGGCCCCACC AGAAAAGGAAA ACCCAATGTTA CACCACACTC ACACACCACCA GAGAAAGGAA ACCCAAGTGGA CCTGCCCAGAG ACTCACATTCT GAGAAAGGCA GCCTATACCCA AGACCACACC AGAAAACAAAA AACACAATC CTACACACCA GAACAAAACAA		COMPACTOR	CACTABTEE	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
ATTATTCTAC CITTECCTAC TTCCCAACTS AGTMACACC TCATACTTT ACCCAACCACCAGACACAG GATTTAGGT TCCCAACTAC AGTAGCCATAC AGTAGCACTA AGTAGCCATAC AGTAGCACTA AGTAGCACTA AGTAGCACTA AGTAGCACTA AGTAGCACTA AGTAGCACTA TAGTCGTGTCA AGCCCAACCG TAGTCGTGTCA TGGTGTGTCA TGGTGTGTCA TGGTGTGTCA TGGTGTGTCA TGGTGTGTCAGACTACTACTAGTGTCAGACTACTACTACTACTAGTGTAGTCAGACTACTACTACTACTACTACTACTACTACTACTACTACTA			NOCCOCN CTC	シンダンダンエンティ	GTCCCTCAGT	TACAGATCIG	GAAATGCCAC	2280
CCAGACAACA GACTTAGGTC TCCACGGTCA ACGIGGTATA CITGAGACA ACCUMICATION ANTICORGAN GACCAGATAT ATACCCCTG TRATGGTCTAGCT GAGGGGTTGACT TTATCTGTT TOTGGGTATA TACCCCTG TRATGGTCTA AGCCCTGACT TTATCTGTT TAGTGGTTCT TGTGGGTATA TACCCCTG TGATGGTTA AGCCCTGACT TTATCAGATA TACTGGGGCA ATTCCAATAA AGCACTTCA AAGCACCT ATCTTCCACACACT ATCTTCCAATACT TTACAGATAG TGTGGTTTACT GAGGATTA AGCACTGTA AGGACTGTA CAGGACAGTA ATCCAAGAGA TGATCAATAAA AGCACTGTA AGGACTGTA CAGGACAGA ATTCCAATAAA AGCACTGTA AGGACTGTA CAGGACAGA ACAGGACAGA AGCTGAAA AGGATTACAT GGAGAAGAG GATACATAAA ATCGTTGCCT ATGATCATAG CAGGACAGGA	40	A STATE OF THE A	C Talabathanana	TTOACTO	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
TATACANTEA GECCAGTAAT AGTACCCTTS TATCTCTACT GECCTEACT TITATCCTT TAGTGGTTCT TOTGGGTATT CTCATCTACT GEAGGAAATG CTTCCAGACT TAGTGGTTCT TOTGGGTATT CTCATCTACT GEAGGAAATG CTTCCAGACT ACTTAGAGGA CAGTACATC CCTAGAGTTA TATCCACACC TCCAGCACCT ATCTTTCCA TTTCAGATGA TOTCGAGCA ATTCCAATAA AGCACTTTCA AAAGCATTAC GACACACAGA ACAGAAATCA TATCATAATA TACTCAATAA AGCACTTACA AAAGCATTAC CAGCAACAGA ACAGAAATCA ATCTATATT GAGCACCAGA AGGATTTAC CAGCAACAGA ACAGAAATCA ATCTACACTA ACCTCCAAG CCCCACCACA ACCACACAGA AACAGAATCA ATCTACACTA ACTTACTCCAACACC CAACCACCAC ACCACACAGA AACAGAATCA ATCTACACCAG CCCCACTGA ATCCACAGCT GAACATAAT AACAGAACAC AAAAATAAAA AACGCCTCCA GCCCATGAA ATCCACAGCT GAACATACA AAAAATAAAA AACGCCTCCAAG CCCCACTGAA ATCCACAGCT GAACATTAC TTCTGGTCAC TCAGAAGAGT GTCAAGTC TTCCCTATTA TACTGTACA GATGACACACA TTCTGGTCAC TCAGAAGAGT GTCAAGTC TTCCCTATTA TACTGTACACACC TACACAGCT GTCAAGTC TTCCCATACC TCAGAAGAGT ACGCCATAC AGAATACACA CACAGTTC GAAAATCAAAA AACGCCCACCA CACAGTACA CACAGTACAC CACAGTACACC AAAAATAAAA AACGCCCACCA AGAATACACC CTCCCAGGAACACACCACAC		0020202202	باشتات شست لا ت	עיייניבייט עייייי	ACCITICATA	CTCGCAGACA	ACCUAACUUG	2400
ACTRAGAGA CAGTACATCE COTAGASTRA TATOCACCAC ACCACACT ATCTTCCAA ATGCAGTAG TGGGGAGA ATTCCAATAA AGCACTTCC AAAGCATGT GCAGACTTA ATGCAGTAG TGGGTTTACT GAAGAATTTG AGACACTGAA AAGCATGTT CCAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA		mama	CCCCACTAAT	እርተልር("እፕር	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTTGG	2460
ACTITAGAGGA CAGTACATCC CCTAGAGTTA TATCCACACC TCCAACACCT TTTTCAGATGA TGTOGAGCA ATTCCAATAA AGCACTTTCC AAAGCACTGT AGAGCTGTAC TGTGGACTTA GGTATTACAG CAGCACACCCA GACCACCCA ACACACCCA GACACACCCA ACACACCCA GACACACCCA ACACACCACAC		AATCCGAGAA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	CCACACTTTT	2520 2580
TTTCAGARTIA TGTGGGAGCA ATTCCAATAA AGCACTTTCC AAAGCATGTT ATGCAAGTAAG TGGGTTTACT GAGAAATTACAG CAGACAGCTC CAACCACCAG GACAACAGA ACACGATCA CTGTGACTTA GGTATTACAG CAGACAGCTC CAACCACCAG GACAACAGA ACACACAAA AGCTTATATT GCTGCCCAAG CACACCACA CTAGCACCAG ACAGACCAAA AGCTTATATT GCTGCCCAAG GCCCATGAA ATCCACAGCT GAAGAACAGAC AAAGAAAGAA AGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTACAGAC CAAGACACACAC CTAGCACAGA ATGCGACACA AAAATTACAAAC CTCCCCAAGA CTCCCCACAGT GATAACAAAC CTCCCCAGAGAGT GTGCAAGTGC TTCCTGTGAAG TTCTGGTCAC CTCACACGCA TGGCCTGACA TGGGAGTACC CACAGTACTAC CTCACACGCA TGGCCTGACA TGGGAGTACC CACAGTACTAC CTCACACGCA TGGCCTGACA TGGGAGTACC CACAGTACTAC CTCACACGCA TGGCCTGACA TGGGAGTACC CAGAGACACAT CACACAGCT GAGAAAGGAAG AAAATAAAA AAGGGCTCCC AGAAAGGAAG ACCCACTGGA ATTTTACTACACACACACACACACACACACACACACAC	15	TAGTGGTTCT	TGTGGGTATT	CTCATCTACT	GGAGGAAATG	TOCALCE	ATCTTTCCAA	2640
AGGACTATA TGGGTTTACT GARGARATTG AGGACACTGAA AGGGTTTAC AGAGACTAA ATCGATTAC CAGGACACTC CAACCACCCA GACAACAG ACAGACACAA AGGACGACAA ACTGACTGAT ATTACATAG CAAGTATAGT GATGCACAG ACAGACCAAA AGCTTATATAT GCTGCCCAAG CCCACTGAA ATCCACAGCT GAGAACGAA AGCTATATATT GCTGCCAAG CCCACTGAA ATCCACAGCT AAAGGAAGAGA AAATTGAAT AAAGGAACGAA AAAATTAAAT AACGTCACCCC TTCTGGTCAC CAAAAAGAAACA CAAAAATTAAAA AAAGGGCTCCC CAGCACTGAA ATCCACAGCT TTCTGGTCAC CACAAGAAGAGT GTGCAAGTGC TTGCCTATTA TACTGTGAGA AATTTACA CACAGTATCA CTACACGCAG TGGCCTAGCA TGGGGATACC CAGAGTGACC AAAAATAAAAA AAAGGGCTCCC AGAAAGGAAG ACCCAGTGAA CGTCACAGTGA AAAATAAAAA AAAGGGCTCCC AGAAAGGAAG ACCCAGTGAA ATCTCACACCAC GAGAATCACAC CGAAAGAAGACA CAAAAATAAAA AAAGAGCCCCACCACCACCACCACCACCACCACCACCACC	43	ACTTAGAGGA	CAGTACATCU	ATTOCABLE	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
AGAGCTGTAC TGTTGACTTA GGTATTACAG CAGACAGCTC CAACCACCA GACAACACAA TTCTTGAAAA GGATGGCAAA CTGACTGATT ATATCAATGC CAATTATGT GATGGCACA ACAGACCAAA AGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGGT GAACATTATGT GGAGAATGAT ATGGGACAT AATGTGGAAG TTTATTCTAT GATACAAAC CTCGTGGAG AAGGAAGGAG AAAATGGAT CAGTACTGGC CTGCCGATGG GATGAAGGAG TACGGGAAC TTCTGGTCAC TCAGAAAGGT GTGCAAGTGC TTGCCTATTA TACTGTGAG AATTTTACT TAAGAAACAC AAAAATAAAA AAGGGCTCC AGAAAGGAAG ACCCAGTGGA AAAAATAAAAA AAGGGCTCC AGAAAGGAAG ACCCAGTGGA CGTGTGGAC CACAGTATCA CTACACGCAG GCCTACCA AGCGCCATGC AGTGGGGCC GTGTGTCGCAGTGA CTGACCATTGT TGACCTTTGT GAGAAAGGAC GCCTATGCCA AGCGCCATGC AGTGGGGCC GTGTGCGACA ACGACACACA CGAAGGACC GCCTATGCCA AGCGCCATGC AGTGGGGCC GTTGTCGCAGA AGATTCAACA CGAAGGACC GCCTATGCCA AGCGCCATGC AGTGGGCC GTTGTCGCAGA AGAATTCAACA CGAAGGACC GCCTATGCCA AGCGCCATGC AGTGGGCC GTTGTCGCAG ACGATACTTAG TGAACCAGCA GCCAACAA TTTGCCTTTCTT AAACACCACT CGTTCACAA CCATACTTAG TAAAAGAAACT GAGGGAGCAAT ATGTCTCTAT TCATGCCTAT GTTAATGCAC AGCCTAATATT ACAGCCAGCA GGCAAACAA AGCTGAAGAA ACACTCCAG CTGCTGAGA ACCATAATTA CAGCCACGCA GACTATTCTG CAGCCCTAAA GCCATGAAGAA ACACTCCAG TCCTGAGCA ACCATAATGC CCACCCCT CTCCTTCATA CCATCAAGGAT TTGCCAGA AGCATGAAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGGA AAACACACAC AGCAATGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGGA AAACACACAC AGCAATGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGGA TTTCTCCAG GACAATGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGGA TTTCTCCAGAGA AAACATGCCAC TCTCTTCATAA GACAATGAC TAATTCTGA GACCTTTATCCAG ACCAATGAT TACTCAGAGAT TAATTGTGA GACCTTTATCAG GACCTTTATCAGA ACACAAATGT CTATTCATATG AAATTGTGA AAACATGCCAC AAACAA TGCCTCTTATTCAGA AAACATGGCA TACACAGAA AAACAATGCCT TATTCATATG AAATTGTAA AAACATGCCAC AAACAA TGCCTCTTATTCAGA AAACAATGCCAC AAAATGCCTCT TAATTCACACA AAACAATGCCAC AAACAA AGCAAGGAAAAAAACAA AAAATGCCTCACCC TTTCTGGACCA AAACAATGCCT CTAATTCACAAGTA ACCACAAGTAT ATGTTATTCAGACAA AAACAAGCACAAATGT CTATTATCACAA AAATGCCTCACCC TTTCTGTATC CTAAAAGTA AACCACAAATGT CTATTATCACACAA AAACAAAGCA AACCAAAGTA ATCCTCAACATA GGACACCAC TTTCTGAGCAA AAACAAATGCCTA AAACAAATGCC TTTCAAAAG		A TOTO A COTAC	TOCCTTTACT	GAAGAATTTG	AGACACTGAA	AGAGTTTTAC	CAGGAAGIGC	2760
TIGCTGAAAA GATGGCAAA CTGACTGATT ATATCATAGC CAGGTTAAG CTAGCGCAAG GATGACGAA GATGACAAA CTGACTGATT ATATCAAGC CAATTATGT GATGGCTAC ACAGACCAAA AGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCC GAGACCAAA AGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCC GAGACCAAA AAGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAGACAAAAAATAAAA AAGGGCTCCC CTGCCAATGG GAGTGACGAG CTGCCGGGAC CACAGTGACA CTACACGCAG TGGCCCTGACA TGGCGCTATCA TACTGTGAGG CTTGCCTTTGT GAGAAAGCAC CACAGTGACA CTCACAGCAG TGGCCTGACA TGGGAGTACC CACAGTGAC CTACACAGCAG TGGCCTGACA TGGGAGTACC CACAGTGAC CTACACAGCAG TGCCCTGCCA AGAGAGCAC CATATATTGT GCTACACACAC CCACAGTGAC ACAGGCACC CTGCCAGTGC AGAGTACACA CGAAGTACACACACCACCC CTCCCACTAC ACAGCCCATCC CTCCCAGTG ACATCACACAC CACAGTACACACACACACACACACACACACACACACACAC		NONCOTOTA C	מיושרים מבויותים בייתי	CCTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	2820
TIGETGAAAA GEGATGGCAAA CTGACTGATT ATATCAATGC CAATTATATT GATGGACAAA ACCACAGAT AACGACCCAAGA ATCCACAGGT GAAGATTAC GAGAAATGAT ATGGGAACAT AAATGTGGAAG TTATTGTCAT GATAACAAC CTCGTGGAG AAGGAAGGAG AAAATGATA CAGTACTGC CTGCCGATGG GAGGAGAGGA		BOB BOB BOOK	* ATACATABAT	ATCCTTCCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
AGGAGATGAT ATGGARCAT AATGTGGAG THATTGTCAT GATAACAAC CTCGTGGGAGAAAGAAGAAAGAAAAAAAAAA	50		CCATCCCAAA	TTACHTACHT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
AAGARGAGA AAAATGRAT CAGTACTGC CTGCGATGG GATGAGGAG TAGGAGAGAGA TTCTGGTCAC TCAGAAGAGT GTGCAAGTGC TTGCCTATA TACTGTGAGG AATTTTACT TAAGAAACAC AAAAATAAAA AAGGGCTCCC AGAAAGGAAG ACCAGTGGA CGTGTGGTC TAACCTTTGT GAGAAAGGCA GCCTATGCCA AGGCCATGC AGGGAGCAT ATGTTGCAG ACTGCAGTGC TGGAGTGGGA GCCTATGCCA AGGCCATGC AGTGGGCCT GTTGTCGTC ACTGCAGTGC TGGAGTGGA AGAACGGCA CATATATTGT GCTAGACAGT ATGTTGCAG AGATTCAACA CGAAGGAACT GTCAACATAT TTGGCTTCTT AAAACACATC GTTTGCAG AGAATTATTT GGTACAAACT GAGGAGCAAT ATGTCTTCAT TCATGCATAC CTGGTTGGAG CCCATACTTAG TAAAGAAACT GAGGAGCAAT ATGTCTTCAT TCATGCATAC CTGGTTGGAG AGTCAAATAT ACAGCAGAGT GACTATATCTG CAGCCCTAAA AGTCAAATAT ACAGCAGAG GACTAATTCTG CAGCCCTAAAA AGTCAAATAT ACAGCAGAGT GACTATATCTG CAGCCCTAAAA AGTCAAATAT ACAGCAGAGT GACTATATCTG CAGCCCTAAAA ACAATTCCAG AGGAAACAA AGCTAGAGGA TTCCCGAGG AGCAAGAGCA CAGCTACATC CATGCATAA CATCATGGG CTATTACCAG AGGAAACAA ACCATAATGC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTTCTGGAGG ATGATATGA ACCATAATGC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTTCTGGAGG AGAACATGAA ACCATAATGC CCAACTGGTG GTTATGATTC CCATGAGCCA AAACATGGCA GAAGATGAA ACCATAATGC CCAACTGGTG GTTATGATTC AAGTGAGCAC AAACATGGCA GAAGATGAA CCAATAATGC CCAACTGGTG GTTATGATTC AAGTGAGCAC AAACATGGCA GAAGATGAA CCAATATGC CCAACTGGTG GTTATGATTC AAGTGAGCAC AAACATGGCA GAAGATGAA CCAAATGCA ACAGAATGAT CTATCTAATG AAGTGAAGGCA CTTTCAGTGT CCTAAATAC CAAATCCAGA ACAGAATGAT CTATCTAATG AAGTGAAGGCA CTTTCAGTGT CCTAAAATGC CAACTGTAG GAAGAGCAT AGTAAACCT TTGAACTTAT AAAGAAGAGA ACCAAATGC AAGGATGAAT CATCATGCAC ACTGGAAGA AAACATGGCA CAGGAGGAT ACCCCATT AGGTAACCT TTGAACTTATA AAAGAAGAGA ACCAAATGC CAACAGAATGAT CATCATGCAC AGCCAGAGT ACGGCAGGAT ACGGCAGGAT AACATGGACA AAACATGGCAC AAGGCCAGGA GAGAATCCC CCACCTCTCT GACCAACC CTTATGCACC TTGTGAGCAC AAGGCAGGAA GAGAACAC ACCAGGTAGC CAACAGAAA ATCCAGCC TTGTGAGCAC AAGGCAGGAA GAGAACAC ACCAGTAACT TTAACACAGA AACCGCAGC AACCAGAGAT ACGGCAGGAT ACCCCACCTTCACCC CTACAACACAAACAAAAAAAA		ACAGACCAA	AGCTTATATI	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATITUI	3000 3060
TTCTGGTCAC TCAGAAGAGT GTGCAAGTGC TTGCCTATTA TACTGTCAGA AATTTTACACACACACTGCAAAAAAAAAA		GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTCAT	CATAACAAAC	TACGGGAACT	3120
TAAGAAACAC AAAAATAAAA AAGGGCTCCC AGAAAGGAA ACCAGTGAC CGTCTGCCAGTG CACAGTATCA CTACACGCAG TGCCCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTG TGACCTTGT GAGAAAGGA GCCTATGCCA AGGCCCATGC AGTGGAGTCC CTGCCAGTG ACTGCAGTC TGGAGTTGGA AGAACACTAC TGGCTCTCT AAAACACACT CGTTCACAA GAATTATT GGTACAAACT GAGGAGCACT ATGTCTCAT TCATGATACA CGGTTCACAA CCATACTTAG TAAAGAAACT GAGGAGCAAT ATGTCTCAT TCATGATACA CTGGTTGAG AGTCAAATAT ACAGCAGAGT GACTATCTG CAGCCCTAAA ACAATTCCAG CTCCTAGACA AGTCAAATAT ACAGCAGAGT GACTATCTG CAGCCCTAAA ACAATTCCAG CTCCTAGACA AGTCAAATAT ACAGCAGAGT GACTATCTG CAGCCCTAAA ACAATTCCAG CTCCTGAGAA AGACTACATC CCTGTGGAAA GATCAAGGGT TGGCATTTCA CCCTGAGG TCATCATTAC CCAGCACCCT CTCCTTCATA CCATCAGGGA TTTCTGCAGA ACCATAATGC CCAGCACCCT CTCCTTCATA CCATCAGGA TTTCTGCAGA AGACATAGAG ACCATAATGC CCAACTGGTG GTTATGATC CTGATAGGCA AACACTGGCA GACATAGAG ACCATAATGC CCAACTGGTG GTTATGATC CTGATAGGCA AACACTGGCA GACATGATAG ACCATAATGC CCAACTGGTG GTTATGATC CTGATAGGCA AACACTGGCA GACATGATAG ACCATAATGC CCAACTGGTG GTTATGATC CTGATAGGCA TTTCTGGAGGA GACATGAGA ACCATAATGC CCAACTGGTG GTTATGATC CTGATAGGCA AACACTGGCA GACATGAGA ACCATAATGC CCAACTGGTG GTTATGATC CTGATAGGCA TTTCTGGAGGA GACATGAGA ACCATAATGC CCAACTGGTG GTTATGATCT TAATTTTCAG GACCTTTAAA CCAAATCCAGA ACAGAATGAT TATTTACTTCA AAGTGAGGCA TTTCAGTGTG CCTAAATCC CCACCAGGTAGC CAAGAAGAT AATCTGATGA AAGTGAGGCA TGGAGGATGA CAACTGGCA AACAGGCAGGA TCGCCAATTAA AAGAAGAGA ACCACATATG GGATGGCCC TATGATGACC AACTGGAGA TTATGGCTA AATTAGCT AACAGTAGAC CAACAGGAA AACACAAAGAA AACCAGAAAACA CAACTGGAAA AACACAGGAA AACAGGAAAACAC CTTTAGGACCA CAACTGGAAA AACACAACAGA AAGGGAGGAT TCTTCAGACAC AACTGGAAAAACAA AACACAGAAAAACAA AACTGAACAAAACAA		AAGGAAGGAC	AAAATGTGAT	CAGTACTGGC	TOCCUATED	TACTORGORG	AATTTTACTC	3180
CACAGTATCA CTACAGGAG TGGCCTGRCA TGGGGTACC AGAGTACTC CTGCCTAGT TGACAGGAG ACCTATGCA AGCCCATGC AGTGGGCCT GTTGTGGTG ACAGCAGTAGGCA GCATACTTCT GAGAAAGGAAC GTACACATAT TTGGCTTCTT AAAACACATC CGTTCACAGA AGATTCAACA CGAAGGAACT GTCACACATAT TTGGCTTCTT AAAACACATC CGTTCACAGA AGATTCATACA CGAAGGAACT GAGGAGGCAAT ATGTCTTCAT TCATGACAGA CTGGTTAGGAGACT TCATGATCATAG GTACACAGAC GGCAAAACAA AGCTAGAGAA ACAATTCCAG CTCCTCATCC TGGACCAGCA GGCAAAACAA AGCTAGAGAA ACAATTCCAG CTCCTGAGGAACAA AGCTAGAGGA ACAATTCCAG AGCAAACAA ACCTACATCA TCATGACACTC TCCTATCATC CCTGTGGAAA GATCAAGGGT TGCATTACCAG AGCAAACAA ACCATAATGC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTTCTGGAGG AGCAATGAACA CCAATAATGC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTTCTGGAGG AGCAATGAA ACCAATAAGC CCAACAGGAT TTTTTTTCTGGAGG ATGAATGAA GACCAAAATGC CCAACAGATGA TATCTTACTG GACCATAAGGA TTTCTGGAGG AGCAATGAA GATGAAGCCTA TAAATTGTGA GAGCTTTAAG GAACATAAGG ACCAAATGA ACACAAAACT TATCTAACTG AGGAAAAACT TATCAAGGA TTTCTAGTGT CCTAAATGC CAACACCAATA GATCAAACT TATCATACTAG AGCAATTAAA ACACCAATAA GAACAAACAT TATCAACTAG AAGGAAGGAA ACCAAAATCA ACAGGAATGAT TATCTACTATG AAGTGAAGCA TTTCAAGTGT CCTAAAATG CAACCCAATAG GAACAAACAT TATCATACAC ATGACACCA ACGGAAGGAT AACACCAAACA ACACAAACAT AAACATCAACA ACAGGAAGGAT AAACATGAACA ACAGGAAGGAT AAACATGAACA ACAGGAAGGAT AAACATGAACA AACAGGAAGGAT AAACATGAAACA ACAGGAAGAA AACACAAACA AACAGAAACAA AACAGAAAACA AACAGAAAAACA AACAGAAAAACAC CAACAGAAAAACAA AACAGAAAAACAA AACAGAAAAAAAA	55	TTCTGGTCAC	TCAGAAGAG1	A PGGGGGGGGG	AGAAAGGAAG	ACCCAGTGGA	CGTGTGGTCA	3240
TGACCTITGT GAGAAAGGCA GCCTATGCCA AGCGCCATGC AGTGGGGCA ATGTTGCAG ACTGCAGTCC TGGAGTTGGA AGAACAGCA CATATATTGT GCTAGACAGT ATGTTGCAG AGATCAACA CGAAGGAACT GTCAACATAT TTGGCTTCTT AAAACACAC CGTTCACAA GAAATTATTT GGTACAAACT GAGGAGCAA ATGTCTTCAT TCATGATACA CTGGTTGGA CCATACTTAG TAAAGAAACT GAGGAGCAAT ATGTCTTCAT TCATGATACA CTGGTTGAG AGTCAAATAT ACAGCAGAGT GACTATTCTG CAGCCCTAA GCAATCCAG CTCCTGAGC AGTCAAATAT ACAGCAGAGT GACTATTCTG CAGCCCTAAA GCAATCCAG CTCCTGAGC AGTCAAATAT ACAGCAGAGT GACTATTCTG CAGCCCTAAA GCAATCCAG CTCCTGAGC AGGAAGCAC AGACTACATC CATGCCTCCT ATATCATGGG CTATTACCAG AGCAAACAA ACCATAATGC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTCTCGGAG AAGCATGAACAA AACCATGAGCA TCATCATTAC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTTCTGGAGG AAGCATGAAC ACCATAATGC CCAACTGGTG GTTATGATCT CTGATGGGCA AAACATGGGC GAAAATGAA CCATAATGC CCAACTGGTG GTTATGATCT CTGATGGGCA AAACATGGGC GAAAATGAA CCATAATGC CCAACTAATAAA GATGAGCCTA TAAATTGGA GACCTTAAG GACCATAATG CTGCCAATAG GCAAATAAA GATGAGCCTA TAAATTGGA GACCTTATAG GACCTTATC CTGCCAATAG GAATGAAC CTTATCTAATG AGGGAAAACT CTTTCATGTG CCTAAAACTG CTGCCAATAG GAAGTGAT TATGTACTTC AAGTGAGGCA TAGGCAGGAGT ACGGCAGGA CCTTTCTGGC CAGCAGTGAT ATGTATCTAC AGTGAAGCAC AAGTGAGGACA AAGAGAGAA ACCAAAATGC CAACATGAT AATCTGATGA GGCCAGGAGT CTTTCCTGG CAACATGAAACTT CTACAAAGTG ATCCCCAGCCC TTGTGAGCAC AGGCAGGAG CTTTCCTGACAC CACCCTCCTC GACAGTGAAT GGTCCAGCAC TTGTCAGCAC AACTAGAGCAC AAGCCAGGAGT CTTCCTAAAATT CACCCAACCC TTGTGAGCAC AACTAGAGAA ATCCCCAGCCC TTGTGAGCAC AACTAGACAC ATGAGCAC AAGTCTTAAGT TAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCAT GAGGAGCTT CCCAAAATT TAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCAT GAGGAGCTT CCCAAAATT TAACACAGA AAGGGTGGG GGGACTCACA TCTGAGCAT GTTTCTCCTAAAATT TAACACAGA AAGGGTCAGG TCCCCACCTCTC GGCAAATTAT TACCATAAC GGAATCCCCACCTCCC CACCTCTCTCAAAATT TAACACAGA AAGGGTGGG GGGACTCACA TCTGAGCAT GTTTCCTCAAAATT TAACACAGA AATCAGTCAG AATTTAAC ATTTTAACA AATTTTAAC AATTTTAACAAACA	23	ON ON OWN MOT	CTR CR CCCRC	マコムこつしていてひしひ	TGGGAGTACC	AGAGTACTCC	CIGCCAGIGC	3300
ACTICACATO COAAGGAACT GTCAACATAT TTGGCTTCTT AAACACACT CGTTCACAA GAATTCAACA CGAAGGAACT GTCAACATAT TTGGCTTCTT AAACACACT CGTTCACAA GAATTATTT GGTACAAACT GAGGAGCAAT ATGTCTCTT TCATGACTAT GTTAATGCA CCATACTTM TAAAGAAACT GAGGAGCAACAA AGCTCAGAGA ACAATTCCAG CTCCTGAGC AGTCAAATAT ACAGCACAGC GGCAAACAA AGCTAGAGAA ACAATTCCAG CTCCTGAGC AGTCAAATAT ACAGCACAGT GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAAGAA ATGCACTC TTCTATCATC CCTGTGGAAA GATCAAGGAT TGCATTCACAG AGGAAAGAA ACACTACATC CAGCCCT CTCCTTCATA CCATCAAGGA TTTCTGCAGG AGGAATGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGACA CAACCATGAACA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGACA AAACATGGCA GACGATGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGACA AAACATGGCA GACGATGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGGACA AAACATGGCA GACGATGAA CCAAATCCAGA AACAAAAGT CTATCTAATG AGGAAAAACT TATAATTCAG GACCTTTATC CAAAATCCAGA TAGCCCCATT AGTAAAACTT TTGAACTTAT AAGGAAGAGA CTGCCAATAG GGATGGGCCT ATGATTGTC ATGATGGCA AAGGAAGAGA ACGGCAGGA CCTTCTCTGTGC TCTGACAACC CTTATGCACA AACTAGAAAA CCAAGGTAGC CAAGGATGAT CATCATGACACA ACCAGGTAGC CAAAGATGT CATCAGACC TTGTGAGCAC AAGGGAGGTG ACGGCAGGA ACCAGGTAGC CAAAGATGT ATCCTCAGCC TTGTGAGCAC AAGGGAGGTG ACGGCAGGA ACCAGGTAGT CAACAAGTG ATCCTCAGCC TTGTGAGCAC AAGGGAGGTG ACGGCAGGA ACCACGATAAT GGCACGTAAT GGTCACCACC TTGTGAGCAC AAGGGAGGTG ACGCAGGAG ACCACCTCTCT GGACAGTAAT GGTCACCACC TTGTGAGCAC AAGGCAGGAG GAAACCAC ACCACCTCTCT GGACAGTAAT GGTCACCACC TTGTGAGCAC AAGGCAGGAG GAGAATCCA CCACCTCTCT GGACAGTAAT GGTCACCACC TTGTGAGCAC AAGGCAGGAG AACAAAGTT CAACTAAAGT AAGCACCACT TCCTGAAATT TACCACCACACACACACACACACACAAAGTG AATCCTCACCC GCCAAATTTA TACCATAAC ATTTCACCACACACACACAC		THE R CHARGE STATE OF	CDCDDAGGCD	なつつうかはヤーハン	AGCGCCATGC	AGTGGGGCCI	Grigitation	3360
60 GAATTCAACA CGAAGGAACT GTCAACATAT TTGGCTTCAT TAAACACATC CGTTCATACACA CGATACACACT GAGGAGCAAT ATGTCTCAT TCATGCATACA CGTGGTTGAGCACACACACACACACACACACACACACACA		\$ CMCC\$ CMC(מבונותיוים מבורית י	_ ACA A CACCCA	CATATATIGI	GCTAGACAGI	AIGIIGCAGC	3420
GARATTATTT GGTACARACT GAGGAGCAT ATGTCTTCAT TCATACATAC CIGOTRACT CATACTTAG TANAGARACT GAGGAGCAT ATGTCTTCATT TCATACATAC CIGOTRAG ACGTCATAT TCATACATAC CATCACTAG GACAACAA AGCTAGAGAA ACAATTCCAG CTCCTGAGC AGCTCAATAT CATCACTAGA CAGGAAACAA AGCTAGAGAA ACAATTCCAG CTCCTGAGC AGCTCAATAT ACAGCACGAGT GACTACTTC CAGCCCTAAA GCAATCACGA GCAATGCAC CAGGAACAA ACCACACAGCA TTCCTGAGAGA ACCACATACAC CAGCACCCT ATACCAGGA TTGCATTCCA GACCATAATC CCAGCACCCT CTCCTTCATA CCATCAGGA TTTCTGGAGG AGCAATGAA GACCAAATGA GATGAGCCA TAAATTGGAG CAACATGAGCA TTGTTTACAG GCAAATAAA GATGAGCAC TAAATTGGAG AAACATGGCA GAAGATGAA CACCAAATGA CATCATACTA AGGAAAACT TATAATTCAG GACCATATAG CAACCAAATGA CATCATACTAG AAGCAGAACAT TAGACCCATT AGAATCCAGA AACACAGGAC CATCATACCA AAGGAAGAA CTTCTCAGAGCA TAGACCCCATT AGAATCACAA AAGGAAGAA AACAGAGGAC ACGGAGGAGA AACACAGAACAC CATCAGCAC AAGCAGGAAGAA AACAGAGGAC ACGGAGGAGA CACCAGATGAAC AATCAGACCA AACTAGAAAA AAGAAGAGAA AACAGAGGAC ACCAGGATGAT CATCAGACCA TAGACCACC CACCACCTCCT GACCAGAACAC CAACAGAACAC CAACAGAACAA AACAGAGAA AACAGAGAA AACAGAGAAA AACAGAGAAA AACAGAGAAA AACAGAGAAA AACAGAGAAA AACAGAGAAAAA AACAGAGAAAAAAAA		3 C 3 FM C 3 3 C 1	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	የ ርተርካል የልጥልግ	. 4416363777	· AAAACACATU	CGTTCACAAA	3480
TCCTCATTCC TGGACCAGCA GGCAAAACAA AGCTAGGAAA ACAATTCCAA AGGGAAAACAA AGCTAGAAAA ACAATTCCAA AGGGAAAACAA AGCTAGAAGA ACAATTCAA CAGCAGAAGA ACAATCAAA ACAATCAAAC ACGGAAAACAA AGCCACAAAA GACAAACAA AGGCAAAGAA AGCATACAACA AGGCAAACAA AGCATACAACA AGCATAAACAC CAGCACACCC CTCCTCATAA CCAATCAAGGA TTGTCATGACA ACCATAAAGC CCAACACAGGA GTATACACGA ATGCATACACAC ACCAAAATGC CCACACACAGGA TTTCTGGAGGA AAACATGGAC ACCAAAATGC CCACAAAACAC CTATCAACAC ACGAAAAACT TATCATACTAC AAGTGAGGAC ACAGAATGA TATCATCATGA AAGGAAAAACT CTTCCAGAAACAC CTTACAGAACC CTTATCAGCAC AACCAAAACC CTTATCAGCAC AACCAGAACAC CTTATCACACAC CAACACACAC CAAACCACAAACC CTTATCACACAC CAACACACAC	60	A > > > (1000)	- ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	• @\$@@\$@@\$\$	י איינייייייאיא	TCATGATAC	CIGGIIGNOG	3540 3600
AGTCAAATAT ACAGCAGAGT GACTATTCTG CAGCCCTAMA GACAATGCAC AGGCAGAGT ACAGGAATGCAC CAGGAAGGCAC TTCTATCATC CCTGTGGAAA GATCAAGGGT TGGCATTCA CCCTGAGT TCATCATGC CAGCACCCT CTCCTCATA CCATCAAGGA TTTCTGAGGC AGCAATGAA GACCAATGAT CTGCTGAGT CTGATGCCCA AAACATGGC GAAAGTGAA GACCAAATGT CTGATGAGTC TATATCTGGGG GAAGATGAA TTTTTATCTG GCCAAATAA GATGAGCCTA TAAATTGTGA GAGCTTTAAG GACCTATAAG ACCAAATGT CTATCATAG AGGAAAAACT TATAATTCAG GACTTTATA CAGCAACAGA ACACAAATGT CTATCATAG AAGGAAGAAC CTTTCAGTGT CCTAAATGC CAAACCCAGA TAGCCCCATT AGGAAACCT TTGAACTTAT AGAGTGAGCA CTTCCAGAAT GGATGGCCCATT AGGAACCAC CTTATGACCA AACTAGAAAA AAAGAAAATCC CAGCAGATGAT CATCCAAGAG ACCAGATGAT CATCCAAGCC CTTGTGAGCCA CAGGAGGAG CCACCAGTTAC CAAACCCAGATAG GGACGAACAC CTTATGAGCAC AACTAGAAAA AGGAGAGGT CCCCCCTCTC GGACAGTAAT GGTCCCAGCC TTGTGAGCAC AAGGCAGGAA GAGGAACCC CACCCTCTCT GGACAGAAA ATCCCCAGCC TTGTGAGCAC AAGGCAGGAA GAGGAATCCC CACCCTCTCT GGACAGAAA ATCCAGCCAGC TTGTGAGCAC AAGGCAGGAA GAGGAATCCCACCCTTTATGT TTAACACAGA AAGGGAGGG GGACCCACA TCTGAGCAT TTCCTAAAATT CACCAACACAA AACGCAGGAG GAGAATCCCACCCACCCACCACCACACACAACAACAAAAAAAA		CCATACTTAC	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCIAI	CTCCTGAGCC	3660
ATGGAACTIC TICIATCATC CCTGTGGAAA GATCAAGGGT TGGCATTTAC TCCCTAGAT ATGCTATACG GAGAAGGCAC AGACTACATC ANTGCCTCT ATACTAGGG TATTACCAG AGCATAGAT ATGCCTCTATA CCATCAGGA ATGCATACATG CCACCACACACACACACACACACACACACACACACACA		TCCTCATTC	TGGACCAGCA	GGCAAAACAA	CACCCCTAA	CCANTICCAC	AGGGAAAAGA	3720
GAGAAGGCAC AGACTACATC AATGCTCCT ATATCATGGG CTATTACCAG AGAAATATGC TCATCATTAC CCAGCACCCT CTCCTTCATA CCATCAAGGA TITCTGGAGG ATGATATGC ACCATAATGC CCAACTGGTG GITATGATTC CTGATGGCCA AAACATGGCA GAAGATGAA TCGTTACTG GCCAAATAAA GATGAGCCTA TAAATTGTGA GAGCTTTAAG TGGCGAAGA ACCAAATGT CTATCTAATG AGGAAAAACT TATAATTCAG GACCTTTATC CAAAACCACA TAGGCCCATT AGTAAAACTT TTGAACTTAT AAAGAAGGA CTTTCAGTGT CCCAAAACC CAAATCCAGA TAGGCCCATT AGTAAAACTT TTGAACTTAT AAAGAAGAA CCTGCCAATAG GGATGGAC ATGATGCACC AACTAGAAAA ACAACGCAGGAG CTTTCCTGGC CTACAAAGCG CAAGATGAACA AACTAGAAAA ACAACAGAAAAA ACAACACACAA AAGGCGAGGAG CTTCCCTGCACA AAGGCAGGAA GAGAAATCAC AAGGCAGGAA ACACACACAA AAGGCAGGAG CTTCCCTGCACA AAGGCAGGAA ACACACACAA AAGGCAGGAG CTTCCCTGCACACA AAGGCAGGAA ACACACACAA AAGGCAGGAG GAGAATCACA AAGGCAGGAA ACACACACAA AAGGCAGGAG CTTCCCTGCACACA AAGGCAGGAA ATCAACCTAGA AAGGCAGGAA CACACTACACA AAGGCAGGAA TCCACCACA TCCCACACACA AAGGCAGGAA TCCACCACA TCCCACACAACAAAAAAAAAA		AGTCAAATA	r ACAGCAGAGI	CACIAIICIG	GATCAAGGG	TGGCATTICA	TCCCTGAGTG	3780
TCATCATTAC CCAGCACCCT CTCCTTCATA CCATCAAGGA TTTCTGGAG AIGATAGAA ACCATAATGC CCAACTGGTG GTTATGATC CTGATGCCCA AAACATGGCA GAAGATGAA TTGTTTACTG GCCAAATAGA GATGAGCCTA TAAATTGTGA GAGCTTTAAG TGGCTGAAGA ACCAAATGT CTATCTAATG AGGAAAAACT TATAATTCAG GACTTTATC TAGAAGCTAC ACAGGATGAT TATGTACTTG AAGTAGAGCA CTTTCAGTGT CCTAAATAC CCAATCCAGA TAGCCCCATT AGTATACTC AACTAGACCA CTTTCAGTGT CCTAAATAC CCACCAGTAG GATGGCCCT ATGATTGTC ATGATGACCA TGGAGGATG ACGGCAGGA ACCAGGTAGC CAAGATGATC AATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAAATTCC CCACCTCTCT GGACAACT ACCCCACCC TTGTGAGCAC AAGGCAGGAA GAGAACTCC AGTCTTAGT TTAACACAGA AAGGGTGGG GGGACTCACA TCTGAGCAT GTTTCCTC AGTCTTAAAATT AGGCAGAAA ATCAGTCTAAT TCCTCAACACT ACCACCACCACACACACACAC	65	CACA ACCCA	¬ እርእሮሞአሮኒሞር	, <i>א</i> אתכתבדתת	ATATCATGG	CTATTACCA	AGCAATGAAL	3840
ACCATARIGE CCAACTGGTG GTTATGATTC CTGATGGCCA AAACATGGGC GAAGATGAT TTGTTTACTG GCCAAATAAA GATGAGCCTA TAAATTGTAA GAGCTTTAAG GTACACTTT TGGCTGAAGA AACCAAATGT CTATCTAATG AGGAAAAACT TATAATTCAG GACCTTTACC TAGAAGCTAC ACAGGATGAT TATGTACTTG AAGTGAGGCCA CTTTCAGTGT CCTAAATGC CCACATAG GGATGGCCT AGGAACACC CTTATGCACCA TAGAGGAGTG ACGCAGGA CCTTTCTGTGC CTACAAGCC CTTATGCACCA AACTAGAAAA AGAAAATTCC GTGGATGT ACCAGGTAGC CAACATGAT AACCTCAGCC TAGTGAGCAC AAGCAGGAG AGGAACCC CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCTGATCG AAATATAGCT GAGAGCTT CCACACTTAGT TAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCAT GTTTCCTTA ACGTTACTT TAACACAGA AACGGCTGGG GGGACTCACA TCTGAGCAT GTTTCCTTA ACAGTACCT TCATGACATA GGATCTCGC GCCAAATTA TAACATTAAC AATGTTGG ATTTTTTAAGA ATGGAATTCT GGTTATTTTT TCTGTATTCA TTTTAACACAGA ATGGATTTTTTTTTT	05	MCN TCN TTN	CONCENCE	CTCCTTCATA	L CCATCAAGG	L TITCIGGAGG	ATGATATGGG	3900
TIGITTACTE GCCAAATAAA GATGAGCTA TAAATTGTGA GAGCTTTACG GTCACTCATT TIGICTGAAGA ACACAAATGT CTATCTAATG AGGAAAACT TATAATTCAG GACTTTATT TIGICTGAAGA ACACAAATGT CTATCTAATG AGGAAAACT TATAATTCAG GACTTATT CAAATCCAGA TAGCCCATT AGTAATACTT TIGIACTTAT AAGGAGATGAT CTGCCAATAG GGATGGCCC ATGATTGTC ATGATGAGCA TIGIAGGAGT AAGAAGAACA CCTTTCTGTGC TCTGACAACC CTTATGCAC AACTAGAAAA AGAAAATTCC GTGGATGT ACAGGTAGC CAAGATGATC AACTCAGCAC AACTAGAAAA AGAAAATTCC GTGGATGT CCACCTCTCT GGACAGTAAT GGTCCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCAC AGTCTTTAGT TTAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCATT GAGAATCTC AGCGTAAATT AGGCAGGAAA ATCAGTCTAG GTCTGTATC TGTTGATTC CCATCACC TCTTAAAATT AGGCAGGAAA ATCAGTCTAG TTCTGTATAC TGTTGATTC CCATCACC ATTTTTGCAG ACTGTAAATT TACTTATTAT GTTTGAATTA AAATGATTGA ATTTCAAGA ATGGAATTC AGGTTTGCTA TCTGTATTC TTTTAACAGA AAATTTCAA ATTTCTAAGA ATGGAATTC AAACTACAGA AAACTTCATTTT TCTGTATTC TTTTAACAGA AAATTTCAA ATTTCTAAGA ATGGAATTC AAACTACAGA AAATTTCAT TTTTAACAGA AAATTTCAA AATAAAACAC TCTTCCTATT GATATCAAC ATTTTAACAC TTACAACTAAAACAC CTTCCTATT GATATCAAC CTCAATGTC TCCAATGACC AAATTTTAT AAAAAAACAC TCTTCCTATT GATATCAAC CCAATGTC TCCCAATGACC AAATTTTAT AAAAAAACAC TCTTCCTATT GATATTCAAC CCAATGTC TCCCAATGACC AAATTTTAT		3 CC3 M3 3 M2	* CCN N CTCCTC	ידד ביד ביד ביד בי	CTGATGGCC	L AAACATGGCA	GAAGATGAAT	3960
TGGCTGAGA ACACAAATGT CTATCTAATG AGGAAAAACT TATAATTCAG GACTTATATTCAGAGCAAAACAAACAAACAAAACA		the Annual of Carried Street	COCDATAR	CATGAGCCT	TAAATTGTG/	A GAGCTTTAAC	GTCACTCTTA	4020
CARATCCAGA TAGOOCCATT AGTANAACTT TTGAACTTAT AAGTAGTATA AAAGAAGACGACCTGCCAATAG GGATGGGCCC ATGATGTTCC ATGATGAGCA TGGAGGATGA ACGCCAGGAG CTTTCTGTGC TCTGACACACC CTTATGCACC ACTAGAAAA AGAAAAATTCC GTGGATGTTAGACCAC ACTAGACAA AAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACTAGACACAACAACAACAACAACAACAACAACAACAACAACA	7 0	MOOCHTON NO.	רביעות מתחמחת א	אדממדריות מדיטיין	: AGGAAAAAC	PATRATTCAC	GACTTTATCT	4080 4140
CTGCCAATAG GGATGGGCCT ATGATTGTC ATGATGAGCA TGGAGGAGTG ACGGCAGCAGC CTTATGCACC AACTAGAAAA AGAAAATTCC GTGGATGT ACGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	70	TAGAAGCTA	C ACAGGATGAT	TATGTACTIC	AAGTGAGGC	A CTTTCAGIGI	ANAGAAGAAG	4200
75 ACCAGETAGE CAGACAGE CATATGCACE AACTAGAAA AGAAAATCE GTGGATGT ACCAGETAGE CAAGATGATC AATCTGATGA GGCCAGGAGT CTTTGCTGAC ATTGGCAC ATCAGTTTCT CTACAAAGTG ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCC CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCTGATGC AAATATAGCT GAGAGCTTT AGTCTTAGT TTAACACAGA AAGGGGTGGG GGGACTCACA TCCTAAAATT AGGCAGAAA ATCAGTCTAG TTCTGTTATC TCTTGATTCC CCACCACC ACAGTAACTT TCATGACATA GGATTCTCC GCCAAATTA TATCATTAAC AATGTGTG ATTTTCTAAGA ATTTCTAAGA ACTGTAATT TACTTATTAT GTTTGAATTGA TTTTAACACGA AAATTTCA TTATAGAGGT TAGGAATTCC AAACTACAGA AAATGTTCT TTTTAATACA GTAGCCTC CTGTATTGT AGGAATTCC AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTA AATAAAACAC TCTTCCTATT GATATTCAC CCCATGACC TCCATGACC ACCATGAC 85 CAAAAAAACAC TCTTCCTATT GATATTCAC ATTTTAACAC TCCATGACC AAATTTAT		CAAATCCAG	A TAGOCCCAT	r AGTAAAACT	TIGARCIA.	TEGAGGAGT	ACGGCAGGAA	4260
ACCAGGIAGO CAAGATGATO AATCIGATGA GECCAGGAGT CITTECTGAC ATTAGACCA ATCAGTITCT CTACAAAGTG ATCCTCAGCC TIGIGAGCAC AAGGCAGGAA GAGAATCCC CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCTGATGG AAATATAGCT GAGAGCTTI AGTCTTAGT TAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCTT TCCTAAAATT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTTGATTTC CCATCACC ACAGTAACTT TCATGACATA GGATTCTGCC GCCAAATTTA TAACATTAAC AATGTGGG ATTTCTAAGA ATGGAATTGT GGTATTTTTT TCTGTATTGA TTTTAACAGA AAATTTTCA TTATAGAGGT TAGGAATTCT GGTATTTTTT TCTGTATTGA TTTTTAATACA AAATTTTTC CTGTATTTGT AGCAATTATC AGGTTTGCTA GAAATTATAC TTTTTAATACA GTAGCCTAGAGAAAATTATCA AAAAAAACAC TCTTCCTATT GATAATTCAC CTCATGGGCC AAAATTTTAC AAATAAAACAC TCTTCCTATT GATAATTCAC CCCTAGGGCC AAAATTTTAC AAATAAAACCA TCTTCCTATT GATAATTCAC CCCTAGGGCC AAAATTTACA			C TOTAL TARGET	י השדמתהבת י	- AACTAGAAA	A AGAAAATTC	C GTGGATGITI	4320
ATCAGTTTCT CHACARAGE ATCCCCAGCC TIGTAGGCAC AGGCAGGAG GAGARTCC CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCTGATGG AAATATAGCT GAGAGCTT AGTCTTAGT THACACAGA AAGGGTGGG GGGACTCACA TCTGAGCAT GTTTTCCCC TCCTAAAATT AGGCAGGAAA ATCAGTCTAG TTCTGTATTC TGTTGATTC CCATCACC ACAGTAACTT TCATGACATA GGATTCTGC GCCAAATTTA TATCATTAAC AATGTGTGC TTTTTGCAAG ACTTGTAATT TACTATTAT GTTTGAACTA AAATGTTGA ATTTTACAGA AAATTTTACAGATTATAAC ATGGAATTCCA AAATTTATTAT TCTGTATTCA TTTTAACAGA AAATTTCAATTTATAACAG TAGGAATTCC AAACTACAGA AAATGTTTCT TTTTAATACA GTAGCCTG CTGTATTGT AGGAATTAC AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTG AAATAAACAC TCTTCCTATT GATATTCAAC ATTTTACACT TCCATGGACC AAATTTAT		A CONCOUNT	ሮ ሮአአሮአምሮልጥ	· AATCTCATCI	A GGCCAGGAG	r CTTTGCTGAG	ATTGAGCAGT	4380
CCACCICICI GGACAGIAAT GGTGCAGCAT TGCCTGATGG AAATATAGCT GAGACTITAGT TTAACACAGA AAGGGTGGG GGGACTCACA TCTGAGCATT GTTTCCTT TCCATAAATT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TCTTGATTC CCATCACC ACAGTAACT TCATGACATA GGATTCTGC GCCAAATTA TATCATTACA AATGTGTGG ATTTTTGCAG ACTTGTAATT TACTTATTAT GTTTGAACTA AAATGTATGA ATTTTTACAGA ATTTTTACAGA ATTTTTACAGAGT TAGGAATTC GAGATTTTT TCTGTATTGA TTTTAACAGA AAATTTCATTTTTATAGAGGT TAGGAATTC AAACTACAGA AAATTTCATTTTTTTTATAGAGGT TAGGAATTC AAACTACAGA AAATTTACAC TTTTAATACA GTAGCCTG CATGTATTTT TCTGTATTAT TCTTTAATACA GTAGCTG CATGTATTCAC TCTTCCTATT GATATTCACA ATTTTTACAC TCCATGTATTCA ACCTAAAGAG AAATTTATCAC TCCATGTACT CCCATGGACC AAATTTAT	75		TO CONTRACTO	ያ አጥርርጥር ል ርር	THYTYGAGCAI	: AAGGCAGGA	A GAGAATCCAT	4440
AGTOTTAGT THACACAGA AAGGGTGGG GGGACTCACA TOTGAGCATT GYTTTCACT TCCTAAAAT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTTGATTC CCATCACC ACAGTAACTI TCATGACATA GGATTCTGC GCCAAATTA TATCATTAAC AATGTGGG ATTTTTGCAGG ACTIGTAATT TACTTATTAT GTTTGAACTA AAATGATCA ATTTTACAGA ATTTTTAAGAGT TAGGAATTCT GGTATTTTT TCTGTATTGA TTTTAACAGA AAATTTCA TTATAGAGGT TAGGAATTCT AACTTACAGA AAATGTTCT TTTTAATACA GTAGCCTG CTGTATTTGT AGCAATTATC AGGTTTGCTA GAAATTATAC AATAAAACAC TCTTCCTATT GATATTCAAC ATTTTACAAC TCCGTGATCTC ACCTAAAG		CONTRACTOR CONTRACTOR	ም ሮሮስሮክሮሞሽል፣	r ርርፕርርእርርል	r TGCCTGATG	G AAATATAGC	r GAGAGCTTAG	4500
TCCTAAAATT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTTGATTAC CCATCACC ACAGTAACTT TCATGACATA GGATTCTGCC GCCAAATTTA TATCATTACA AATGGTGTG ACTITTGCAAG ACTIGTAATT TACCTATTAT GTTTGAACTA AAATGATTGA ATTTTCAAGA ATGGAATTAT GGTATTTTTT TCTGTATTGA TTTTAACAGA AAATTTTCATTTTTATAGAGGT TAGGAATTATC AAACTACAGA AAATGTTTGT TTTTAATACA GTAGCCTG CTGTATTTGT AGCAATTATC AGGTTTGCTA GAAATGAACA TTTTAATACA GTAGCCTG AATAAAACAC TCTTCCATAT GATATTCAAC ATTTTACAC TGCAGTATTC ACCTAAAG		A CONCRETER OF	ጥ ጥጥአአርክርክር	A AACCCCTTGG	GGGACTCAC	A TCTGAGCAT	r Greerer	4560
80 TITTIGCAG ACTIGIAATT TACTTATIAT GITTIGACTA AAATGATIGA ATTITACA ATTICTAAGA ATGGAATTGT GGTATTTTT TCTGTATTGA TITTAAGAGA AAATTTCA TTATAGAGGT TAGGAATTCC AAACTIACAGA AAATGATTCT TITTAGTGTC AAACTTATTT CTGTATTGT AGCAATTATC AGGTTTGCTA GAAATATAAC TITTAATACA GTAGCCTG AATAAAACAC TCTTCCTATT GATATTCAAC ATTITACAGA TGCAGTATATC ACCTAAAG 85		**************************************	T ACCCACCAA	A TCAGTCTAG	TTCTGTTAT	C TGTTGATTT	CCATCACCIG	4620 4680
ATTICTAAGA AIGGAATTGT GGTATTTTT TCTGTATTGA TTTTAACAGA AAATTTCTA TTATAGAGGT TAGGAATTCC AAACTACAGA AAATGTTGT TTTTAATACA GTAGCCTG CTGTATTTGT AGCAATTACA AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTG AATAAAACA TCTTCCTATT GATATTCAAC ATTITTACAAC TGCAGTATTC ACCTAAAG 85 **CONTRACTOR*** CTATATTATT CTABATACTG CCCTAGTGTC TCCATGGACC AAATTTATATTATTATTATTATTATTATTATTATTATTA	00	ACAGTAACT	T TCATGACAT	A GGATTCTGC	GUCAAATTI	A TATCATTAA	AMIGIGIGCC TOLOROPHIA A	4740
TTATAGAGGT TAGGAATTCC AAACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTCCCGTATTTGT AGCAATTACA AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCTTCAAAAAAAC TCTTCCATAT GATAATCAAC ATTTTACAAC TGCAGTATTC ACCTAAAG AAATTTATT	80	TTTTTGCAA	G ACTTGTAAT	T TACTTATIA	r GTTTGAACT	A AAAIGAIIG	TEATHTREE A	
CIGTATITGT AGCAATTATC AGGITTGCTA GAAATATAAC TITTAATACA GIAGCCIG AATAAAACAC TCITCCATAT GATATTCAAC ATTITACAAC TGCAGTATTC ACCTAAAG 85			ም ማእርርንአምምር	בסמדשממת יי	A AAATGTTTG	T TITTAGIGI	C AAATTTTTAG	4000
AATAAAACAC TCTTCCATAT GATATTCAAC ATTTTACAAC TGCAGGACC AAATTTAT		CONCRETE TOTAL	ጥ አብሮአክሞየልጥ	للتركي المستدين والم	A GAAATATAA	C TITTAATAC	a gragectigta	4920
X CARABANCE CONTACTOR GENERAL CONTACTOR CONTACTOR TOCATGGACC ARATTERIA		*******	C TOTOGRAPH	ተ ሮኔጥልጥሞሮልል።	C ATTTTACAA	C TGCAGTATT	C ACCIAAAGIA	4700
THE PARTY OF THE P	85	G111771177	سل لا بلماست لا بلماست بالم	רייים במערבייים ייי	CCCTAGIGI	C TCCATGGAC	C AAATTTATAT	5040
TTATAATTGT AGATTTTAT ATTITACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAAT		COURS OF A POPULAR OF THE PARTY	The Part of the Pa	T ATTTTACTA	C TGAGTCAAG	T TITCIAGIT	C TGTGTAATIG	2100
TITAGITTAA TGAOGTAGIT CATTAGCTGG TCTTACTCTA CCAGTTTTCT GACATTGT		TTTAGTTTA	A TGACGTAGT	T CATTAGCTG	G TCTTACTCT	A CCAGTTTTC	T GACATIGIAT	5160

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٥	AAATACCTTC ATGGTTTTTA	ATTTTGAAAG	AAGTTTTTAT TGCAAAAATA	GAGAATAACA	CCTTACCAAA	TGGAAAATAG CATTGTTCAA AAAAAAAAA	5280
5		186 Protein cession #: 1		•			
10	1	11	21	31	41	51	
10	LSILPEVGTE PCTDTVDWIV	HWGKCNMSSD ENLDPKAIID PKDTVSISES AVCSSEPENV	GVESVSRFGK QLAVFCEVLT	QAALDPFILL MQQSGYVMLM	NLLPNSTDKY DYLQNNFREQ	YIYNGSLTSP QYKFSRQVFS	60 120 180 240
15	PELIGTEEII TNRSPTRGSE NDGSKTVLRS	QDLGAILNNL KEREEGKDIE PSGKGDVPNT PHMNLSGTAE PSSENPETIT	EGAIVNPGRD SLNSTSQPVT SLNTVSITEY	SATNQIRKKE KLATEKDISL EEESLLTSPK	PQISTTTHYN TSQTVTELPP LDTGAEDSSG	RIGTKYNEAK HTVEGTSASL SSPATSAIPF	300 360 420 480 540
20	DITAQPDVGS PPTEVTPHAF IPLVIVSALT IPIKHFPKHV	GRESFLQTNY TPSSRQQDLV FICLVVLVGI ADLHASSGFT	TEIRVDESEK STVNVVYSQT LIYWRKCFQT BEFETLKEFY	TTKSFSAGPV TQPVYNEASN AHFYLEDSTS QEVQSCTVDL	MSQGPSVTDL SSHESRIGLA PRVISTPPTP GITADSSNHP	EMPHYSTFAY EGLESEKKAV IFPISDDVGA DNKHKNRYIN	600 660 720 780
25	NVEVIVMITN KGSQKGRPSG RTGTYIVLDS EVLDSHIHAY	LAQLAEKDGK LVEKGRRKCD RVVTQYHYTQ MLQQIQHEGT VNALLIPGPA	QYWPADGSER WPDMGVPEYS VNIFGPLKHI GKTKLEKQFQ	YGNFLVTQKS LPVLTFVRKA RSQRNYLVQT LLSQSNIQQS	VQVLAYYTVR AYAKRHAVGP EEQYVPIHDT DYSAALKQCN	NFTLRNTKIK VVVHCSAGVG LVEAILSKET REKNRTSSII	940 900 960 1020 1080
30	VMIPDGQNMA YVLEVRHFQC	SLEGEGTDY I EDEFVYWPNK PKWPNPDSPI VDVYQVAKMI ESLESLV	DEPINCESFK SKTPELISVI	VTLMAEEHKC KEEAANRDGP	LSNEEKL11Q MIVHDEHGGV	DFILEATQDD TAGTFCALTT	1140 1200 1260 1320
35	Nucleic Act	187 DNA sec id Accession Lence: 148-4	#: EOS sec	Meuce			
40	1	11	21	31	41	51	
40	CAAAAAAAAC	CACGCACGAT ATTTCCTTCG CCGCAGACCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	60 120 180
45	CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG	GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC	CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA	GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT	ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC	ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA	240 300 360 420 480
50	GTCAGCGGAG AAATGCAATA GAGATGCAAA GGAAAAGGGA	GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA	AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT	AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAGG	AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA	TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG	540 600 660 720 780
55	TTAGATCCAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG	TCATACTGTT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTTC	GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACTTA	CCAAACTCAA GACACAGTTG GTTTTTTGTG CAAAACAATT	CTGACAAGTA ACTGGATTGT AAGTTCTTAC TTCGAGAGCA	TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG	840 900 960 1020 1080
60	AGTTCAGAAC TGGGAAAGAC CAGTTGGATG GGTGCTATTC TGCACTAATG	CAGAAAATGT CTCGAGTCGT GAGAGGACCA TCAATAATTT GCTTATATGG	TCAGGCTGAC TTATGATACC AACCAAGCAT GCTACCCAAT AAAATACAGC	CCAGAGAATT ATGATTGAGA GAATTTTTGA ATGAGTTATG GACCAACTGA	ATACCAGCCT AGTTTGCAGT CAGATGGCTA TTCTTCAGAT TTGTCGACAT	TCTTGTTACA TTTGTACCAG TCAAGACTTG AGTAGCCATA GCCTACTGAT	
65	GAAGAGGGAA AACCAAATCA ACGAAATACA	AAGACATTGA GGAAAAAGGA ATGAAGCCAA	AGAAGGCGCT ACCCCAGATT GACTAACCGA	ATTGTGAATC TCTACCACAA TCCCCAACAA	CTGGTAGAGA CACACTACAA GAGGAAGTGA	CAAGGAGGAG CAGTGCTACA TOGCATAGGG ATTCTCTGGA TAAATTAGCC	1500 1560 1620
70	GAAGGTACTT AACTTGTCGG AGTTTATTGA	CAGCCTCTTT GGACTGCAGA CCAGTTTCAA	AAATGATGGC ATCCTTAAAT GCTTGATACT	TCTAAAACTG ACAGTTTCTA GGAGCTGAAG	TTCTTAGATC TAACAGAATA ATTCTTCAGG	TCACACTGTG TCCACATATG TGAGGAGGAG CTCCAGTCCC ATTTTCCTCC	1800 1860 1920
75	GAAAACCCAG GAAGATTCAA GTGTGGTTTC AGCTTTCTCC	AGACAATAAC CTTCATCAGG CTAGCTCTAC AGACTAATTA	ATATGATGTC TTCAGAAGAA AGACATAACA CACTGAGATA	CTTATACCAG TCACTAAAGG GCACAGCCCG CGTGTTGATG	AATCTGCTAG ATCCTTCTAT ATGTTGGATC AATCTGAGAA	AAATGCTTCC GGAGGGAAAT AGGCAGAGAG GACAACCAAG GGAAATGCCA	2040 2100 2160 2220
80	CATTATTCTA TCCAGACAAC GTATACAATG	CCTTTGCCTA AGGATTTGGT AGGCCAGTAA	CTTCCCAACT CTCCACGGTC TAGTAGCCAT	GAGGTAACAC AACGTGGTAT GAGTCTCGTA	CTCATGCTTT ACTCGCAGAC TTGGTCTAGC	TACCCCATCC AACCCAACCG TGAGGGGTTG	2340 2400 2460
85	CTAGTGGTTC TACTTAGAGG ATTTCAGATG CATGCAAGTA	TTGTGGGTAT ACAGTACATC ATGTCGGAGC GTGGGTTTAC	TCTCATCTAC CCCTAGAGTT AATTCCAATA TGAAGAATTT	TGGAGGAAAT ATATCCACAC AAGCACTTTC GAGACACTGA	GCTTCCAGAC CTCCAACACC CAAAGCATGT AAGAGTTTTA	TTTTATCTGT TGCACACTTT TATCTTTCCA TGCAGATTTA CCAGGAAGTG AGACAACAAG	2580 2640 2700 2760

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                                                                                         3120
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                                                                                         3240
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                                                                                         3720
                                                                                         3780
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                                                                                         3960
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                                                                                         4020
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        CATANTECCC AACTGGTGGT TATGATTCCT GATGGCCAAA ACATGGCAGA AGATGAATTT
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                                                                                         4260
25
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        TTCTGTGCTC TGACAACCCT TATGCACCAA CTAGAAAAAG AAAATTCCGT GGATGTTTAC
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                                                                                         5340
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                                                                                         5400
        5460
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        Seq ID NO: 188 Protein sequence:
        Protein Accession #: BOS sequence
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        MRILKRPLAC IQLLCVCRLD WANGYYROOR KLVEEIGWSY TGALNOKNWG KKYPTCNSPK
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                                                                                           420
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65
         IKHFPKHVAD LHASSGFTEE PETLKEFYQE VQSCTVDLGI TADSSNHPDN KHKNRYINIV
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EVIVMITNLV EKGRRKCDQY WPADGSEEYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG
                                                                                           960
                                                                                         1020
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                                                                                         1260
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                                                                                    540
                                                                                    600
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                                                                                     1500
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			ACAAAATTTT				5760
	COMPANION	moore a mos o	CCTGCACATT	mcammora a a	TO CONTRACT TO THE	AMERICAN V V V V	5820
	GGTACAATGC	TCCCAATCAC	CCIGCACATI	IGATICIAAA	IGGCITTIAL	111111111111111111111111111111111111111	
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85	MUNUL LUNUM		Warretting	CULCITION	CULTURAL	COMPOSITION TO THE	0000
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WO 02/086443
         MPALMLGCCL CYSLLLPAAR ATSRREVCDC NGKSRQCIFD RELHRQTGNG FRCLNCNDNT
         DGIHCEKCKN GFYRHRERDR CLPCNONSKG SLSARCDNSG RCSCKPGVTG ARCDRCLPGF
                                                                                           120
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                                                                                           600
         NCEHGAFSCP ACYNOVKIOM DOPNOOLORM EALISKAOGG DGVVPDTELE GRMOOAEOAL
                                                                                           660
         QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTE
                                                                                            720
         RLITOMOLSL AESEASLENT NIPASDHYVG PNGFKSLAGE ATRLAESHVE SASNMEQLTR
                                                                                            780
         ETEDYSKOAL SLVRKALHEG VGSGSGSPDG AVVQGLVEKL EKTKSLAQQL TREATQABIE
                                                                                           840
15
        ADRSYQHSLR LLDSVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTREND EFKRTQKNLG
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                                                                                           900
                                                                                           960
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                                                                                          1080
        AQKVDTRAKN AGVTIQDTLN TLDGLLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP
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                                                 31
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                                                                                            360
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                                                                                           540
                                                                                           600
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                                                                                            660
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                                                                                          1020
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                                                                                          1080
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                                                                                          1440
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                                                                                          1680
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                                                                                          1740
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                                                                                          2160
        AGAAAAAAA AAAAAAA
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        Protein Accession #: NP_057613
                                   21
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70
        MSVIVETPSG RERLYCKGAD NVIFERESKD SKYMEETECH LEYPATEGER TECVAYADES
        ENEYEWLKY YQEASTILKD RAQRLEECYE IIEKNLLLLG ATAIEDRIQA GYPETIATLL
                                                                                           120
        KABIKIWULT GDKQETAINI GYSCRLVSQN MALILLKEDS LDATRAAITQ HCTDLGNLLG
         KENDVALIID GHTLKYALSP EVRRSFLDLA LSCKAVICCR VSPLQKSEIV DVVKKRVKAI
                                                                                           240
75
        TLAIGDGAND VGMIQTAHVG VGISGNEGMQ ATMNSDYAIA QFSYLEKLLL VHGAWSYNRV
TKCILYCFYK NVVLYIIELW FAFVNGFSGQ ILFERWCIGL YNVIFTALPP FTLGIFERSC
TQESMLRPPQ LYKITQNGEG FNTKVFWGHC INALVHSLIL PWPPMKALEH DTVFDSGHAT
                                                                                           300
                                                                                           360
                                                                                            420
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                                                                                           480
        PDMRGQATMV LSSAHFWLGL FLYPTACLIE DVAWRAAKHT CKKTLLEEVQ ELETKSRVLG
KAVLRDSNGK RLNERDRLIK RLGRKTPPTL PRGSSLQQGV PHGYAPSQEE HGAVSQEEVI
                                                                                           540
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        Nucleic Acid Accession #: BC017001
85
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                                                              41
                                                                           51
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WO 02/086443 PCT/US02/12476 AACSCTGGGC AGGGCCGGCG CGGGTCGGGG GGCCCCGAG GGGCCCGGGC CGAGCGGCGG OGOGCAGGGC GGCAGCATCC ACTOGGGCCG CATOGCOGCG GTGCACAACG TGCCGCTGAG 120 CGTGCTCATC CGGCCGCTGC CGTCCGTGTT GGACCCCGCC AAGGTGCAGA GCCTCGTGGA 180 CACGATCOGG GAGGACCCAG ACAGOGTGCC CCCCATOGAT GTCCTCTGGA TCAAAGGGGC CCAGGGAGGT GACTACTTCT ACTCCTTTGG GGGCTGCCAC CGCTACGCGG CCTACCAGCA 300 ACTGCAGOGA GAGACCATCC CCGCCAAGCT TGTCCAGTCC ACTCTCTCAG ACCTAAGGGT 360 GTACCTGGGA GCATCCACAC CAGACTTGCA GTAGCAGCCT CCTTGGCACC TGCTGCCACC 420 TTCAAGAGCC CAGAAGACAC ACCTGGCCTC CAGCAGGCTG GGCCATGCAG AAGGGATAGC 480 AGGGTGCAT TCTCTTTGCA CCTGGCGAGA GGGTCTGACT CTGGGCACCC CTCTCACCGG CTACAAGGCC TTGGACTCAC TGTACAGTGT GGGAGCCCCA GTTCCCACCT CTGTGACAAT 10 600 AGGATCATGG CCTTACCCTT GAAGCATTAC CGAGAAGGAG AACAGAGATG GGCTTGAAGA 660 GCCACGTGCT GCCGGCTCCA AATTCCCAAG GACAAGGATC CCTCTGCATT TTTGTCTATG 720 TAAACAAACA GAAGATTGTT TTTCCACATA GCATGGATTC TGGAGATGGG TGGCTAATGG 840 15 TATTGGTTCA ACAACTCCAC GGAGGTAGGG GTCACGTCTT GGATCCTTTT GCCTTAATCT 900 CAGTGCTCGT TACTTCATGG TCCCAAGATG GCTGCTGTAT CCCCAAGAAT CATGTCTGCG 960 TTCAAGGAAG GAGGGTGGA GGAAGAGGAA GGGCCAAACT AGCTGGACCC GTCACCTTCT ATCAGAAAGT AAAACCTCGT CAGAAGTCTG TTTCCTGCTC TCTCCCTCTG CATATCTTCA 1080 20 CTTAGATGCC CTTGGCCCGA GCCAGCTACC ATTGCACCTC TAGCTGCAAA CAAAGCTAAG 1140 ACAGCAGGGA ACAGAATTGT CATGGCTGAA TAGACCAATC GTGTTCCATC TACTGAGACT 1200 GGCACACTGC CTCCTGCAAT AAAACTGGGA TCCCATTACC AAGAGAGAAA TGCAGAATTG 1260 TGTACCAGTT AGCTTTTGCT GTGTAACAAA CCATCCCCAA ACTTGGCAGC TAGAAACAAA 1320 CCCTGTATTT TCCCACAATC CTATGGGTTG GCAATTTGGG CTGGGCTCAA CAGGGCAGTT 1380 CTGCTGCTCA CACCTGGGAT CCCTCATGGA GCTAAGGTCA GCTGTTACCT CAGCTGGGCC 25 1440 TGGATGGTCT AGGATAGCCT TACTCACTTG CCTGGCAGGT GACAGGCTGT TGGCTGGAAT 1500 TECTTEGTTC TCCTCCATGT GECCTCTCCA GCAGGCTAGC TCAGGCTTAT TCACATGATG 1560 GCTTCAGGAT TCCAAAGAGA GTGAGAGTAG AAGCTGAAAG ACTTCTTGAG TTCTTGGCCT GGAACTGGGA CTAGGACAGT GTCACTTCTG CTAAGTTCTT TTGGTCAGAG CAAATCACAA GGCTTTACCC AGATTCAAGG GATGAGAAAC AGACTACATG TCTTGATGAG GGGAACCACA 1620 1680 30 AAGAGCTTGT GGCCATTTTT CACCTATCAC AAATAATTTT GGATGGGTAT TTATTTGGAT 1800 AAAGGTATTT CCCTCTTCCC CCTTTCTCTC TGTCTCATGG GGCCTCACTC TGCCAAGTTG 1860 GAAGGCACTA AGACATTOTC CTGGCCCTCA GGGTCTAGGG GAAGAGGTGT TGGGGCAGGA 1920 AGTGAGTCTC TCCATGGGCT GGACCCACTG TAGTAGGAGT GCCTCCTTGT CTGCACTGCT
GGTATGGGGT TAGGCCAGGT AGGACATTCC AGAGGGGGCTT CTGAAAACCA AGAGTCCCTG 35 2040 GGGAAAGGGA ACAGAGTAAG GCAGGCCTTG TTCTCACTGC CCTCTAAGGG AACTTGGTCA 2100 CTCGGCACTT TTAAGCCTCA GTTTCTCCAG TTCAATAATA AGGACAAGAG CTTTTCCCAT GCATTCTCTT TCCCCGGGAA AGTTGACTGA GGTGACCAGT AATAGAATTG AAAAGGGAGA 2160 GTGTCTTCAG TGCAATGTGG CATCCTGGAT TGGGTCTTGG AACAAAAACA GGACATTAGT 2280 40 GGGAAAATTG GAAATCTGAA AAAAGTCTGA ATTTTAGTTA ATATACCAAT TTCAGTCTCT. 2340 TGGTTTTGAC AGATGTACCA TGGTGATGTA AGATGTTGAC CTTGGGGTAG GCTGGGTGAA 2400 45 Seq ID NO: 224 Protein sequence: Protein Accession #: AAH17001.1 51 41 50 TLGRAGAGRG APEGPGPSGG AQGGSIHSGR IAAVHNVPLS VLIRPLPSVL DPAKVQSLVD TIREDPDSVP PIDVLWIKGA QGGDYFYSFG GCHRYAAYQQ LQRBTIPAKL VQSTLSDLRV 120 55 Seg ID NO: 225 DNA seguence Nucleic Acid Accession #: NM_021048 Coding sequence: 1..1110 60 21 31 41 11 ATGCCTCGAG CTCCAAAGCG TCAGCGCTGC ATGCCTGAAG AAGATCTTCA ATCCCAAAGT GAGACACAGG GCCTCGAGGG TGCACAGGCT CCCCTGGCTG TGGAGGAGGA TGCTTCATCA 120 TOCACTTCCA CCAGCTCCTC TTTTCCATCC TCTTTTCCCT CCTCCTCCTC TTCCTCCTCC 180 TOCTOCTGCT ATCCTCTAAT ACCAAGCACC CCAGAGGAGG TTTCTGCTGA TGATGAGACA CCAAATCCTC CCCAGAGTGC TCAGATAGCC TGCTCCTCC CCTCGGTCGT TGCTTCCCTT CCATTAGATC AATCTGATGA GGGCTCCAGC AGCCAAAAGG AGGAGAGTCC AAGCACCCTA 65 240 300 360 CAGGTCCTGC CAGACAGTGA GTCTTTACCC AGAAGTGAGA TAGATGAAAA GGTGACTGAT 420 TTGGTGCAGT TTCTGCTCTT CAAGTATCAA ATGAAGGAGC CGATCACAAA GGCAGAAATA CTGGAGGAGTG TCATAAAAAA TTATGAAGAC CACTTCCCTT TGTTGTTTAG TGAAGCCTCC GAGTGCATGC TGCTGGTCTT TGGCATTGAT GTAAAGGAAG TGGATCCCAC TGGCCACTCC 480 70 540 600 TTTGTCCTTG TCACCTCCCT GGGCCTCACC TATGATGGGA TGCTGAGTGA TGTCCAGAGC 660 ATGCCCAAGA CTGGCATTCT CATACTTATC CTAAGCATAA TCTTCATAGA GGGCTACTGC 720 ACCCCTGAGG AGGTCATCTG GGAAGCACTG AATATGATGG GGCTGTATGA TGGGATGGAG 780 75 CACCTCATTT ATGGGGAGCC CAGGAAGCTG CTCACCCAAG ATTGGGTGCA GGAAAACTAC 840 CTGGAGTACC GGCAGGTGCC TGGCAGTGAT CCTGCACGGT ATGAGTTTCT GTGGGGTCCA 900 AGGECTCATE CTGARATTAG GAAGATGAGT CTCCTGARAT TITTGGCCAR GGTRARATGG AGTGATCCAR GATCCTTCCC ACTGTGGTAT GAGGAGGCTT TGARAGATGA GGARGAGAGA 960 GCCCAGGACA GAATTGCCAC CACAGATGAT ACTACTGCCA TGGCCAGTGC AAGTTCTAGC 1080 80 GCTACAGGTA GCTTCTCCTA CCCTGAATAA Seq ID NO: 226 Protein sequence: Protein Accession #: NP 066386 85 31 41 MPRAPKRORC MPEEDLOSOS ETOGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSSS

5	SSCYPLIPST QVLPDSESLP ECMLLVFGID TPEEVIWEAL	RSBIDEKVTD VKEVDPTGHS NMKGLYDGME	LVQPLLFKYQ FVLVTSLGLT HLIYGEPRKL	LTQDWVQENY	LESVIKNYED MPKTGILILI LEYRQVPGSD		120 180 240 300 360
10	Nucleic Ac	227 DNA seid Accessionuence: 82-1	#: NM_005	025.1			
	1	11	21	31	41	51	
		(POTTONIA)	CACAACCTCC	AGCATCCCGT	CACCCCTTCC	l Concinciaco	60
15				CTTGGACTCT			120
	AGTATGGCTA	CAGGGGCCAC	TTTCCCTGAG	GAAGCCATTG	CTGACTTGTC	AGTGAATATG	180
				GAAAATATTC			240
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20				TATGTGATGA			420
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				AATGTAGCCG			540
				AAAGATTTGG GTCTATTTCA			600 660
25				TTCACTAAAG			720
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				ATACCATATG			840
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						CATGGGACGA	1260
35	GTCATGCATC	CTGAAACAAT	GAACACAAGT	GGACATGATT	TCGAAGAACT	TTAAGTTACT	1320
				AGCACATTAT			1380
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40				TTAAAATAAA			
40		228 Protein	-				
	PIOCEIN ACC	-cooron &	15_003010.1				
15	1	11	21	31	41	51	•
45	1	1	1	1	1	1	
45	 Maplglpsll	 VLQSMATGAT	 PPEEAIADLS	31 VNMYNRLRAT KEFSNMVTAK	 GEDENILPSP	 LSIALAMGMM	60 120
45	 MAPLGLPSLL ELGAQGSTQK NEEPLQMMKK	VLQSMATGAT EIRHSMGYDS YFNAAVNHVD	 PPEEALADLS LKNGEEFSFL FSQNVAVANY	 VNMYNRLRAT KEFSNMVTAK INKWVENNTN	 GEDENILPSP ESQYVMKIAN NLVKDLVSPR	LSIALAMGMM SLFVQNGFHV DFDAATYLAL	120 180
	 MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW	VLQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR	 PPEEAIADLS LKNGEEPSFL FSQNVAVANY TFSFTKDDES	VNMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ	 GEDENILPSP ESQYVMKIAN NLVKDLVSPR GEFYYGEFSD	LSIALAMGMM SLFVQNGFHV DFDAATYLAL GSNEAGGIYQ	120 180 240
45 50	MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL	VLQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR ISMMLVLSRQ GITEIFIKDA	PPEEALADLS LKNGEEFSPL FSQNVAVANY TFSFTKDDES EVPLATLEPL NLTGLSDNKE	 VNMYNRLRAT KEFSNMVTAK INKWVENNTN	GEDENILPSP ESQYVMKIAN NLVKDLVSPR GEPYYGEPSD NSVKKQKVEV FLEVNEEGSE	LSIALAMGMM SLFVQNGFHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQE	120 180
	 MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac:	ULQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Bed	PPERAIADLS LKNGEEFSFL FSQNVAVANY TFSFTKODES EVPLATLEPL NLTGLSDNKE RNRRTGTILF LLENCE ##: NM_0030	 VNMYNRLRAT KEFSNMVTAK KINKWENNTN EVQIPMMYQQ VKAQLVEEWA IFLSKAIHKS MGRVMEPETM	GEDENILPSP ESQYVMKIAN NLVKDLVSPR GEPYYGEPSD NSVKKQKVEV FLEVNEEGSE	LSIALAMGMM SLFVQNGFHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQE	120 180 240 300
50	MAPIGIPSLL ELGAQGSTQK NEEPIQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequ	VLQSMATGAT VLQSMATGAT VLQSMATGAT VSMIVUSRQ GITEIPIKDA IVDHPPPFLI 229 DNA Bed Accession Lence: 12-39	 PPEEAIADLS LKNGEEPSPL FSQNVAVANY TFSPTKDDES EVPLATLEPL NLTGLSDNKE RNRRTGTILF PLENCE 4 #: NM_0030	VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IFLSKAIHKS MGRVMEPETM	GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFERL	 LSIALAMGMM SLFYQNGFHV DFDAATTLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI	120 180 240 300
50 55	 MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac:	ULQSMATGAT VIQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA sec	PPERAIADLS LKNGEEFSFL FSQNVAVANY TFSFTKODES EVPLATLEPL NLTGLSDNKE RNRRTGTILF LLENCE ##: NM_0030	 VNMYNRLRAT KEFSNMVTAK KINKWENNTN EVQIPMMYQQ VKAQLVEEWA IFLSKAIHKS MGRVMEPETM	GEDENILPSP ESQYVMKIAN NLVKDLVSPR GEPYYGEPSD NSVKKQKVEV FLEVNEEGSE	LSIALAMGMM SLFVQNGFHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQE	120 180 240 300
50	 MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIFYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequ	ULQSMATGAT VLQSMATGAT EIRESMGYDS YFNAAVNHVD KSQFRPENTR ISMALVLSRQ GITEIPIKDA IVDHPPFPLI 229 DNA Sec d Accession ence: 12-39	FPEEAIADLS FPEEAIADLS LKNGEEPSFL FSQNVAVANY TFSFTKDDES EVPLATLEPL NUTGLSDMKE RNRRTGTILF TUENCE 1 #: NM_0030 8	VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IFLSKAIHKS MGRVMEPETM	GEDENILFSP GEDENILFSP ESQYYMKIAN MINKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL	LSIALAMGMM SLFVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI	120 180 240 300
50 55	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequ 1 CGACATCAGA CAGCCCTTAC	ULQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFRPENTR ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Bedd Accessionence: 12-3: 11 GATGAGGACA CCTGCGGCTGC	FPEEAIADLS LKNGEEFSFL LKNGEEFSFL FSQNVAVANY TFSFTKDDES EVPLATLEPL NLTGLSDMKE RNRRTGTILF Puence #: NM_00308	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 595 31 TCCTTGCAGC CCAGCTCCAG	GEDENILPSP GEGYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV PLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG	LSIALAMGMM SLIFVQNGFBV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG	120 180 240 300 360
50 55	MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequ 1 GSACATCAGA CAGCCTTAC TCTGCCCGGC	ULQSMATGAT VLQSMATGAT VLQSMATGAT VFNAAVNHVD KSQFPENTT ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Bee 1d Accession Dence: 12-39 11 GATGAGGACA CCTGCGCTGC CAGCTCTCGC	FPEEAIADLS FPEEAIADLS LKNGEEPFFL FSQNVAVANY TFSFTKDDES EVPLATLEPL NLTGLSDNKE RNRRTGTILF THENCE 1 #: NM_0031 8 21 GCATTGCTGC CACGTGTGCA TTCTGCAAGA	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IFLSKAIHKS MGRVMEPETM 595 31 TCCTTGCAGC CCAGCTCCAG CCACGAACAC	GEDENILPSP GEDENILPSP ESQYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT	LSIALAMGMM LSIALAMGMM SLPYQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTCTGG CTGAGGGGGA	120 180 240 300 360 60 120 180
50 55 60	MAPLGLFSLL ELGAQGSTQK NEEPLQMMKK INAVYPKGNW VLEIPYEGDB IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding Bequ 1 GACATCAGA CAGCCTTAC TCTGCCGGC ATCTGGTGAA	ULQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR ISMULVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Bed d Accession ence: 12-39 11 GATGAGGACA CCTGCGCTGC CAGCTCTCGC GAAGGACTGT		VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 595 31 TCCTTGCAGC CCAGGCTCAGG CCACGACAC GCACCACAG GCACCACAG	GEDENILFSP GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG	LSIALAMGMM LSIALAMGMM SIPVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG CTGACGGGGA CAAGGCCAGG	120 180 240 300 360
50 55	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequil CGACATCAGA CAGCCCTTAC TCTGCCCGGC ATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	ULQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFPENTT ISMMLVLSRQ GITEIFIKDA IVDHPPFFLI 229 DNA Bee 1d Accession Lence: 12-39 11 GATGAGGACA CCTGCGCTGC CAGCTCTCGC GAAGGACTGT CAGCCAGCTCC ACCCACCCGC ACCCACCCGC	FPEEAIADLS FPEEAIADLS LKNGEEFSFL FSQNVAVANY TFSFTKDDES EVPLATLEPL NLTGLSDNKE RNRRTGTILF JUENCE #: NM_0036 8 21 GCATTGCTGC CACGTGTGCA TTCTGCAAGA GCGAGTGT ACCGCCTCG ACCGCCTCG	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEM IPLSKAIHKS MGRVMEPETM 395 31 TCCTTGCAGC CCAGCTCCAG CCACGAACAC GCACACCCAG GCCAGGAGGA CCCAGGAGGA CCCAGGAGGA CCCACGAGGGC CCCACGGGGCCCCAGGCCCAGGCCCAGGCCCAGGCCCAGGCCCAG	GEDENILPSP GEDYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDPEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGTGCAAT CCTCAGCCTG	LSIALAMGMM LSIALAMGMM SLIPVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRPTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTTGG CTGAGGGGGA CAAGGCCAGG GAGAAGCTGC GGGCTGGCCC	120 180 240 300 360 60 120 180 240
50 55 60	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequipulation of the coding sequi	ULQSMATGAT EIRESMGYDS YFNAAVNHVD KSQFRPENTR ISMALVLSRQ GITEIPIKDA IVDHPPFPLI 229 DNA Bed d Accession DEDCe: 12-39 11 GATGAGGACA CCTGCGCTGC CAGCTCTCGC GAAGGACTGT CACCAGCTCC ACCCACCGC GCCGTCACCG GGCCGTCATC	FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL NUTCLSOMKE RNRRTGTILF TUENCE 1 #: NM_003(8 21 GCATTGCTGC CACGTGTGCA GCGAGTGGCA ACCCAGTGCT ACCCAGTGCT ACCCAGTGCT TTAGCCCCCCA	VMMYNRLRAT VMMYNRLRAT KEFSMMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMEPETM 595 31 TCCTTGCAGC CCAGCTCCAG CCACGCTCCAG GCCACGACAC GCACACCCAG GCCACAGAGGA GCCACACAGGC GCCTGTGACC	GEDENILFSP GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGTGCAAT TCTCCAGCCTG	LSIALAMGMM LSIALAMGMM SIFVQNGFHV DFDAATTLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG CTGAGGGGAAGGCCCG GGGAGGCCCC GGAAGGCCCC	120 180 240 300 360 60 120 180 240 300 360 420
50 55 60	MAPLGLPSLL ELGAQGSTQK NEEPLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequity Carcada Cagccttac TCTGCCCGGC ATCTGGTGAA TCAGCAGCGG ACAACGCTGC TGAGCCTCTT TCATGCCTTT	ULQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFRPENTR ISMMIVUSRQ GITEIFIKDA IVDHPPFPLI 229 DNA sec dd Accession ence: 12-39 dence: 12-39 carcacacacacacacacacacacacacacacacacaca	FPEEAIADLS FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL NLTGLSDNKE RNRRTGTILF PLENCE 1 #: NM_0030 8 21 GCATTGCTGC CACGTGTGCA TTCTGCAAGA GCGGAGTGT ACCAGTGCT ACCAGTGCT ACCAGTGCT ACCAGTGCT ACCAGTGCT ACCAGGGCT CTCTGGGGAT	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IFLSKAIHKS MGRVMHPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGACAC GCCACACCAG GCCACAGGAGGA GCCACAGGAGGA GCCACAGGAGGA CCACACAGGACCAC TCCACACACTC TCCACACCTC TCCACACCTC	GEDENILFSP GEDENILFSP ESQYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGTGCAAT CCTCAGCCTG TTOCCCCAG	LSIALAMGMM LSIALAMGMM SIFVQNGFBV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGGG CTGAGGGGGA CAGGCCCC GGGAAGGCCCC CCGGCAACGG	120 180 240 300 360 60 120 180 240 300 360 420 480
50 55 60 65	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Accoding sequit Cagacataa Cagacataa Tagacagaa Atagaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	ULQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFRENTR ISMMLVLSRQ GITEIFIKDA IVDHPPFPLI 229 DNA Bee Ld Accession Lence: 12-3: 11 GATGAGGACA CCTGGCTGC CAGCTCTGC GAAGGACTGT CACCAGCTCC ACCCACCGG GGCGTCATC CCTTCCCTTT AGCCCCAGGC	FPEEAIADLS FPEEAIADLS FRONAVANY TFSFTKDDES EVPLATLEPL NLTGLSDMKE RNRRTGTILF TUENCE 1 #: NM_0030 8 21 GCATTGCTGC CACGTGTGCA TTCTGCAAGA GCGGAGTGGT ACCCAGTGCT ACCGCTCG TTAGCCCCCA CTCTGGGGATT TGAGGGCTTCT	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 395 31 TCCTTGCAGC CCAGCTCCAG CCACGACACC GCACACCCAG GCCAGGAGGA CCCACGAGGGG CCCACAGTGC CCCGACACCC CCCCCCCCCC	GEDENILPSP GEDYMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGTGCAAT CCTCAGCCTG TCTCCCCCAG TGGGACCAGG	LSIALAMGMM LSIALAMGMM SIFVQNGFHV DFDAATTLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG CTGAGGGGAAGGCCCG GGGAGGCCCC GGAAGGCCCC	120 180 240 300 360 60 120 180 240 300 360 420
50 55 60	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding Bequit Cascataga Cascataga Cascataga Tasgaacga Attegtga Tasgacga Tasgaacga Tasgaacga Tasgaacga Casgaacga Catgaatga Casagaacga Catgaatga Caagaacga Catgaatga Caagaagaaca Nasagaaca Caagaagaaca Caagaagaaca Caagaagaaca Caagaagaaca Caagaagaaca Nasagaaca N	ULQSMATGAT EIRHSMGYDS YFNAAVNHVD KSQFRPENTR ISMULVLSRQ GITEIPIKDA IVDHPFFPLI 229 DNA Bed d Accession Dence: 12-39 11 GATGAGGACA CCTGCGCTGC GAAGGACTGT CACCAGCTCT CACCAGCTCT CACCAGCTCC CACCCCC GGCCGTCATC CCTTCCCTTT AGCCCCAGGC CGTGCCCAGC CGTGCCCAGGC CGGCCGTCATC CCTTCCCTTT CAGCCCCAGC	FPEEAIADLS FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL INTEGEO ##: NM_0030 8 21 GCATTGCTGC CACGTGTGCA GCCAGTGTGCA GCCAGTGCT ACCCAGTGCT ACCCAGTGCT TTAGCCCCCC CTCTGGGGAT TGAGGGCTTC CTGGGGAT TGAGGGCTCC CTCTGGGGAT CGAGGGCCCC CTCCATGGAA	VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGACAC GCACACCCAG GCCACAGAGGG GCCAGAGGGG GCCAGGAGGC CCACGAGGGC CCCGGAAGTC CCCGGAAGTC CCCGGAAGTC CCACACCCC	GEDENILFSP GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG ASTGGAGCCT CTACACCTG CCTGGCATT CCTCAGCCTG TCCCCCAG TCTCCCCAG TCTCCCCAG ACGGACAGAGAGAGAGAGATG ACGAAGGATG	LSIALAMGMM LSIALAMGMM SIPVQNGPHV DFDAATTLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG CTGAGGGGAA CAAGGCCAGG GGGAAGGCCCC CCGGCAACGG TCCAGGTGGG TCCAGGTGGG TCCAGGTGGG TCCAGGTGGG AAGCCCCC TGGATCCCCG TGGATCCCCG	120 180 240 300 360 120 120 240 300 360 420 480 540 600 660
50 55 60 65	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding Bequit Cascataga Cascataga Cascataga Tasgaacga Attegtga Tasgacga Tasgaacga Tasgaacga Tasgaacga Casgaacga Catgaatga Casagaacga Catgaatga Caagaacga Catgaatga Caagaagaaca Nasagaaca Caagaagaaca Caagaagaaca Caagaagaaca Caagaagaaca Caagaagaaca Nasagaaca N	VLQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFRPENTR ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Beeld Accessionence: 12-3: 11 GATGAGGACA CCTGCGTGC CAGCTCTGC GAGGACTGT CACCAGCTCC ACCACCGC GGCGTCATC CCTTCCCTTT AGCCCCAGGC TGATGACTTG CAGCCCCCAGG TGATGACTTG TGATGACTTG TGATGACTTG TCAGCCCCCAGG TCATCTCTTTT	FPEEAIADLS FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL INTEGEO ##: NM_0030 8 21 GCATTGCTGC CACGTGTGCA GCCAGTGTGCA GCCAGTGCT ACCCAGTGCT ACCCAGTGCT TTAGCCCCCC CTCTGGGGAT TGAGGGCTTC CTGGGGAT TGAGGGCTCC CTCTGGGGAT CGAGGGCCCC CTCCATGGAA	VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGACAC GCACACCCAG GCCACAGAGGG GCCAGAGGGG GCCAGGAGGC CCACGAGGGC CCCGGAAGTC CCCGGAAGTC CCCGGAAGTC CCACACCCC	GEDENILFSP GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG ASTGGAGCCT CTACACCTG CCTGGCATT CCTCAGCCTG TCCCCCAG TCTCCCCAG TCTCCCCAG ACGGACAGAGAGAGAGAGATG ACGAAGGATG	LSIALAMGMM LSIALAMGMM SLIPVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTTCTGG CTGAGGGGGA CAAGGCCAGG GAGAAGCTGC GGGCTGGCCC CGGCAACGG TCCAGGTGGG AAGGCCCC CCGGCAACGG AAGGCCCC CCGGCAACGG AAGGCCCC	120 180 240 300 360 120 180 240 306 420 480 540 600
50 55 60 65	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Accoding sequitary of the sequence of the se	VLQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFRENTR ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Beed d Accession ence: 12-3: 11 GATGAGGACA CCTGCGCTGC CAGCTCTGC GAGGACTGT CACCAGCTCC ACCACCGC GCCGTCATC CCTCCCTTT AGCCCAGGC TCATTCTGTT AAACC 230 Protein	FPEEAIADLS FPEEAIADLS FROM NAVANY TESTINDES EVPLATLEPL NLTGLSDMKE RNRRTGTILF PLEASE FROM NAVANY TESTINDES FOR NAVANY TEST	VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGACAC GCACACCCAG GCCACAGAGGG GCCAGAGGGG GCCAGGAGGC CCACGAGGGC CCCGGAAGTC CCCGGAAGTC CCCGGAAGTC CCACACCCC	GEDENILFSP GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG ASTGGAGCCT CTACACCTG CCTGGCATT CCTCAGCCTG TCCCCCAG TCTCCCCAG TCTCCCCAG ACGGACAGAGAGAGAGAGATG ACGAAGGATG	LSIALAMGMM LSIALAMGMM SIPVQNGPHV DFDAATTLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG CTGAGGGGAA CAAGGCCAGG GGGAAGGCCCC CCGGCAACGG TCCAGGTGGG TCCAGGTGGG TCCAGGTGGG TCCAGGTGGG AAGCCCCC TGGATCCCCG TGGATCCCCG	120 180 240 300 360 120 120 240 300 360 420 480 540 660
50 55 60 65 70	MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequity of the se	VLQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFRENTR ISMMLVLSRQ GITEIFIKDA IVDHPFFFLI 229 DNA Beed d Accession ence: 12-3: 11 GATGAGGACA CCTGCGCTGC CAGCTCTGC GAGGACTGT CACCAGCTCC ACCACCGC GCCGTCATC CCTCCCTTT AGCCCAGGC TCATTCTGTT AAACC 230 Protein	FPEEAIADLS FPEEAIADLS FROM NAVANY TESTINDES EVPLATLEPL NLTGLSDMKE RNRRTGTILF PLEASE FROM NAVANY TESTINDES FOR NAVANY TEST	VMMYNRLRAT VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGACAC GCACACCCAG GCCACAGAGGG GCCAGAGGGG GCCAGGAGGC CCACGAGGGC CCCGGAAGTC CCCGGAAGTC CCCGGAAGTC CCACACCCC	GEDENILFSP GEDENILFSP ESQYVMKIAN NIVKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG ASTGGAGCCT CTACACCTG CCTGGCATT CCTCAGCCTG TCCCCCAG TCTCCCCAG TCTCCCCAG ACGGACAGAGAGAGAGAGATG ACGAAGGATG	LSIALAMGMM LSIALAMGMM SIPVQNGPHV DFDAATTLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTGTGG CTGAGGGGAA CAAGGCCAGG GGGAAGGCCCC CCGGCAACGG TCCAGGTGGG TCCAGGTGGG TCCAGGTGGG TCCAGGTGGG AAGCCCCC TGGATCCCCG TGGATCCCCG	120 180 240 300 360 120 120 240 300 360 420 480 540 600 660
50 55 60 65 70	MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequity of the se	VLQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFPENTR ISMMLVLSRQ GITEIFIKDA IVDHPPPFLI 229 DNA see Id Accession lence: 12-3: 11	FPEEAIADLS FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL NLTGLSDNKE RNRRTGTILF GLEE #: NM_0030 8 21 GCATTGCTGC CACGTGTGCA TTCTGCAAGA GCGGAGTGGT ACCCAGTGT ACCCCTCG TTAGCCCCCA CTCTGGGGAT TGAGGGCTTC GAGCAGCCCC CTCTAGGAA TTGTTGCCGT Sequence: P_003686 21	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEWA IPLSKAIHKS MGRVMHPETM 395 31 TCCTTGCAGC CCAGCTCCAG CCACGACAC CCACGACAC CCACCCAG GCCACGAGGA CCCACACCCAG GCCACGAGGA CCCACACCCAG TCCACACCCC GGCTGGACC CTCCACACCCC CCCGAAAGTC CACAGACCCC GGTGGAGGA TTATTTTGTA	GEDENILPSP GEDENILPSP GESYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGGCAAT CCTCAGCCTG TCCCCCAG TCGCACTG TCTCCCCAG TCGCACTG TCTCCCCAG TCGGACCAGG ACAGAGGATG ACAGAGGATG ACAGAGGCTTC CTCAAATCTC	LSIALAMGMM LSIALAMGMM SLIPVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRPTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTTGG CTGAGGGGGA CAAGGCCAGG GGAGAGCTGC GGGAAGGCCCC TCCAGGTGGG AAGCACCCC TGGATCCCCG TACATGGAGA 51	120 180 240 300 360 120 180 240 300 360 420 540 600 660 720
50 55 60 65 70	MAPLGLPSLL ELGAQGSTQK NEEFLQMMKK INAVYPKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequity of the se	VLQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFPENTT ISMMLVLSRQ GITEIFIKDA IVDHPPFFLI 229 DNA see Id Accession Lence: 12-3: 11	FPEEAIADLS FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL NLITGLSDNKE RNRRTGTILF NLIGHER GCATTGCTGC CACCTGTGCA TTCTGCAAGA GCGAGTGT ACCCAGTGTA ACCCAGTGTA ACCCAGTGTA ACCCAGTGTA ACCCAGTGT TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCCCCC	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEM IFLSKAIHKS MGRVMEPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGAACAC GCACACCCAG GCCAGGAGGA CCCACAGTGC GCCAGAGGGC TCCACACTC CACAGTC CACAGTC CACAGTC CACAGTC CACAGTC CACAGCT TTATTTTGTA 31 NCKHSVVCPA	GEDENILPSP GEDENILPSP GESYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGGCAAT CCTCAGCCTG TCTCCCCAG TCTTCCCCAG TCTTCCCCAG TCTTCCCCAG TCGGACCAGG ACAGAGGATG AGAAGCCTG CTCAAATCTC 41 SSRFCKTINT	LSIALAMGMM LSIALAMGMM SLIPVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRPTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTTGG CTGAGGGGGA CAAGGCCAGG GGAGAGCTGC GGGAAGGCCCC TCCAGGTGGG AAGCACCCC TGGATCCCCG TACATGGAGA 51	120 180 240 300 360 120 120 240 300 360 420 480 540 600 660
50 55 60 65 70	MAPLGLFSLL ELGAQGSTQK NEEFLQMMKK INAVYFKGNW VLEIPYEGDE IDLKDVLKAL SRMAVLYPQV Seq ID NO: Nucleic Ac: Coding sequity of the se	VLQSMATGAT VLQSMATGAT EIRRSMGYDS YFNAAVNHVD KSQFPENTT ISMMLVLSRQ GITEIFIKDA IVDHPPFFLI 229 DNA see Id Accession Lence: 12-3: 11	FPEEAIADLS FPEEAIADLS FPEEAIADLS FSQNVAVANY TFSFTKDDES EVPLATLEPL NLITGLSDNKE RNRRTGTILF NLIGHER GCATTGCTGC CACCTGTGCA TTCTGCAAGA GCGAGTGT ACCCAGTGTA ACCCAGTGTA ACCCAGTGTA ACCCAGTGTA ACCCAGTGT TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCA TTAGCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCA TTAGCCCCCCCCCC	VMMYNRLRAT KEFSNMVTAK INKWVENNTN EVQIPMMYQQ VKAQLVEEM IFLSKAIHKS MGRVMEPETM 31 TCCTTGCAGC CCAGCTCCAG CCACGAACAC GCACACCCAG GCCAGGAGGA CCCACAGTGC GCCAGAGGGC TCCACACTC CACAGTC CACAGTC CACAGTC CACAGTC CACAGTC CACAGCT TTATTTTGTA 31 NCKHSVVCPA	GEDENILPSP GEDENILPSP GESYVMKIAN NIUKDLVSPR GEFYYGEFSD NSVKKQKVEV FLEVNEEGSE NTSGHDFEEL 41 CCTGGCTGTG CAACTGCAAG AGTGGAGCCT CTACACCCTG CCTGGCAAT CCTCAGCCTG TCTCCCCAG TCTTCCCCAG TCTTCCCCAG TCTTCCCCAG TCGGACCAGG ACAGAGGATG AGAAGCCTG CTCAAATCTC 41 SSRFCKTINT	LSIALAMGMM LSIALAMGMM SLIPVQNGPHV DFDAATYLAL GSNEAGGIYQ YLPRFTVEQB AAAVSGMIAI 51 GCTACAGGGC CATTCTTGTG CTGAGGGGGA CAAGGCCAGG GAGAAGCTCC CGGCAACGG TCCAGGTGGG AAGCCCCC TGGATCCCCG TACATGGAGA 51 VEPLEGNLVK	120 180 240 300 360 120 180 240 300 360 420 480 540 600 660 720

Coding sequence: 126-752

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45	1	11	21	31	41	51	
45	 GAGCAACCTC CGACCCAGAG	AGCTTCTAGT CTTCTCCAGC	 ATCCAGACTC GGCGGCGCAG	CAGOGCCGCC CGAGCAGGGC	CCGGGCGCGG TCCCCGCCTT	ACCCCAACCC AACTTCCTCC	60 120
45 50	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG CGAGGGGCTG	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CGCGGGCGCC CCTTCCTGGG CCTATGCCGG GCGTGTCGCA	CAGOGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGG	CCGGGGGGGG TCCCGGCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGGGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT	
	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTG TGACTCCTTG CATCCTCCTG CTTGGAAGAC TCTTGCAGGGT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT CTGAATCTGA GAGTGATAG GATGAGTGC CTGGCTATTT	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCTTCCTGGG CCTATGCCGG GCGTGTCCAGA GCAGCACATT CAATCTTTGT AGAAGATGGCAC TAGTTGCCAC	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG GCAAGCAACC GGCCACCGTT GATGGCTGTC AGCATGGTAT	CCGGGCGCGG TCCCCGCCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT ATTGGGGTG GGCAATAGAA	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGCGCTGCA GCACTGCCAT GGCAATGTT GGTAGGTTGG GTATGAAGTCT TGGTGGTTGG GGATATTTCT TCGTTCAAGA	120 180 240 300 360
50	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG CGAGGGGCTG TGACTCCTTG CATCCTCTG CATGGAGAG ATTCTATGAGAC ATTCTATGACAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GAGTGATAG GATGAGTGC CTGGCTATTT CCTATGACCC	ATCCAGACTC GCCGGCGCAG GGAGTCCGGG CCCTTCCTGGG CCTTCCTGGG CCAGCACATT CAATCTTTGT AGAAGATCAG TAGTTGCCAC CAGTCAATGC	CAGGGCGGC GGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG GCAGCACCGT GATGGCTGTC AGCATGGTATC CAGGTACGAA	CCGGGCGCGG CCTT GCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCGCCC CAGATCCAGT CGTGCCTTGA GGCATGAAGT ATTGGGGGTG TTTGGTCAGG	ACCCCAACCC AACTTCCTCC CGCCTTCTGC CGCGGGCTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TGGTTCAAGA CTCTTCAACA CTCTTTCAC	120 180 240 300 360 420 480 540 600
50	GAGCAACCTC CGACCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CCAGGGGCTG TGACTCCTTG CATCCTCCTG CTTGGAAGAC TCTTGCAGGT ATTCTATGAC GGAAAAACA GAAAGACTAC	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTACT TGGATGTCCT CTGAATCTGA GAGTGATAG GATGAGGTGC CTGGCTATTT CCTATGACCC GCTGCTTTCC GCTGTTCTCC GCTGTGACACA	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCTTCCTGGG CCTATGCCGG GCAGCACATT CAATCTTTGT AGAGAGAAGATGAC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGCACAAAG CAGGCAAAAAG GAGGCAAAAAG	CAGCSCCGCC CGAGCAGGGC TTGCCCACCT CGAGCGAGTC ATGGATCGGC CGACAACATC GAGCACCGGG GCAAGCACCTT GATGCATCGTT AGCATGGTTACGAA GGCAGGTTACCA GGCACGATCCAACACTC AGGTACCAACACTC AGGTACCAACACTC AGGTACCAACACTC AGGTACCAACACTC AGGTACCAACACACACACACACACACACACACACACACAC	CCGGGCGCGG CCTTCCCCACCTT GCAAACTCTC ATGGCCAACG GCCATCCTCA GTGACCGCCC CAGATCCAGT CGTGCCTTGA GGCATTAGAGT ATTGGGCAGT CTTGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAAACA	ACCOCAACOC AACTTCCTCC CGCCTTCTGC CGCGCTCCCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG TCGTTCAAGA CTCTTCAACA GTTCCTGTCC CTTCCAGCGG AACCGAAAAT	120 180 240 300 360 420 480 540 6600 720 780 840 900
50 55	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGG CGAGGGGCTG TGACTCCTCTG CATCCTCCTG CATCCTCCTG CATCTCAAGAC TCTTGCAGGT ATTCTATAGAC TCGGAGAGACTAC GGACAATAACA GGACATTGAG GTATGGTATT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCC AGGATTTACT TGGATGTCCT TGGATCTCA GAGGTGATAG GATGAGGTGC CTGGCTATTT CCTATGACC GCTGCTTCTC ACCTCTTACC GTGTGACCAA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGGGGGCAG GGAGTCCGGG CCTATGCCGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGCACAAG GAGGCAAAAG GAGGCAAAAG CAAACAAA	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCAGGGC CTGCCACCT CGAGCACATC CGACAACATC GAGCACCGT GATGGCTGT GATGGCTGT CAGCTACGAA CAGGTACGAC GGCAGCTGT CAGGTACGAA AGCATCCA AGCATAGAAT AAAAACCCAT	CCGGGCCGG CCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCCCC CAGATCCAGT CGTGCCTTGA ATTGGGGTG GGCATAGAA TTTGGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAAACA TTTGGTAAACT GTGTTAAAAT	ACCCCAACCC ACCTTCTCC CGCCTTCTGC CGCGTTCTGC CGCGTGCCT AGGCCATGTA GCAAGTCTT TGGTGGTTGG GTATGAAGT CTCTTCTAAGA CTCTCTTCTAAGA CTCTCTTCTCCAGCGG AACGAAAAT ACTCAGTGCT ACCGAAAAAT ACTCAGTGCT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
50 55 60	GAGCAACCTC CGACCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CCAGCGCTG CAGCCCCTTG CATCCTCTG CATCCTCTG CTTGGAGAC TCTTGCAGGT ATTCTATGAC TGGCTGGGCT CGGAAAAACA GAAAGACTAC GGACATTGAG GACATTGAG TATAGGTATT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GGATGATGAC GATGAGGTGC CTGGCTATTT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATAAAACAAA TAATCTTATT	ATCCAGACTC GGCGGCGCAG GGAGTCCGGG CCTATGCCGG CCTATGCCGG GCGGCACATT CAACACTTTGT AGAAGATCAACA TCAGCACACT CCAGCACACT CCAGCACACT CCAGCACACT CAACACCAAG GAGCAAAAG TAACATTAGC CAACACAAG TAACATTAGT TTATCTTCTT	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCAGGGC ATGGATCGGC GGACAACATC GAGCAACCATC GAGCAACCGGG GCAAGCAACC GGTGGTGTT AGCATGGTAT CAGGTACGAA GGGAGGTGCC GCCCTATTCCA GAGAAAATCA ACCTTAGAAT TCCTCAATAT	CCGGGCCGCG CCAAACTCTC ATGGCCAACG GCCATCTCA GTGACCGCC CAGATCCAGT CGTGCCTTGA GGCATGAGAT TTTGGTCAGG CTACTTTGCT AAACCTCCAC TGTTGAAACA TTTGGTAAACA TTTGGTAAACA TTTGGTAAACA TTTGGTAAACA TGTTGAAACA AGGAGGGAAA	ACCCCAACCC ACCTTCTCC CGCCTTCTGC CGCGTTCTGC CGCGTGCA GCACTGCCCT TGGTGGTTGG GTATGAAGT TGGTTCAAGA CTCTCTTCAGC GTTCCTGTCC CTTCCAGCGG AACCGAAAAT GTAATCTGAA ACCCAGTGCT ATTTTACCAT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080
50 55	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CGAGGGGCTG CATCCCTG CATCGCAGT ATTCTATGAC TCTTGCAGGT ATTCTATGAC GAAAAACA GAAAGACTAC GGACATTGAG GTATGGTATT AAACATGGCT TTGATTACT TTGATTACT TATATATAGA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT CTGAATCTGA GATGAGGTGC CTGGCTATTTC CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGGGGGCAG GGAGTCCGGG CCTATGCCGG CCTATGCCGG CCTATGCCGC CCTATGCCGC CCTATCTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATTGC CAGTCAATGC TCTGCCTTCT CAACACCAAG GAGGCAAAAC TAACATTAGG CAAACAAACA TTATCTTCT GAGTAATCAT TACATGTTTT TACATGTTTTT TACATGTTTTT TACATGTTTTT TACATGTTTTT TACATGTTTTT	CAGGECCECC GAGGAGGGG TTGCCCACCT GAGGAGTC ATGGATCGGC GGACAACATC GAGCACCGT GATGGCTGTC GATGGCTGTC GATGGCTGTC GAGGAGAACC GCCCTATCCA GAGAAAATCA ACCTTAGAAT AAAACCCAT TCCTCAATATG TCTAATATAAA	CCGGGCCGG CCAAACTCTC GCAAACTCTC GCAAACTGTCA GTGACCGCC CAGATCCAGT CGTGCCTGA ATTGGGGTG GGCATGAAGT ATTGGGGTG GGCATGAAGT ATTGGGGTG GGCATGAAGT ATTGGTCAGG CTACTTTGCT AAACTGCAC TGTTGAAACA TGTTGAAACA AGGAGGGAAG GGGAAGGGAA	ACCCCAACCC ACCTCTCTCC CGCCTTCTGC CGCGTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CGATATTTCT TCGTTCAAGA CTCTCTTCAC GTTCCTGTCC CTTCCAGGGG AACCGAAAGT ATTTTACCAT ATTTTACCAT ACTCTTAAA AAATACTATT	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080 1140 1200
50 55 60	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGG CGAGGGGCTG TGACTCCTCG CATCCTCCTG CATCCTCGTG ATTCTATGAGAC TCTTGCAGGT ATTCTATGAGCT CCGAAAAACA GAAAGACTAC GGACATTAGG GTATGGTATT AAACATGGCT TTGTATTACTA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCC AGGATTTACT TGGATGTCCT CTGAATCTGA GGATGATAG GATGAGGTGC CTGGCTATTT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCAT ATACTATCAT TACAATACAT TATOTATATAT TGGTACTATC	ATCCAGACTC GGGGGGCAG GGAGTCCGGG CCTATGCCGG CCTATGCCGG GCGTGTCCAC GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTCAATGCCAC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAACACAAG GAGGCAAAAG GAGGCAAAAG TAACATTAGG CAAACAAACA TTATCTTCTT GAGTAATCAT TACATGTTTT ATACTTAAAA	CAGCGCCGCC CGAGCAGGGC TTGCCCACCT CGAGCAGGGC TTGCCCACCT CGACAACATC GACAACATC GAGCAACCGGG GCAACCGGT GATGGATAC GGCCACCGTT GATGGATAC AGCATAGGAA ACCTATAGAAT ACTCAAATGT TCTATAAAA TATCTCTAAA	CCGGGCCGCG CCAAACTCTC ATGGCCAACG GCCATCGTCA GTGACCCCC CAGATCCAGT CGTGCCTTGA ATTGGGGTG GGCATAGAA TTTGGTCAGG CTACTTTGCT AAACTGCAC TGTGAAACA TTTGGTAAACA GGGAAGGGAA	ACCCCAACCC ACCTTCTCC CGCCTTCTGC CGCCTTCTGC CGCCTTCTGC CGCACTGCCCT AGGCCATGTA GCAAGTCTT TGGTGGTTGG GTATGAAGT CTCTTCTCAC GTTCCTTCAC GTTCCTGTCC CTTCCAGCGG AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTACCAT GCTCCTTAAA ACTCAGTGCT ATTTACCAT GCTCCTTAAA AAATACTATT	120 180 240 300 360 420 540 600 600 780 840 900 1020 1080 1140 1200 1260
50 55 60 65	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGG CGAGGGGCTG TGACTCCTCG CTTGGAAGAC TCTTCTACTAG ATTCTATTAGA TGGCTGGGCT CGGAAAAACA GGACATTGAG GTATGGTATT AAACATGGCT TTGTATTACT TTATTATTAGA CTCATTATTAGT CCATTATTGT CCATTATTGAT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCG GATGATGG GATGAGGTGC CTGGCTATTT CCTATGACC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGGGCAG GGAGTCCGGG CCTTCCTGGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTCATTGCCAC CAGTCAATGC CAGTCAATGC TAGCCATCT CAACACCAAG GAGGCAAAAG GAGGCAAAAG TAACATTAGG CAAACAAACA TTATCTTCTT GAGTAATCAT TACATGTATTA ATTAGGTATAAA ATTAGGTATAT	CAGGGCGGC CGAGGAGGG TTGCCCACCT CGAGGAGTC ATGGATCGGC CGACAACATC GAGCAACATC GAGCACCGT GATGGCTGTC GATGGCTGTC GAGGAGGAGT CAGGTACGAC AGCATGGTAT CAGGTACCAA AAAAACCAT CCTCAATTAT ACTCAAATGG TCTTTTTTCT CCTTTTGGTTT CCTGGGGGGGGGT	CCGGGCCGCG CCAACTCTC ATGGCCAACG GCCATCGTCA GCGATCCTCG GCATCCTCG GGCATCCAGT CGTGCCTTCGA ATTGGGGTG GGCATGAAGT TTTGGTCAGG CTACTTTGAACA TTTTGGTAATC GTGTTAAAAT AGGGGGAAG GGGAAGGGGT ATTGGTAAAAT ATGGGGTAT GTGTTAAAAT ATGGTAAT ATTGGTAAAT ATGGTAAAT ATGGTAAAT ATGGTAAT CCTTTTGCCCAC CCTTTTGCCCAC	ACCCCAACCC ACCTCTCTGC CGCCTTCTGC CGCGTTCTGC CGCGTGCCCT AGGCCATGTAG GCAACGTCTT TGGTGGTTGG GTATGAAGTC CGATATTTCT TCGTTCAAGA CTCTCTTCAC GTTCCTGTCC CTTCCAGCGG AACCGAAAAT GTAATCTGAT GTAATCGAA ACTCAGTGCT ATTTTACCAT ACTTTAACTAT GCATATCTTAAT ACATATCTAAT	120 180 240 300 360 420 540 600 720 780 840 900 1020 1080 1140 1200 1260 1380
50 55 60	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGG CGAGGGGCTG TGACTCCTCTG CTTGGAAGAC TCTTGCAGGT ATTCTATTAGAC GGACATTGAG GGACATTGAG GGACATTGAG GTATGGTATT AAACATGGCT TTGTATTACT TTGTATTACT TATATTACAC CTCATTATGAT CCATTATTGAT CCATTATTGAT CAGTCAATT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCCT CTGAATCTGA GGAGTGATAG GATGAGGTGC CTGGCTATTT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGGGGGCAG GGAGTCCGGG CCCTTCCTGGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTCATCC CAGTCACTC CAACACAAG GAGGCAATAG TAACATCATC CAACACAAG GAGGCAAAAG TAACATTAGG CAAACAAACA TTATCTTCTT GAGTAATCAT TACATGTTTT ATACTTAAAA ATTGGTAATT TCTTTCAATT	CAGCGCCCCC CGAGCAGGGC TTGCCCACCT CGAGCAGGGC CTGCCACCT CGAGCAACATC GAGCACCGT GAGCACCGT GATGGCTGT GATGGCTGT CAGCTACGAA ACCTTAGAAT ACCTCAATAGA TCTCTTATAAA TATCTCTAAA TTTCTTTTC GCTTTGGGTC CTGAGCGCCCTTTCCCCCTCACCACCT TCCTCATCCCCCCTCCACCACCCT TCCTCATCCCCCCCC	CCGGGCCGCG CCAAACTCTC ATGGCCAACG GCCATCGTCA GCGATCCTCA GGCATCACG CGGGCCCCC CAGATCCAGT CGTGCCTTGA ATTGGGGGTG GGCATAGAA TTTGGTCAGG CTACTTTGAAACA TTTGGTAAACA TTTGGTAAACA GGGAAGGGAA	ACCCCAACCC ACCTTCTGC CGCCTTCTGC CGCGTGCCC CGCCTTCTGC CGCGTGCCC CGCCATGCCCT AGGCCATGTAG GCAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA CTCTGTTCAC GTTCCTGTCC CTTCCAGCGG AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAC AATTACTATT GCATATTTAACTT CATATTTAACTT CATATTTATT	120 180 240 300 360 420 480 540 660 720 780 900 900 91020 1080 1140 1260 1320 1380 1440
50 55 60 65	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCAGTGG CCACCAGTGG CATCCCTG CTTGGAAGAC TCTTGCAGGC TCTTGCAGGC TCTTGATGAC AGAAGACTAC GGACATTGAG GTATGGTATT AAACATGGC TTGTATGAC TTGTATTACT TATATATACA TCTATTATAC CCATATTGT CCATATTGT CCATATTGT CCATATTGT CATTTTTTA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTAGT GATGAGGTGATAG GATGAGGTGATAT CCTATGACCC GTGTGACCC GTGTGACCA ATACTATAT ACAAAACAAA	ATCCAGACTC GGGGGGCGC GGAGTCOGG GCAGGGGCCC CCTTCCTGGG CCTATGCCGG GCAGTCACAT CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGC CAGTCAATGC CAGTCAATGC CAGTCAATGC TAGTAGAAG GAGGAAAAG TAACATAAG GAAGAAACA TTATCTTCTT GAGTAATCAT TACATGTATA ATACTTAAAT ATTCTTCATTA TCTTTCATTA TAGACACTG TAGACACTTG TCTTTCAATT ATAGCACTTG TGAATCTAAC TTATGCACTTG TGAATCTAAC TTATGCACTTG TGAATCTAAC TGAATCTAAC TTATGCACTTG TGAATCTAAC TGA	CAGGECCECC CGAGCAGGGC TTGCCCACCT CGAGCAGGGGC CGACACATC GAGCACCT GAGCACCGG GCCACCGT GATGGCTGT GATGGCTGTC GAGCACGT GATGGCTGTC GAGGAGAACC GCCCTATCCA GAGAAATCA ACCTTAGAAT ACAAAATCA TCCTCAATAT TCTCTAATAT TTTCTTTTTC GCTTTGGGTG CTTCATGGTT CTTCATGGTT CTTCATGGTT CTTCATGGTT CTTCATGGTT CTTCATGGTT CATCATTCATA	CCGGGCCGCG CCGAACTCTC GCAACTCTC GCAACTCTC GCACCCC GCGCCCCC GGACCCCC GGGCATGCA GCCATCGTCA GCCATCGTCA GCCATCGTCA GGCATGCAG GGCATGCAG GGCATGCAG GGCATGCAG GGCATGCAA TTTGGCGTC TTTGGTCAG CTACTTTGCT AAACCTGCAC TGTTGAAACA TGTGTAAACA GGGAAGGGAA	ACCCCAACCC ACCCCAACCC CGCCTTCTGC CGCGTTCTGC CGGGGTTGCA GCACTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAG CTTCCTTCAC GTTCCTGCC CTTCCAGCGG AACCGAAAAT ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAATACTAAT GTATTTAACTA AAATACTATT GTATTTAACTAT GTATTTAACTAT TGTATTTAACTAT ACATATGTAA AAGACCTAGC TATACTTTAT TTGTTTTTTTTGTG TAGTTTCTAA	120 180 240 300 360 480 540 600 780 900 960 1020 1140 1200 1320 1380 1440 1560
50 55 60 65 70	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGG CGAGGGGCTG TGACTCCTCTG CATCCTCCTG CATCCTCCTG CATCCTCAGAGAC TCTTGCAGGT ATTCTATAGAC GGACATTGAG GGACATTGAG GTATGGTATT AAACATGGCT TTGTATTACT TATATATAGA CTCATTATGAT CCATTATGAT CAGTCAAATT CAGTCAATTTACT TTACATTGAT TTACATTAGAT TTACATTGAT TTACATTAGAT TTACAT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG CCTGAGCCAG TTCATTCTCC AGGATTTACT TGGATGTCCT TGGATGTGC GGTGATATG GGATGATGG GCTGCTATTT CCTATGACCC GCTGCTATTT CCTATGACCC ATGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGGGGGCAG GGAGTCCGGG CCCTTCCTGGG CCTATGCCGG GCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTCACAC GAGCACATT CAATCATTGCCAC CAGTCAATAG GAGGCAAAAG ATACATTAGG CAAACAAACA TTACATGTTT ATACATTATAAA ATTGGTATAT TTCTTCAATT ATAGCACTTG TGAAATCAAAC TTATCTTCAATT ATAGCACTTG TGAAATCAAAC TTATCATTCAATT ATAGCACTTG TGAAATCAAAC ATTACATAAA	CAGCGCCCCC CGAGCAGGGC TTGCCCACCT CGAGCAGGGC TTGCCCACCT CGAGCACCT CGACCACCT CGACCACCT CGACCACCT CGACCACCGT CGACCACCGT CACCGCT CCTCATCGCT CCTCATCGCT CCTCATCGCT CCTCATCGCT CCTCATCGCT CCTCATCGCT CCTCATCGCT CACCGCT CACCGCT CACCGCT CACCGCT CACCGCT CACCGCT CACCGCT CACCGCT CACCGCT CACCCCCT CACCCCCC CACCCCC CACCCCCC CACCCCCC CACCCCC CACCCCC CACCCCC CACCCC CACCCC CACCCC CACCCC CACCCC CACCCC CACCC CACC CACCC	CCGGGCCGCG CCAAACTCTC ATGGCCAACG GCCATCGTCA GCGATCCAGT GGGAAGAGT ATTGGGCTGA ATTGGGGTG GGCAATAGAA TTTGGTCAGG GCAATAGAA TTTGGTAAACA TTTGGTAAACA TGTGTAAACA GGGAAGGGAA	ACCCCAACCC ACCTTCTGC GGCTTCTGC GGCGTTCTGC GGCATGCCCT AGGCCATGTAG GCAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA CTCTCTTCAG GTTCCTGTCC CTTCCAGCGG AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAACT ACTTTAACT ACTTTAACT ACTTTAACT ACTTTTAACT TGATTTTACTAT TCATATCTTAAT ACAGACCTAGC TATATTTTTTTTTT	120 180 240 300 360 480 540 600 720 780 900 960 1020 1140 1260 1320 1320 1340 1500 1560 1680
50 55 60 65	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG CCACCCTGC CATCCTCG CATCCTCTG CATCCTCTG CATCCTCTG ATCTGAGAC TGGCTGGGCT ATCTGAGGCT AGACAACCA GAAAGACTAC GGACAATTGAG GTATGGTATT AAACATGGCT TATATATACAC TATATATACT TATATATACT TATATATA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCT TGGATGTAGC GATGAGCCG GCTGCTTCTC ACCTCTTACC GCTGCTTCTC ACCTCTTACC GTGTGACCAA ATACTATAT TGATACTAT TGATACTAT TGATACTAT TGATACTAT TGATACTAT CCATATCTC AAGGATGATT TCATTTACTC AAGGATGATT CCATAATCTC CATATCTC AATTTATTAC CCTGTTGACC AATTTATTAC CCTGTTGACC AAATATTTTT	ATCCAGACTC GGGGGGCAG GGAGTCOGGG CCTATGCCGG CCTATGCCGG CCTATGCCGG CCTATGCCAGT CAATCTTTGT AGAAGATGAG TAGTTGCCAC CAGTCAATGCCAC TAGTTGCCAC TAGTTGCCAC TAGTTGCCAC TAGTTGCTTCT CAACACAAG GAGGCAAAG TAACATTAGG CAAACAAACA TTACTTCTT TACATGTTTT ATACTTAAA ATTCGTATAT TCTTCATTA TCTTTCATTA TCTTCATTA TCTTCACACA CAATTGAGAC CCAATTGAGT	CAGGGCGGC CGAGGAGGGGC TTGCCCACCT CGAGGAGGGGC CGACAACATC GAGCACCATC GAGCACCGT GATGGCACGG GCAAGCAACG GGCACGGT GATGGCTGT AGCATGGTAT AGCATGTAT ACCTTAGAAT ACCTTAGAAT ACTCAAATAT TTTCTTAAAA TATCTCTAAA TATCTCTAAG CTTTGGGGG CTTTGGGTG CTTCATGGTG CTTCATGGTG CTTCATGGGTAT ACTCATGGTAT ACTCATGGTG CTTCATGGTG CTTCATGGTG CTTCATGGTG CTTCATGGTAT ACATTTCATA TTTGGGGGCA ACCTCTGAC ACCTCTACA ACCTCTGAC ACCTCTACA ACCTCTGAC ACCTCTACA ACCTCTGAC ACCTCTACA ACCTCTGAC ACCTCTACA ACCTCTAC ACC	CCGGGCCCG CCGAACTCTC GCAACTCTC GCAACTCTC GCAACCCCC GGAACCCCC CAGATCCAGT CGTGCCTCA GCCATCGTC GGCAATGCAA TTTGGGGTG GGCAATAGAA TTTGGGTATT GTGTTAAAAC TTTGGTATT GGGTAGT AAACCGCAC TTTGGTAACA TTTGGTATT GCTTAAAAC ATAGGTAAT CCTTTGCCAC GCCCTTTTCA AACCCCTTATA GCCTACTTTT CCTTTGCCAC GCCCTTTTCA AAGCCCTTAT TGCTACATTT AATCTTTCTG TCTGACCCAT TCTGACCCCAT	ACCCCAACCC ACCCCCAACCC GCCTTCTGC CGCGTTCTGC CGCGTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGGG GTATGAAGTG CGATATTTCT TCGTTCAAG GTTCCTGTCC CTTCCAGCGG AACCCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT GCTCCTTAAA AAATACTAAT GTATTTAATT GTATTTAATT TTATTTATT TTATTTAT	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1560 1680 1740
50 55 60 65 70	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGG CGAGGGGCTG TGACTCTCTG CTTGGAAGAC TCTTGCAGGT ATTCTATTAGC TGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTTGAAAACTAC GGACATTGAG GTATGGTATTACT TTGATTACT TATATATAGA CTCATTATTATC TTATTATTAC TTTATTATC TTTATTATC TTTATTATC TTATTATTAC TTATTATTAC TTATTATTAC TTATTATTAC TTATTATTAC TTATTATTAC TTATTTTTA TTTCATTGGT TGCTTTGGT TGGTAAAAT TTTGCTTTGA CACAACTTTA TTTGCTTTGA CACAACTTTA ACCATCTTTTTTTTTT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCG GATGATGGG GATGATGG GCTGCTATTT CCTATGACC GCTGCTATTT CCTATGACC TGTTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGCGGGGCAG GGAGTCCGGG CCTTCCTGGG CCTTCCTGGG CCTTCCTGGG CCGTGTCGCA GCAGCACATT CAATCTTTGT AGAAGATGAG TAGTCATGC CAGCACATGC CTACACCAAG GAGGCAATAGC CAACACAAG GAGGCAAAAG TAACATTAGG CAAACAAACA TTACTTCTT AGAGTAATCAT TTCTTCAATT ATACTTAAAA ATTGGTAATT TTCTTCAATT ATAGCACTTG TGAAATCTAACA TTACTTCAATT ATAGCACTTG TGAAATCAGAC TTCCCACACA CCAAATTGAGT TTTTAAGCTA TTTTAAGCTA TTTTAAGCTA TTTTAACTTA	CAGGGGGGGG TTGCCACCT GAGGAGGGG TTGCCACCT GAGGAGGGG TTGCCACCT GAGGAGGAGT CAGGACAACATC GAGCACCGT GATGGCTGT GATGGCTGT AGCATGGTAT CAGGTACGAC GGGAGAGTACC GCCCTATCCA GAGAAAATCA ACCTTAAATG ACTCAAATGG TCTATTAAAA TATCTCTAAA TATCTTATT ACATTTCATT ACATTTCATT ACATTTCATT ACATTTCATT ACATTTCATT ACATTTCATA ACATGGGT CATGGTTAT ACATTCATA ACATCGGT CATGGTTAT ACATTCATA ACATCGGT CATGGTTAT ACATTCATA ACATGGT CATGGTTAT ACATTCATA ACATGGT ACTTCATGGT CTTGTGGGGCA ACCCTGTAC AGCGGCATGC CTTATTCATA TGTTTTCCCA TGTTTTCCCA TGTTTTCCCA TGTTTTCCCA TGTTTTCCACT TGTTTTCACT TGTTTCACT TGTTTTCACT TGTTTTCACT TGTTTTCACT TGTTTTCACT TGTTTTCACT TGTTTCACT TGTTTCACT TGTTTTCACT TGTTTTCACT TGTTTTCACT TGTTTCACT TGTTTTCACT TGTTTCACT TGTTTTCACT TGT	CCGGGCCGCG CCAAACTCTC ATGGCCAACG GCCATCGTCA GCGATCCAGT GGCAATCCAGT CGTGCCTCGA ATTGGGGTG GGCAATAGAA TTTGGTCAGG GCCATTGCA AACCTGCA TTTTGGTAAACA TTTGGTAAACA AGGGGAAG GGGAAGGGTA ATAGGTAAAT ATAGGTATT GTCTTAAACA ATTGGTAAACA ATAGGTAAT ATAGGCCTTAT CCTTTGCCAC GCCCTTTTCCA AACCCTTAT GCTACACTTT TCTGACCCAT TGTTCCCCCA GTTTTATATCC CCTTGTACCCAC TGTTCCCCCA TGTTCCCCCA TGTTTCCCCCA TGTTTCAATTA	ACCCCAACCC ACCTCTCTCC CGCCTTCTGC CGCGTTCTGC CGCGTGCCCT AGGCCATGTAG GCAACTCCTT TGGTGGTTGG GTATGAAGTC CTCTCTCAGC GTTCTGTCCAGCG ACCCGAAAAT TGATCTCTCAGCG AACCGAAAAT GTAATCTGAA ACTCAGTGCT ATTTTACCAT ACTCTTAACA ACTCAGTGCT ATTTTACCAT TGATTTAATT ACATATCTAAT TGTTTTTGT TAGTTTTCTG TAGTTTCTTA CATGCCTTAAAC CCCTAAAACT TCATGCCTTAACT TCATGCCTTTT	120 180 240 300 360 480 540 660 720 780 900 960 1080 1140 1260 1320 1340 1500 1560 1680 1740 1680 1740 1860
50 55 60 65 70 75	GAGCAACCTC CGACCCAGAG GCGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG CCACCAGTGG CATCCTCCTG CTTGGAAGAC TCTTGCAGGC TATCCTCTG ATTCTAGAC TGGCTGGGCT ATTCTAGAC TGGCTGGGCT ATAGACTAC GGACATTGAG GTATAGTATT AAACATGGCT TATATATACA CTCATTATGAC CTATTTTTA TTTCATTGAT TATATATAC TTATTTTTTA TTTCATTGAT CAGCAAGAAG GTGATAAATT TTTCATTGAT AGCAAGAAG TTATTTTTTA TTTCATTGAT AGCAAGAAG ACCAACTTTA ACCTTTTTTTA TTTGATTTGA	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG GCCACCTTCG CCTGAGCCAG AGGATTTACT TGGATGTCCT TGGATGTCT TGGATGTAGC GATGAGGTGT CCTATGACCC GCTGCTTCTC ACCTCTTACC GCTGCTTCTC ACCTCTTACT ACAAAACAAA	ATCCAGACTC GGCGGCGCGC CCTTCCTGGG CCTATGCCGG GCTGTCGCG CCTATGCCGG GCTGTCGCG TAGTTGCCAC CAGTCAATC CAGCCATT AGAAGATGA TAGTTGCCAC CAGTCAATGC CAGTCAATGC CAGTCAATGC TAGTTGCTCT CAACACAAG TAACACTAG TAACATTAG TAACATTATT TACATGTTT ATACTTATA ATTCTTCATTA TCTTTCATTA TCTTCACTA TAAGACC CAATTGAGT TTTTAAGTAT TTTTAAGTAT TTTTAAGTAT TTTTAAGTAT TTGTTTTA	CAGGGCCGCC CGAGGAGGGGC TTGCCCACCT CGAGGAGGGGC CGACAACATC GAGCACCACGG GCAACACT GAGCACCGGG GCCACCGTT GATGGCTGTC AGCATGGTAT AGCATGGTAT AGCATGTAT ACCTTAGAAT ACCTTAGAAT ACTCTAATAT TTTCGTATT CTTCATAGT TTTTCTTAA ATTCTTAAA ATTCTTAAA ATTCTTAAA ATTCTTAAA ATTCTTAAA ATTCTTAAA ATTCTTAAA ATTTCTAAA ACTTTAGGGCG CTTATTCATA ATTCTTAAA AGCTGCAAGC CTTATTCCTAA AGCTGCAACA	CCGGGCCCG CCGAACTCTC GCAAACTCTC GCAAACTCTC GCGACCCCC GGGCATCGTC GTGACCGCCC CAGATCCAGT CGTGCCTTCA GCCATCAGT GGCAATAGAA ATTGGGGTG GGCAATAGAA TTTGGTCAGG CTACTTTGCT AAACCTCCAC TGTTGAAACA TTTGGTAATAT GCGTAGTAAACA GCGAGGAGG GGCAGGAGG ATAGAACA TTTGGTTAAATA GCCTTTTCC GCCTTTTCA AATCTTTTTGCCAC GCCTTTTCA AATCTTTTTTC GCTACATTT AATCTTTTTTC GCTACATTT AATCTTTTTCAG TTTGACCCCA TTTTTATATC AGTGCTAATTA AGTGCTAGACTA	ACCCCAACCC ACCTCTCTCC CGCCTTCTGC CGCGTTCTGC CGCGTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGTG GTATGAAGTG CGATATTTCT TCGTTCAAGG GTTCCTGTCC CTTCCAGGGG AACCGAAAAT GTAATCTAA ACTCAGTGCT ATTTTACCAT GCTCTTAAA AAATACTAAT GTATTTAATT TTATTTAACTTAAT TGATTTAATT TTATTTATT TTATTTATT TTATTTAT	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1320 1380 1400 1560 1560 1680 1740 1860 1860 1920
50 55 60 65 70	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG CGAGGGGCTG TGACTCCTG CTTGGAAGAC TCTTGCAGGT ATTCTATGAGT ATTCTATGAGT ATTCTATGAGT TGGATGATTAACATGGT TTGTATTACT TTATATATAGA CTCATTATTATT TTATTTTTTA TTTCATTGGT TGCTTAGATAAAT TTTCATTGGT TGCTTTGATAAAT TTTCATTGGT TGCTTTGATAAAT TTTCATTGGT TGCTTTGATAATT TTTGTTTTAA TTTCATTGGT TGCTTTGATAAATT TTTGCTTTTGA ACCAAGAAT TTTGTTTTGATTGT TATAATCTCC GATAATTTGT TATAATCTCC GATAATTTGT TATAATCTCC GATAATTCC TTATTTTTTTAACCTTTTGT TATAATCTCC GATAATTTCC TTATTTTTTTTTT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG GTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCCT TGGATGTGCT CTGAATCTGA GATGAGGTGC CTGGCTATTT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAAACAAA	ATCCAGACTC GGGGGGCAG GGAGTCCGGG CCTTCCTGGG CCTTCCTGGG CCTTTCTGGCA CAGCACATT AGAAGATGAG TAGTTGCCAC CAGTCAATTCT CAACCATCA CAGCACATT AGAAGACAAT TAGTCCTTCT CAACACCAAG GAGGACAATT CAACATTAGG CAACAACAAC TAACTTCTT GAGTAATCAT TACATGTATTA TACATTAAAA ATTGTATAT TCTTCAATT ATAGCACTTG TGAACACCACCA CCAATTGAGT TTTTAAGCTA TTGAGTATAT TCTCTCTGTA TTGAGATAAT TTGAGATAAT	CAGGECCECC GAGCAGGGC TTGCCCACCT GAGCAGGGC TTGCCCACCT GAGCACACT GAGCACACT GAGCACCGG GCACACGT GATGGCTGT GATGGCTGT AGCATGGTAT AGCATGGTAT AGCATGGTAT AGCATGGTAT AGCATAGAA AAAACCCAT TCCTCAATAG TCTCTATAAA TTTCTTTTCC CTTTGGGTG CTTCATGGTT TTTGGAGGC ATCCTGATCT ATCGTATC TTTGGAGGC ATCCTGATCA TTTTGGAGCA TCCTGATCA TTTTGGAGCA TCCTGATCA TTTTGGAGCA TCCTGATCA TTTTGGACGA TCCTTATCCAA TGTTTTCCCA TGTTTCCCA TCTTATCATA TGTTTTCCCA GCTGTAACCA GCTGTACCA GCTGCTACCA GCTCCA GCTCCAC GCCCA	CCGGGCCCG CCAAACTCTC GCAAACTCTC GCAAACTCTC GCGACCCCC GGGATCCAGT GCGACCCTGA ATTGGGGTG GGCATGAAG ATTGGGGTG GGCATGAAG TTTGGTCAGG CTACTTTGCT AAACCTGCAC TGTTGAAACA AGGGGAAG ATTAGAGA TTTGGTTAAAAT AGGGGAAGGGAT ATAGGCAAGT ATAGGTAATT GCCTTTTCC GCCTTTTCC AACCCTTTTC AACCCTTTTC AACCCTTTTC TCTGACCCAT TGTTCCCCCA GTTTTTATAT AGTGCTAGAACA AGTGCTAGAAC AGTGCTAGAAC AGTGCTAGAAC AGTCACTTAA	ACCCCAACCC ACCTCTCTCC CGCCTTCTGC CGCGTTCTGC CGCGTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGTG CGATATTTCT TCGTTCAAGA CTCTCTTCAC GTTCCTGTCC CTTCCAGGGG AACCGAAAGT ATTTTACCAT ATTTTACCAT ACTCTTAAA ACTCAGTGCT ATTTTAACT ATTTTAACT TGATTTTATT TCATATGTAA AAGACCTAAC TATGTTTTAT TTGTTTTTGTG TAGTTTTTACT TTGTTTTTGTG TAGTTTTTAC TAGTTTTTAC TTGTTTTTAC CGTGTTTTAA CATGACCTAAA AGGACCTAC CGTGTTGTAA CCCCTAAACT TCATGCGTTT TCTTCTGCAGT TCTTTCTGCAGT TCTTTCTCAC AGGTAGTGTG	120 180 240 300 360 420 480 540 600 720 780 900 900 1020 1140 11260 11380 1440 15500 1680 1740 1680 1740 1860 1860 1980
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50 55 60 65 70 75	GAGCAACCTC CGACCCAGAG GCGGGGCCCA ACCTGCCACC GCTGTTGGGC GCCCCAGTGG CGAGGGGCTG CGACCCCTG CTTGGAAGAC TCTTGCAGGT ATTCTATGAGT ATTCTATGAGT ATTCTATGAGT TGGATGATTAACT TGGATTAACT TTATATTACT TTATATTATTAC TTATTTTTTA TTTCATTGGT AGCCAAGAAG GTATGAGT TTTGTTTACT TTTTTTTTA TTTCATTGGT AGCCAAGAAG GTATGATTACT TTTTTTTTTA TTTCATTTGT TACATTCATTTGT TACATTCATTTGT TACATTCATTTGT TACATTCATTTGAT ACCTTTTTTTTTA ACCTTTTTTTTTA ACCTTTTTTTT	AGCTTCTAGT CTTCTCCAGC GCCACCTTCG CCTGAGCCAG GCCACCTTCG CCTGAGCCAG TTCATTCTCG AGGATTTACT TGGATGTCCT TGGATGTCCT CTGAATCTGA GATGAGGTGC CTGGCTATTT CCTATGACCC GCTGCTTCTC ACCTCTTACC GTGTGACACA ATACTATCAT ACAAACAAA TAATCTATT TGCTTCCCATT TCATTTACTC AAGGATGATT CCATAATCTC CATAATCTC AAGGATGATT CTCTATCTCC AAATTTATT CTCTATCTCC AAATTTATT CTCTATCTCC AAATTTATT TCATTTACTC CAAAATTTATT CCCCATTCC TAATAAGGTG TGACAAAATAT ATCTGCCAAA AGTTTATATT CAGCTGCCTT TCACTGCCT TCACTGCCTT TCACTGCCT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCCTT TCACTGCTT TCACTGCTT TCACTGCT TCACTT TCACTGCT T	ATCCAGACTC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CAGGECGEC CGAGCAGGG TTGCCCACCT CGAGGAGGAGT CAGGAGAGACACC GGACAACATC GAGCACCGT GATGGCTGT GATGGCTGT CAGGTACACA GGGAGGAGT CAGGTACCA GGGAGGAGT CCCTATCCA GAGAAATCA ACCTTAGAAT AAAACCCAT TCCTCAATAT ACTCAAATGG CTTTATTAAA TTTCTTTTC CATCGTTATA TTTTGGAGGC ATCCTGATCAT TTTTGGAGGC ATCCTGATCAT TTTTGGAGCA TCCTGATCAT TTTTGAACATG GCTTTACAT TTTTGAACATG GCTTTAACAT TTTTTCCA GCTGTAACA GCTGTAACA GCTGTAACA GCTGTAACA GATACTTAAC GAAGTCACTG ACCAGTCTAA	CCGGGCCCG CCAAACTCTC GCAAACTCTC GCAAACTCTC GCAACTCTCA GTGACCGCC CGGATCCAGT ATTGGGGTG GGCATCAGA ATTGGGGTG GGCATGAAG TTTGGTCAGG CTACTTTGCT AAACTGCAC GTGTTAAAAT AGGGGAAG ATTGGTAAAC ATTGGTAAT ATTGGTAAT GTGTTAAAAT AGGGGAAG GTCATTTAAT CTTTTGCCAC GCCTTTTCA AACCCTTAT AATCTTTCTG TCTTACCAT TCTTACCAT TGTTCACCAT TGTTCACCAT TGTTCACCAT TGTTCACCAT AGGCTAATTA AGTGTAATTA AGTGTAATTA AGTGTTAAAT AGTGTTAAAC AGTTAGAAG AACTATACCT TCCACTGAA	ACCCCAACCC ACCTCTCTCC CGCCTTCTGC CGCGTTCTGC CGCGTGCCCT AGGCCATGTA GCAAAGTCTT TGGTGGTTGG GTATGAAGT CCGTTCTCAC GTTCCTCTCAC GTTCCTGTCC CTTCCAGGGG AACCGAAAT ACTCATTCAA ACTCAGTGCT ATTTTACCAT ACTCTTCAA ACTCAGTGCT ATTTTACCAT ACTCAGTGCT ATTTTAACT TGTATTTAATT ACATTAGTA AAATACTATT TGTATTTATT TGTATTTATT TGTATTTATT TGTTTTTGTG TAGTTCTTAA AGGACCTAGC TATACTTAAT CGTGCTTTTAT TTGTTTTTGTG GGTGTTGTAA CCCCTAAACT TCATGCGTTT TCTTCTGCAGT TCTTTCTGCAGT TCTTTCTTCAC AGGTAGTGTG ATGAGTGTG ATGAGTGTC ACACACTTAC CAAAACCTAC CAAAACCTAC	120 180 240 300 360 420 480 540 600 720 780 900 950 1080 1140 1260 1380 1440 1560 1680 1740 1860 1980 1980 2010 2010
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50 55	Seq ID NO: Nucleic Ac: Coding seq 1 AATTTTCAGA TAAATGTATT GTGAAACCAT TCTGTTATCCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC	246 DNA sec id Accession sence: 897-3 11 AGITTCGTAT TAGITCTCATT TACITCTTAT TAATATGGAC TGAGTATTAA GGAGGTGAAA AAGAAAAGTC TACITCTGT	quence 1 #: XM_058 4400 21 GGGGATGGTT GCTCAATAGA AGGTTTTCACA AGGTTTTGAGAAAGC CCTCACTAGA ATGAAAATGC CAAAGACTTC TATTTTTAAG	31 TTATATARAAT AGAGATTTCT TTCCTATACATT TCCTAACATT TARAGGACA TGAACTAGTG CAGCATTTCC AACCCAGGAG	41 TCAGGITTIT AATAGAAAG AGATITGITC GCCACTITAG ATGITAGIGI TITICAAGCA AGGITCITAG GAAAGCITTA	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA	120 180 240 300 360 420 480
50	Seq ID NO: Nucleic Ac: Coding sequing AATTTTCAGA TAAATGTATT GTGAAACCAT CTGTTATCCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC TTATTTCTGT TTGTCCAGGC	246 DNA secid Accession lence: 897-3 11 AGITTCGTAT TAGTCTCGTAT TAGTCTCGTAT TAGTATGGAC TGAGTATAA GGAGGTGAAA AAGAAAAGTC TACTGTCTGT TGCCTATCTG GTTTATGTAT CAAGTGCAAT	Tuence 1 #: XM_058 1400 21	31 TTATATAAAT AGAGATITCT TTCCTGATACT TCCTAACATT TAAAGGATAT AAAAGGACAT TGAACTAGTG CAGCATTCC AACCCAGGAG TTGTTTTTTT TCATAGCTCC	41 TCAGGTTTTT AATAGAAAG AGATTGTTC GACACGTTTA GCACTTTAG TTTTCCAAGCA AGGTCCTAGA GAAAGCTTTA AAAGACAGGA TGGACTTAAG	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT TATTGGAAGG GAGGAACAAG TAATAGAACA TCTCACTCCA TGATCTGCCT	120 180 240 300 360 420 480 540 600
50 55	Seq ID NO: Nucleic Ac: Coding seq 1 AATTTTCAGA TAAATGATT GTGAAACCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC TTATTTCTGT TTGTCCAGGC GCCTTTGCCT	246 DNA sec id Accession ience: 897-1 11 AGTITICGTAT TAGTCTCATT TRATTATGGAC TGAGTATTAA GGAGGTGAAA AAGAAAAGTC TACTGTCTGT TGCCTATCTG GTTTATGTAT CAAGTGCAAT CCTGAGTAGC	TUENCE 1 #: XM_058 4400 21 GGGGATGGTT GCTCAATAGA AGTTCTTCACA AGTTCTTGAG TTGGAGAAGC CCTCACTAGA ATGAAAATGG CAAAGACTTC TATTTTTAAG AAGGGGTTTT GGCACGAACC TGGGACTACA	31 TTATATARAT AGAGATTCT TTCCTTATAC TCCTACATT TTARAGGACA TGAACTAGT CAGCATTTCC AACCCAGGAG TTCATTAGCTCC GGCATGAGCC GGCATGAGCC	41 TCAGGTTTTT AATAGAAAG GAGAGGTTTTG GCACTTTAG ATGTTAGTGT TTTCCAAGCA AGGTCCTAGA GAAAGCTTTAA AAAGACAGGA TGGACTTAAG CCCATGCCTTAGA	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TCTCACTCCA TCACTCCCT GCTAAGTTTG	120 180 240 300 360 420 480 540 600
50 55	Seq ID NO: Nucleic Ac: Coding sequence Antitroaga Anantotat GTGAAACCAT CTGTTATCCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC TTATTCTGT TTGTCCAGGC GCCTTTGCCT TTTTTTTTTT	246 DNA secid Accession tence: 897-3 11 ASTITUCATA TAGTOTIATA TAGTOTIATA TAATATGAC TGAGTATTAA AGGAGATGAA AAGAAAGTC TACTGTCTGT TGCCTATTCTG GTTTATGTAT CAAGTGCAAT CCTGAGTAGC TGTTTGTTTG	Huence #: XM_058 400 21 GGGGATGGTT GCTCAATAGA ATGTTTCACA AGTTCTTGAG ATGAGAAGC CCTCACTAGA ATGAAAATGG CAAAAGACTTC TATTTTTAAG AAGGGGTTTT GGCACGAACC TGGGACTACA TTTGTTTTTG	31 TTATATARAT TAGGATTTC TCCTGTTAC TCCTAACAT TTAAGGACA TGAACTAGTG CAGCATTTC CAGCATTTC AACCCAGGAG TTGTTTTTT TCATAGCTCC GGCAGGAGGCC GGCAGGGGGGTTG	41 TCAGGITTIT AATAGAAAA AGATICGTIC GAGAGGITTI GCCACITIAG TCTCCAGCA AGGTCCTAGA GAAAGCTTA AAAGACAGGA TGGACTTAAG TGGACTTAAG TTTTTTTTTT	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGACAAG TCTCACTCCA TGATCTGCCT GCTAAGTTTG TGTAGAGACAG TGTAAGTTTG TGTAGAGACAG	120 180 240 300 360 420 480 540 660 720 780
50 55	Seq ID NO: Nucleic Ac: Coding sequing sequing AATTTTCAGA TAAAATGTATT GTGAAACCAT CTGTTATCCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC TTATTTCTGT TTGTCCAGGC GCCTTTGCT TTTTTTTGTT TAGTCTTGCT TTAGTCTTGCT TTAGTCTTGCT	246 DNA secial Accession lence: 897-3 11 AGTITICGTAT TAGTICTAGT TICTICTAGT TAGTICTAGT TAGTICTAGT TAGTICTAGT TACTICTAGT TGCTATCTG TGCTATCTG TGTTATGTAT CAGTICAAT CAGTICAAT CTGAGTAGT TGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCTAGTTGCCAG	TUENCE 1 #: XM_058 1400 21 GGGGATGGTT GCTCAATAGA ATGTTCACA AGTTCTTGAG ATGTATCACA AGTTCTTGAG CCTACTAGA ATGAAAATTG CAAAGACTTC TATTTTTAG AAGGGGTTTT GGCACGAACC TGGGACTACT GTTTTTTTTTT	31 1 TTATATAAAT AGAGATTICT TCCTGATAC TCCTAACATT TAAAAGGACA AAAAGGGACA AACACAGGAG TGGTTTTTT TCATAGCTCC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC GGCATGACC ACCCCTGGC	41 TCAGGTTTT AATAGAAAAG AGATTGTTC GAGAGGTTTT GCCACTTTAG TTTCCAAGCA AGGTCCTAGA GAAAGCTTTA AAAGACAGGA TGGACTTAAG CCCATGCCTG TTTTGTTTTT TTCAAGTGAT	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGACAAG TAATAGAACA TCTCACTCCA TGATCTGCCT GCTAAGTTTG TGTAGAGACG CCTCCTGCCT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60	Seq ID NO: Nucleic Ac: Coding sequity AATTTTCAGA TAAATGTATT GTGAAACCAT CTGTTATCCA ATAGAGGGAA TGGGATGAGA ACTGGTAACC TTATTCTGT TTTGCAGGCT TTTTTTTGTT TTGTCCAGGC GCCTTTGCT TTTTTTTTTT	246 DNA secid Accession lence: 897-3 11 AGITTCGTAT TAGTCTCGTAT TATCTCTTTA TATATGGAC TGAGTATAA AGGAAAAGTC TACTGTCTGT TGCCTATCTG GTTTATGTAT CAGGGCAAT CCTGAGTAGC TGTTTGTTTG TTGCCAG GAGTGCCAG GAGTGCCAG	quence 1 #: XM_058 400 21	31 TTATATAAAT AGAGATTCT TTCCTGTTAC TCCTAACATT TTAAAGGACA TGAACTAGTG CAGCATTCC AACCCAGGAG TTGTTTTTT TCATAGCTCC GGGGGGGTTG AACTCCTGGC TTGGATTCAG	41 TCAGGTTTT AATAGAAAG AGATTGTTC GAGAGGTTTT GCCACTTAG ATGTTAGTGT TTTCCAAGCA AGGTCCTAGA GAAAGCATTA AAAGACAGGA CCCATGCCTG TTTTGTTTTT TTCAAGTGAT CTTCATT	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TCTCACTCCA TGATCTGCCT GCTAAGTTTG TGTAGAGACG CCTCCTGCCT TCCACACATGG	120 180 240 300 360 420 480 540 660 720 780
50 55	Seq ID NO: Nucleic Ac: Coding seq 1	246 DNA secial Accession ience: 897-1 11 1	Quence #: XM_058 4400 21 GGGGATGGTT GCTCAATAGA AGTTCTCACA AGTTCTTCACA AGTTCTTGAG TTGGAGAAGC CCTCACTAGA TTGAAAATGG CAAAGACTTC TATTTTTAAG AAGGGGTTTT TGGACGAACC TGGGACTACA TTTGTTTTTG GCTAGTCCTAG ATTACAGCAC CTGGACCCTG	31 TTATATARAT AGAGATITOT TCCTTGATIAC TCCTACATIT TTARAGGACA TARAGGGACA TAGACTAC AACCAGGAG TTGTTTTTT TAGACTAC GGCATGAGCC GGCATGAGCC GGCATGAGCC GGCATGAGCC GGCATGAGCA TTGGATTCAG AACCCAGGA GAAGCTATT	41 TCAGGTTTT AATAGAAAAG AGATTGTTC GCACTTTAG ATGTTAGTGT TTTCCAAGCA AGAGCCTTAA AAGACAGGA TGGACTTAA CCCATGCCTG TTTGTTTT TTCAAGTAAT TTCAAGTAAT CTTCTTCATT GCAATGCCTC GCAATGCCCTG	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCTTCCT TATTGGAAGG GAGGAACAAG TATAGAACA TCTCACTCCA TCACTCCT GCTAAGTTTG TGTAGAGACG CCTCCTGCCT TCCAACAAGG TCCCACATAGG TCCAACAAGG TATGACAAAA	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50 55 60	Seq ID NO: Nucleic Ac: Coding sequing sequing AATTTTCAGA TAAATGTATT GTGAAACCAT CTGTTATCCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTA ACTGGTAACC TTATTTCTGT TTGTCCAGGC GCCTTTGCT TTTTTTTGTT TAGTCTTGCT CAGCCTCCCA AAGAAACTTA ACCATCAAAT	246 DNA secial Accession and A	TUENCE 1 #: XM_058 1400 21 GEGGATGGTT GCTCAATAGA ATGTTCACA AGTTCTTGAG TTGGAGAAGC CCTCACTAGA ATGATATTTTAG CAAAGACTTC TATTTTTTTTTT	31 1 TTATATAAAT AGAGATTTCT TCCTGATAC TCCTAACATT TTAAAGTATT TAAAAGGACA AACCAGGAG AACCAGGAG GGGGGGGTTG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC TTGGATTCAG AACTCCTGGC	41 TCAGGTTTTT AATAGAAAG AGATTGTTC GAGAGGTTTT GCCACTTTAG TTTCCAAGCA AGGTCCTAGA GAAAGCTTTA AAAGACAGGA TGGACTTAAG CCCATGCCTG TTTTGTTTTTTTTCAAGTGAT TTCAAGTGAT CTTCTTCATT GCAATGCCCC CAAGTGCAGA	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGACAAG TCTCACTCCA TGATCTCCT GCTAAGTTTG CTAAGTAGT TGTAGGACG CCTCCTGCCT TCCAACATGG TATGCAAAAA AAGAATCATC	120 180 240 300 420 480 540 660 720 780 840 900 1020
50 55 60	Seq ID NO: Nucleic Ac: Coding sequing	246 DNA Secial Accession ience: 897-3 11 AGITTCGTAT TAGTCTCGTAT TAGTCTCGTAT TAGTCTCGTAT TAGTCTGGT TGCTGTTGT TGCTATCTG GTTTATCTGT TGCTATCTG TTTTATTATCAGTGCAAT CCTGAGTAGC TGTTTGTTTG TGTTTGTTTGCAG GAGTGCTAGC CACGACTCC CAGGGCTTGC AAGCAAATTG	quence 1 #: XM_058 1400 21 GGGGATGGTT GCTCAATAGA AGTTCTTGAG AGTCTTGAG TTGGAGAAGC CCTCACTAGA ATGATTTTAAG CAAAGACTTC TATTTTTAAG AAGGGTTTT GGCACGAACC TGGGACTACA TTTGTTTTTG ACTACTAGCAC CTGGACCTCG ATTACAGCAC CTGGACCCTG GGGACTTCCTT GCTACTTGTC	31 TTATATAAAT AGAGATITCT TTCCTGTTAC TCCTAACATT TTAAAGGACAT TGAACTAGTG CAGCATTTCC AACCCAGGAG TTGTTTTTTT TCATAGCTCC GGCAGGGGCTTG GGCAGGCCC TTGGATCAG AACTCCTGGC TTGGATCAG AGAACTCAGC TTGGATCAG AGAACTCCTAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC TCGATCAGC	41 TCAGGTTTT AATAGAAAG AGATTTGTTC GACACGTTTT GCACACTTTAG ATGTTAGTGT TTTTCCAAGCA AGGTCCTAGA GAAAGCATTAA AAGACAGGA CCCATGCCTG TTTTGTTTTT TTCAAGTGAT CTTCTTCATT GCAATGCCCC CAGTGCCCC CAGTGCCCC	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TCTCACTCCA TGATCTGCCT GCTAAGTTTG TGTAGAGACAGG TATGACAACA TGTCCTGCCT TCCAACATGG TATGACAAAA AAGAATCATC GTTCCTCGAG GTTCCTCGAG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080
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50 55 60	Seq ID NO: Nucleic Ac: Coding sequing sequing AATTTTCAGA TAAATGTATT GTGAAACCAT CTGTTATCCA ATAGAGGGAA TGGGATGAGA GATCATGTTT GTTGAGTGTAC TTGTTCAGGC GCCTTTGCT TTGTTCAGGC GCCTTTGCT TTGTTTTTTTTTT	246 DNA Secild Accession lence: 897-3 11	Huence #: XM_058 400 21 GGGGATGGTT GCTCAATAGA AGTTCTTGAG TTGGAGAAGC CCTCACTAGA ATGATTTTTAAG CAAAGACTTC TATTTTTAAG GCACGAACC TGGGACTACT GCTAGTACT GCTAGTACT GCTAGTACT GCTAGTACT GCTAGTCTC GCTAGTCTC GCTAGTCTC GCTAGTCTC ATTACAGCAC TTGGACCTT GCTACTTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTGTC AGACAAGAGA AAAGAITTGT	31 \ \text{TTATATAAAT} \AGAGATTICT \text{TTCCTGTTAC} \text{TCCTGACATT} \text{TTATATATATT} \text{TATATATATT} \text{TATATATATT} \text{TATATATATT} \text{TATATATATT} \text{TATATATATT} \text{TATAGATTCC} \text{AGCATTTCC} \text{AGCATTTCCTATAGCTCC} \text{GGCATTGGCTTATAGCTCTTGATTCATAGCTATTCATTATCCTTCAATGC} \text{ATCATCTTATCCTTCAATGC} \text{ATCATCTATTATCCTTCAATGC} AGCAGAGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG	41 TCAGGTTTT AATAGAAAAG AGATTGTTC GAGAGGTTTT GCCACTTTAG TTTTCCAAGCA AGGTCCTAGA AGACCTTAAG CCCATGCCTG TTTTGTTTTT TTCAAGTGAT TTTCAATGTTT TTCAAGTGAT CTTCTTCATT GCAATGCCCC CAAGTGCAGA TGGCCACCAG TTGTATTAGG TGGCCACCAG TTGTATTAGG CAGCACCTGG CAGCACCCCAC CAGCACCCCC	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGACAAG TAATAGAACA TGATCTCCA TGATCTCCA TGATCTCCT TCTAAGTTTG CTTAAGAGACG CCTCCTGCCT TCCAACATGG AAGAATCATC GTTCCTCGAG CAAGATCTTC GTTCCTCGAG CAAGATCTTC CTTCCTCGAG CAAGATCTTC CTTCTCTCGAG CAAGATCTTC CTTTGTCTCGGG CTTTGTCTCGGG CTTTGTCTCGGG	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1200 1260
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50 55 60 65 70	Seq ID NO: Nucleic Ac: Coding sequity ATTOTICAGA TRAATGTATT GTGAAACCAT CTGTTATCCA ATAGAGGAA ACTGGTAACC TTATTCTGT TTGAGTTAT GTTGAGTTAT GTTGAGTTAT GTTGAGTTAT CTTGATTTTCTGT TTGTCTGGT TTGTTTTTTTGT TTGTCTTGCT CAGCCTCCCA AAGAACTTA ACCAACA CTGAACTAAA CTGAACTAAC GCACACACACA ATAACCTAGA GTACACACAC ATAACCTAGA GTTGCTTCTT	246 DNA Secial Accession in Acc	quence #: XM_058 400 21 GGGGATGGTT GCTCAATAGA AGTTCTGAG AGTCTTGAG TTGGAGAAGC CCTCACTAGA AGTTTTTAAG AGGGTTTT TATTTTTAAG GCAAGAACC TGGGACTACA ATTACTGTTTTA GCTACTAGA ATTACAGCAC CTGGACCCTG GCTACTTGT GCTACTTGT GCTACTGT AGACAGACC TGAGACCCTG AGACAGACC TGAGCTGT CCAAGCTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTGTC TCAAGCTCT TGAGTTCCCA TGGGTTCCCA TGGGTTCCCA TGGGTTCCCA TGGGTTCCCA TGGGTTCCCA	31 1 TTATATAAAT AGAGATITCT TTCCTGTTAC TCCTAACATT TTAAAGTATT TAAAGGACT TGAACTAGTG CAGCATTCC AACCCAGGAG TTGTTTTTTT TCATAGCTCC GGCATGAGC GGGGGGGTTG AACTCCTGGC TTGGATTCA AGAACTATTA AGAAGCTATT CCTTCAATGC ATGACTAGAG CTCTGGCTGA ATGACTAGAGAG CTCTGGCTGA AATCTCTTCCT TGGAGCAA AATCTCTCCC TTGGAGCAA AATCTCTCCC TTGCAGCAA AATCTCTCCC TTTCCATCCA TTTTCCTCCT	41 TCAGGTTTTT AATAGAAAG AGATTGTTC GACAGGTTTT GCACACTTAG ATGTTAGTGT TTTCCAAGCA AGGTCCTAGA AGAGCATTAA AAAGACAGGA ACGTCCTAGA TCTAGTTTT TTCAATGGACTTAG CCATGCCTG TTTTGTTTT TTCAATGGACTTAGG CAAGTGCAGA TCGCACCCCA TTGTATTGAG GAGCACTTGG GAGCACTTGG CAGCACCCCA CATAGTTACA GTATGTTCTG ATGCTAGACCA	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TCTCACTCCA TGATCTGCCT GCTAAGTTTG TGTAGAGACC CCTCCTGCCT TCCAACATGG TATGACAACA AAGAATCATC CATTCCTCAGG CAAGATGTTG CAGTCCCTC CTTCTCCAGG CAAGATGTTG CAGTCCCTC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC CAGTCCCTCC TTTGTCTCGGG GAACATAAGA CCATGGAAAA CTAGAAGACT TAGAATGGTA	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1260 1380 1380 1340 1440 1500
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50 55 60 65 70 75	Seq ID NO: Nucleic Ac: Coding sequity AATTTTCAGA TAAAACATT GTGAAACCAT GTGAGAACCAT GTTGAGTGTA ACTGGTTACCA ACTGGTAACC TTATTCTGT TTGTCCAGGC GCCTTTGCT TTGTCCAGGC GCCTTTGCT TTGTTTTTTTTTT	246 DNA secidid Accession ience: 897-3 11	quence #: XM_058 400 21 GGGGATGGTT GCTCAATAGA AGTTCTTGAG AGTTCTTGAG AGTTCTTGAG ATGATATTTTAAG ATGATATTTTAAG AAGAGATTC TATTTTTAAG GCTAGTACT ATTGTTTTT GCTAGTCTCA ATTACAGCAC CTGGACCTTGGACCTTG AGATTCCTT AGCTACTTGT AGCAAGAGA AAGAGTTCCT TGAGCTGTC CAAGCTGTC AGAGCAGAAGC CTGAGATTCCT AACACAGCC CGAGTTCCCA ACTGACAAGC ACTCAGAAGC Bequence: P_058553.1 KNHQIRACRF	31 \TTATATAAAT AGAGATITCT TCCTGATACT TCCTACACTT TCAAAGTATT TAAAGGACT TCAAACTT TAAAAGGACT TCAACACTT TCAAAGCACT TCAACCT AGCATTACT AAACGGACC AGCATTACT AACCCCTGGC TTGGATCAG AGAACTCCTTG AACCCCTGGC TTGGATCAG AGAACTCTTAT CCTTCAATGC ATGACAGAAG CTCTGGAGCAA ATCTCTCC ACACTTTTT TTCCAATAA TTTCCTCCT ACACTTTTT TTCCAAATAA 31 PYHLIKCREN	41 TCAGGTTTT AATAGAAAAG AGATTGTTC GAGAGGTTTT GCCACTTTAG ATGTTCAGTGT TTTTCCAAGCA AGGTCCTAGA GAAAGCCTTA AAAGACAGGA TGGACTTAAG CCCATGCCTG TTTTGTTTT TTCAAGTGAT CCTCACTG CAAGTGCAGA GAGCACTAG GAGCACTAG GAGCACTAG CAGCACCCA CATAGTTACA GTATGTTCTC ATGTTACT GTATGTTCTC ATGCCACCCT ACCTTGATA 41 HPDVASKLAT	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TGATCTCCT GCTAAGTTTG TGTAGAGACG CCTCCTGCCT TCCAACATGG TATGACACAA AGGATCATC GTTCCTCGAG CAAGATGTTG CAGTGCCCT TTTGTCTCGAG CAAGATGTTG CAGTGCCCTC TTTGTCTCGGG GAACATAAGA CCATGGAAAAA CCATGGAAAAA CCATGGAAAAA CCATGGAAAAA CAAGAATCTC TAGAATCCTCA CAGATTG 51 CPFNARHQVP	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1140 1200 1250 1320 1320 1320 1350 1440 1500
50 55 60 65 70 75	Seq ID NO: Nucleic Ac: Coding Bequity Antitroaga Ataanactat Graaaaccat Gratatcaga Gatcatgiti Gritatcaga Gatcatgiti Gritatcaga Gatcatgiti Gritatcaga Gatcatgiti Tigitoaga Gatcatgiti Tigitoaga Gatcatgiti Tigitoaga Gatcatgiti Tigitoaga Gacticaga Gacticaaa Cactacaaa Accatcaaat Crigaatgiag Crigaaataa Gataaccaaac Crigaaataa Gataaccaaac Crigaaataa Gataaccaaac Tigitoagataa Gataaccaaac Crigaaataa Gataaccaaac Tigitoatga Acaaccaaac Tigitoatga Acaaccaaac Tigitoatga Acaaccaaac Ataaccaaac Titaatgcaa Seq ID NO: Protein Acc 1 MEETITOSLD RABISHISS	246 DNA secid Accession sence: 897-3 11 AGTITCGIAT TAGTCTCAGT TICTCTITTA TAATATGGAC TGAGTATTAA GGAGGTGAAA AAGAAAAGTC TACTGTGTGTTTGCTATTTTTTTTTT	quence a #: XM_058 400 21 GGGGATGGTT GCTCAATAGA ATGTTCACA AGTTCTTGAG ATGAAAATGG CAAAGACTTC TATTTTTAG AAGGGGTTTT GGCACAGA ATTACAGCA ATTACAGCAC CTGGACCTG AGGTTCCTT GCTACTTGT AGGACACC CTGACACTGT AGACACTGC AGGTTCCTA ACTACAGCA CTGAATACCT CAGAGTTCCCA ACTGACAGC CTGAATACCT CAGAGTTCCCA ACTGACAGC ACTCAGAAGC ACT	31 TTATATAAAT AGAGATTTCT TCCTGTTAC TCCTAACATT TTAAAGTATT TTAAAGTATT TTAAAGTATT TCAAGGAC TGAACTATGTC CAGCATTTCC GGCAGGAG TTGTTTTTT TCATAGCTCC GGGGGGGTTG AACTCCTGGC TTGGATTCAG CTTCGATTCC CTTCAATGC CTTCGATGC CTTCGATGC ATCTCATCAA TCATCTTAT TCCTCATCAC ATCTCATCAC ATCTCATCAC ATCTCATCAC ATCTCATCAC ATCTCATCAC ATCTCATCAC ATCTCATAC ATCTCATCAC ATCTCATAC ATTTTCTCCT ACACTTTTTT TTCCAAATAA 31 PYHLIKCRRN ETLARSTNQC	41 TCAGGTTTTT AATAGAAAG AGATTGTTC GAGAGGTTTT GCCACTTTAG TTTCCAGCA AGGTTCTAG GAAAGCTTTA AAAGACAGGA TGGACTTAG CCCCATGCCTG TTTTGTTTT TCAAGTGAT TCTCTTCATT TTCAAGTGAT TCTCTTCATT TTCAAGTGAT CCCCCAGAGCACCAC CAAGTGCAGA GAAAGCCTTCG CAGGCACCAC CATAGTTACA GTATGTTCT ATGCCAGACC AACTTGATA ATCTAATTA CCTCCCCCT ACCTTTGATA 41 HPDVASKLAT PPCDEDWIND	51 CCCACAATAA GATTCAAACT TCTTGTGACT CCCTTAGTGC CACTGAAGAT GGCCCTTCCT TATTGGAAGG GAGGAACAAG TAATAGAACA TGATCTCCT GCTAAGTTTG TGTAGAGACG CCTCCTGCCT TCCAACATGG TATGACACAA AGGATCATC GTTCCTCGAG CAAGATGTTG CAGTGCCCT TTTGTCTCGAG CAAGATGTTG CAGTGCCCTC TTTGTCTCGGG GAACATAAGA CCATGGAAAAA CCATGGAAAAA CCATGGAAAAA CCATGGAAAAA CAAGAATCTC TAGAATCCTCA CAGATTG 51 CPFNARHQVP	120 180 240 300 360 420 540 660 720 780 960 1020 1080 1140 1260 1380 1380 1350 1560

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Nucleic Acid Accession #: NM_003392
Coding sequence: 758..1855

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	<u> </u>	CCCCCCTCCT	-	maga serroge		TOGGOTOGTA	60
	TTAAGGAAAT	GAAACATACG	ATTECCEATE	GGAGCTGCAT	TTCCCAGCTG	GGCACTCTCG	120
10	OGOGCTGGTC	CCCGGGGCCT	CGCCCCCCAC	CCCCTGCCCT	TCCCTCCCGC	GTCCTGCCCC	180
	CATCCTCCAC	CCCCCCCCCCCCCT	GGCCACCCCG	CCTCCTTGGC	AGCCTCTGGC	GGCAGCGCGC	240
	TCCACTCGCC	TCCCGTGCTC	CTCTCGCCCA	TGGAATTAAT	TCTGGCTCCA	CTTGTTGCTC	300
	GGCCCAGGTT	GGGGAGAGGA GCACAGCACC	CGGAGGGTGG	CCGCAGCGGG	CTCCCCAGIG	CACCCACA	360 420
15	GAGGGACIGA	AGGGGGGGGG	ACCAGGGCTT	TGACTCAACA	GAATTGAGAC	ACGITTGTAA	480
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	CTCTCTCCCA	CATGGTACAC	ATCCAGAAGG	TAAAGAAATA	CATTTTCTTT	TTCTCAAATA	2220
45	ተረጉር አጥር አጥል	TREGRATEGET	AGGTTCCAGT	TGAAAGAGGG	TGGTAGAAAT	CTATTCACAA	2280
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•	AATGGAAGAT	AGAATATAAA	ATAAAACGTT	ACTIGIAAAA	AAAAAAA		
		249 Protei					
85	Protein Ac	cession #:	NP_003383				
0,5	1	11	21	31	41	51	
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Protein Accession #:NP_002649.1
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Seq ID NO: 294 Protein sequence: Protein Accession #: NP_001489

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WO 02/086443
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			ECDSPSYQKR KDRMMQKPGS				120
			YEKIFEMLEG				180
35	LKKKLKRMI	* I I I I I I I I I I I I I I I I I I I		TOUR TRYINGS	rrotina	NG-MGDI VIGI	200
	Seq ID NO:	297 DNA sec	quence				
	Nucleic Ac	ld Accession	n #: Eos se	quence			
40	Coding sequ	ence: 247-	315				
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	•		21	21	43	53	
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	Coding sequ	ence: 247-8	315				
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### PRESIDENTS GENTRISALLY PURPORTED FREEINMANN NI.SDGQRTVT GIANNULVP 180 CHERNESURS TYPGINADMI. DSIRRORED FROEINMANN NI.SDGQRTVT GIANNULVP 180 CHERNESURS T	20	1			31	41	51	
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TESLIGENUS YIPDGIRADILI DSIRPOREDE PRERIINMENN NISDGORTYT GILANDILIP COMPRISED THE PITTENS ANKICEPIL LETTESPESTE HAMBINUS PRESSIVINI GORDFRAYUL SAGYISHEYS YIGKVATGRY GPSIGASGAI MYULANUTKI IPBGELAIII GORDFRAYUL SAGYISHEYS YIGKVATGAI GORDFRAYUL SAGYISHEYS YIGKVATGAI GARAGACA THE ACCESSION II NO 000625 COCIGGOCCACAGT GRAGACAGT TAGACACAGT GAGTACTATA CACAGGAICAG CACAGGACTACA CACAGGAICAG CACAGGACTACA CACAGATAGA CACACACAGA GAGACACA TACACACACA GAGACACACA CACACAGAGAA TACACACACA CACACAGAGAA CACACAGAGAA GAGACACACA CACACAGAGAA ATACACACACA CACACAGAGAA CACACAGAGAA GACACACAC								
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DEPETRAGE NALITATION AMILGREFF BRABHLIGAL FGIVYVTGE ELIWENREPL 360 Seq ID NO: 312 DNA sequence Seq ID NO: 312 DNA sequence Seq ID NO: 312 DNA sequence Coding sequence: 1953656 35								
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ACACAAATT CAGGTACGCT GTOTTTGGCC TOGGCTCCAG CATGTACCCT CGGTTCTGGC 2100 CCTTTGCTCA TGACATTGAT CAGAAGCTGT CCCACCTGGG GGCCTCCAG CTCACCCCGA 2160 TGGGAGAAGG GGATGAGCTC AGTGGGCAG AGGACGCCTT CCGCAGCTGG GCCGTCCAAC CCTTCAAGGC AGCCTGTGAG ACGTTTGATG TCCGAGGCCA ACACGCCCAC CAGGCTCGG CAGGACCCAC AGCCTTACAC CTCCAAATGTG ACCTGGGAC CGCACCACTA CAGGCTCGTG CAGGACCACCAC AGCCTTACAC CTCCAAATGTG ACCTGGGACC CAGACCACTA CAGGCTCGTG CAGGACCACCAC AGCCTTACACAG CCGCCACACACAC CAGGCTCGTG CAGGACCTAC CAGGCTCGTG CAGGACCTACC CAGGCTCGTG CAGGACCTAC CAGGCTCGTG CAGGACCTAC CAGGCTCGTG CAGGACCTAC CAGGCTCGTG CAGGCCCACCAC ACCCCCACCAC CTGGCGAGAT CTACAAAGTC CAGACTCCAC CTGGGGAGCAC CTTGGGGGTTT 2520 GCCCAGGCAA CCAGCCGGCC CTGGAGGCCCT ACCACCTAC GGCAGCACCAC TGGGGGAGCAC CTGGGGGAGCAC CTGGGGGTG CACCCCCACAC CAGGCCCTCG CTGGAGGGCC TGGATGAGAG TGGCAGCTAC TGGGCCCAC 2700 ACACGCCCAC CCAGCTGCTG CTCCAAAAGC TGGCCCCACG CACACGAA GAGCCTGAGA CACCCCCACC CAGGCTGCT CTCCAAAAGC TGGCCCCACC CAGCTGCAC CAGCCCCCCAC CAGCCCCCCC CAGCTGCTG CTCCAAAAGC TGGCCCCACAC CAGCCCCCACAC CAGCCCCCCC CAGAGTACACC CAGAGTACACC CAGACTACCC CAGAGTGCAC CAGACTACCC CAGAGTACACC CAGAGTACACC CAGAGTACCAC CAGAGTACCAC CAGAGTACCAC CAGAGTACACC CAGAGTACCAC CAGAGTACACC CAGAGTACCAC CAGAGTACCAC CAGAGTACCAC CAGAGTACACC CACCCCCCACATT CCCGGAGGGCC CAGAGTACCAC CAGAGTACACC CAGAGTACACC CACCCCCCCCCACATT CCCGGAGGGCC CAGAGTACCAC CAGAGTACC								
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175								
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PCT/US02/12476

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2220

2340

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306

WO 02/086443 Coding sequence: 317-1123

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20	COCCOTTOCO	CCCCCACCTC	AGGTGACCTA	CACCACCCCC	TTCCAGACCA	CCAGTTCCTC	780
••	CHARLES A COLOR	CALCIOCOCCUPACE	CCTCTGCGGC	CAATGTAGCC	TGTGGGGAAG	GTGACAAGGA	840
	CONCACTORG	DC-TC DT-TATT	TOTTTTCCAA	GGAGAAGGCC	CCCGATGTGT	TCGACTGGGG	900
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43	COMMITTEE & TYPE	TOTAL ACTO	CAACCTCTCT	CTTGGCGTGC	CACGGTGGGG	ATTICGIGAC	2340
	MOM 2 M 2 M C 2	Andread Mathematical Laboratory	بالملماء المائدة مان	TCAAATTCCA	ATGTGACCAA	TTCCCGATCA	2400
	CCCMCCCCCCCC	**************************************	TARGEGETT	CCCTGAATAT	CTTCTCTGCT	CACTTCCACC	2450
	***********	A A A A COTTO A C	TOTAL CONTRACTOR	TCATTAGGAT	TGAAATGATI	TGTTTCTCTT	2520
50	COMP CC MOD	**************************************	המידים בידים ד	TCAATTAGGT	AAGAAGATCI	GGTTTTTTGG	2580
	TO A A CCCA A	CATCTTCCCA	CTGGAAACAT	TTCTTTACAT	TIGCATICCI	CCATTTCGCC	2640
	******************************	בירות ממיים ביותים	יייבאדא(ביויי	CACATCCTCC	AGAATGGCC	GAAGIGCAAI	2700
	TAACCTCTTA	GGTGGCAAGG	AGGCAGGAAG	TGCCTCTTTA	GTTCTTACAT	TTCTAATAGC	2760 2820
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	ALCOUNTS A A A	THE STATE OF THE PARTY.	GGAGGGAAGG	AAGAGGGAAA	GAGATGACTA	ACTAAAATCA	3360
		*****	י ראאאמררים ייי	TATATTATAT	CCTCATTITA	LAAAGTTACAT	3420
65	CONCORD BEEN	* ************************************	CATABTECAS	TOGATAGTG	GCACTCTTT	Tererere	3480
	manamana a	* ********	, מכמכמכמכמ	' ACACACACAC	: AGAGACACU	CACCATTCIG	3540 3600
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15		* ************************************	י אבו מאריידים או	NTEGETGGA:	r GCGCTGCTG	A CCAACATCAG	4140
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HYOSGPUPGT AINGTLPLSH M

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		GAGCCGGACC					840
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50 55 60 65 70	Protein Acc 1 MADRITOLOD LIARTAKDID ALADIAQSQL Seq ID NO: NUCLEIC AC: Coding sequ 1 ATGGAGAATC CTGCGCGTGG CATTTCAAAG TTCTTAGACC ACAGTACAGA ACTGTTACAAG ACTGTTACAAG TTCTTGGAA TTCTCTTGGAA TTCTCTTGGAA AAAGCTGTG TTCTTTGGATC CATTCCATAT AAAGTTAGAT ATAAATTTC CATGCCTGTG Seq ID NO:	11 AVNSLADQFC VLIDSLPSEE KTESGTHSQS 372 DNA Section accession ac	NP_0042 21 NAIGVLOQCG STAALQAASL LPDS Quence #: AJ27105 GCGCATGTC CGTACAGAAC TGGTGCCAAA AGAGCCTGTT TCAGTGGTGG CCTAAATAAA AGGATACCTG TGGACTGTG GGCTGACATG TGTGACATG TGTGTTATTC GTTTTATTG TTATTTTTTTTTT	31 PPASFNNIQT YKLEEENHEA 1	AINKDQPANP ATCVEDVVYR 41 AGCGACACCG GCATCACTGA TCTATGAATT CCCAGAGGCA CAAAGCAGGA AAAGCGAAG ATCTTGTGCA TCTTGGGAAA GCCAGATGCT TGCTGGGAAATTT TCACATGGCT TGCTCTCAGT TGCCATATCC TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATTTT	TEEYAQLFAA GDMLLEKIQS 51 GAGGCTATAT AAACGTGCTG TCACCTGGAG GGTAAACATT AAAGGCACCA CTCTCCTGAA ATTCTTGGGA ATTCTTGGGA AGAGTCCTTT GGCAGTTGTG TCTGATCCAG AATGCAGAAC CAGGTACTCT TCGTTACACT GATTCAGTCC AGTGAAAATC AGGTTTATAC AGGTTTATAC	120 60 120 180 240 360 420 480 540 660 720 780 840 900 1020	
50 55 60 65 70 75	Protein Acc 1 MADRITOLOD LIARTAKDID ALADIAQSQL Seq ID NO: NUCLEIC AC: Coding sequ 1 ATGGAGAATC CTGCGCGTGG CATTTCAAAG TTCTTAGACC ACAGTACAGA ACTGTTACAAG ACTGTTACAAG TTCTTGGAA TTCTCTTGGAA TTCTCTTGGAA AAAGCTGTG TTCTTTGGATC CATTCCATAT AAAGTTAGAT ATAAATTTC CATGCCTGTG Seq ID NO:	11 AVNSLADQFC VLIDSLPSEE KTESGTHSQS 372 DNA Section accession ac	NP_0042 21 NAIGVLOQCG STAALQAASL LPDS Quence #: AJ27105 GCGCATGTC CGTACAGAAC TGGTGCCAAA AGAGCCTGTT TCAGTGGTGG CCTAAATAAA AGGATACCTG TGGACTGTG GGCTGACATG TGTGACATG TGTGTTATTC GTTTTATTG TTATTTTTTTTTT	31 PPASFNNIQT YKLEEENHEA 1	AINKDQPANP ATCVEDVVYR 41 AGCGACACCG GCATCACTGA TCTATGAATT CCCAGAGGCA CAAAGCAGGA AAAGCGAAG ATCTTGTGCA TCTTGGGAAA GCCAGATGCT TGCTGGGAAATTT TCACATGGCT TGCTCTCAGT TGCCATATCC TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATCT TGCATATTTT	TEEYAQLFAA GDMLLEKIQS 51 GAGGCTATAT AAACGTGCTG TCACCTGGAG GGTAAACATT AAAGGCACCA CTCTCCTGAA ATTCTTGGGA ATTCTTGGGA AGAGTCCTTT GGCAGTTGTG TCTGATCCAG AATGCAGAAC CAGGTACTCT TCGTTACACT GATTCAGTCC AGTGAAAATC AGGTTTATAC AGGTTTATAC	120 60 120 180 240 360 420 480 540 660 720 780 840 900 1020	

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WO 02/086443

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WO 02/086443

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10	GATGATAGCA	CAACITIOIG	MINIMAIAA	TCCACAAAAC	PANCAGOOC	CONCINCION	2340
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20	ATTARCTATC	ATGAGAATAG	CACAAGAAAG	COUNTRACE	MUTCH ACTIVE	AGATTTCCCT	2940
20	TGGGTCCCTC	CAATAACATG	TGGAAATTCI	GGTAGATACA	ATTCAAGTIG	AGAIII I GOGI	3000
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	CANGARAGA	ATGGTGGGGT	THEFTGTTTGT	TTGGTTTTGT	TTTTGTTTTA	CAGCTGGAGT	3360
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	AGAATACAAA	OCCATOCKS!	CALL CHARGES	TTCACATGAG	COCCUCACTG	CTGACTTGCA	3480
30	CATIGGCATT	MUMMAGGUAC	CIMCAIGIAT	AGGTACAATG	CALVEY S CALCAGO	TO TO THE PARTY OF	3540
30	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGIACAAIG	GIAGAACIGI	AMICCIGICC	
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	VALUE OF THE PARTY	TEGATTCACC	TTACTCTTCT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	WITCHOOT			. Candara av	TCAAAGGAAT	ATTTAGATGC	6960
	THUMINAMIT	WETCETWALL					

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				TTTCTCCATT			480
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WO 02/086443

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	Nucleic According sequents of the sequents of	id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG	#: NM_014 1314 21 CCGGACTTCG CGCGGCGGCC AGCAAAAGCA	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA	CAGAACCTCG CGTCCCTGGC CCAGAGATTA	CCCAGCGCCC CGTAATTTG TTCTCAACCT	120 180
50 55	Nucleic According sequents of the control of the co	Id Accession Lence: 64 11	#: NM_014 1314 21 CCGGACTTCG CGCGGCGCC AGCAAAAGCA GGACATAAAA	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC	CAGAACCTCG CGTCCCTGGC CCAGAGATTA AGCAACCAGC	CCCAGCGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA	120 180 240
	Nucleic Actioning sequence of the control of the co	Id Accession nence: 64	#: NM_014 1314 21 CCGGACTTCG CGCGGGGCC AGCARAAGA AGGATTCATG	31 CCGCAOGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA	CAGAACCTOG CGTCCCTGGC CCAGAGATTA AGCAACCAGC TCACCTTTCA	CCCAGOGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGOGGCC	120 180
	Nucleic Actioning sequence of the control of the co	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAGC CCCTGGTCAC	#: NM_014 1314 21 CCGGACTTCG GGACAAAGCA AGCAAAAGCA AAGATTCATG TACCCCAGGC	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACTACCAACAA	CAGAACCTOG CGTCCCTGGC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACACTGCAAC ACTCACACAC	CCCAGOGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGOGGCC CACCAGCCCA AGCTCCTCCA	120 180 240 300
55	Nucleic Ac: Coding sequence Coding sequ	Id Accession lence: 64 11	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG ATTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAAA ACACCCAACA GCCCCTTATT	CAGAACCTOG CGTCCCTGGC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACACTGCAAC ACTCACACAC CACTGCCACC	CCCAGCGCCC CGTAATTTTG TTCTCAACCT TAAGCAAGCA AACAGCGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC	120 180 240 300 360 420 480
	Nucleic Actional Sequence of the Coding Seque	Id Accession nence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC CCCTGGTCAC TTACAGTCGG	#: NM_014 1314 21 CCGGACTTCG CGCGGGGCC AGCANANGCA AGGATTCATG TACCCCAGCA AACCCAGGCC CCCTAGCTTCA	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCACACA GCCCCTTATT TCAACCGTCA	CAGAACCTOG CGTCCCTGGC CCCAGAGATTA AGCAACCAGC TCACCTTTCA ACACTGCAAC ACTCACACAC CACTGCCACC GCCACACAACA	CCCAGCGCCC CGTAATTTIC TTAGCAAGCA AACAGCGCCA AACAGCGCCCA AGCTCCTCCA AGCTCCTCAC TGGGAACACC	120 180 240 300 360 420 480 540
55	Nucleic Actioning sequence of the control of the co	Id Accession ience: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC CCCTGGTCAC TTAGAGTCGG GTAACTGGG GTAACCAGAC GTTACCAGCAGC	#: NM_014 1314 21 CCGGACTTCG CGCGGCGCC AGCARAAGCA GGACATAAAA AAGATTCATG TACCCCAGCA AACCCAGCCC CCCTAGCTTA AACCAGTTCA AACCAGTTCA	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCCTTATT TCAACCGTCA GCAACTTTAT	CAGAACCTOG CGTCCCTGGC CCCAGAGATTA AGCAACCAGC TCACCTTTCA ACACTGCAAC ACTCACACAC CGCCACACAAC CGCACACACAC CGATAGCACT	CCCAGCGCCC CGTAATTTTG TTCTCAACCT TTAGGCAGCA AACAGCGGCCC AACAGCCCA AGCTCCTCCA CACCATCACC TGGGAACACC GCACAAAAGC	120 180 240 300 360 420 480 540
55	Nucleic Ac: Coding sequence Coding sequ	Id Accession lence: 64 11	#: NM_014 1314 21	31 COGCAOGCTG GCGCTCTTCG GTTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCCTTATT TCAACCGTCA GCAACTTTAT CATGCCCCAG	CAGAACCTOG CGTCCTGGC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACACTGCAAC ACTCACACAC CACTGCCACA CGCACAACAAC GGATAGCACT GAACAACGGC	CCCAGGGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGGCCCA CACCATCACC TGGGAACACC GGCACAAAAGC AGCTGCCCAC	120 180 240 300 360 420 480 540
55 60	Nucleic Ac: Coding sequing sequing sequing sequing sequing sequing caccacacacacacacacacacacacacacacacacac	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC CCCTGGTCAC TTACAGTCGG GTAACCTGG GTAACCAGAC AGAAGCTGG GTAACCAGAC AGAAGCTGG TCCAAGACTGG	#: NM_014 1314 21 CCGGACTTCG CGCGGGGCC AGCANANGA AAGATTCATG TACCCCAGCA AACCCAGCC CCCTAGCTTA AACCAGTCA CACCTTCCA TCAACCCACC ACTGCCTCC ACTGCCTCC ACTGCCTCC	31 CCGCACGCTG GCGCTCTTCG GTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGGTCA GCAACTTTAT CATGCCCAG ACGGTCCTG GCAACTTTAT CATGCCCAG ACGGTCCTG	CAGAACCTCG CCTGGCC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACCTGCAAC ACTGCCACC ACTGCCACC ACTGCCACC GCCACCACACA CGATAGCACT GAACACGGC GACCACCAC GAAGCCACACC GAAGCCACAC	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC GCACAAAAGC GCACAAAAGC AGCTGCCCAC TGCACCTCAG CTGTATAAAA	120 180 240 300 360 420 480 540 600 660 720 780
55	Nucleic Ac: Coding sequence 1	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTTAGCAGC TTCCAACAGC TTCCAACAGC TTACAGTCAG GTAACAGC GTAACAGC GTAACAGCTGA GAAGCCTGA GGAAGCCTGA GCACAGCTGG TCAAGACTGG GGATACAGCT	#: NM_014 1314 21 CCCGGACTTCG CGCGGCGCGCC AGCARAAGCA AGACTATAAA AAGATTCATG TACCCCAGCA AACCCAGCC CCCTAGCTTA AACCAGTTCA CACCCTTCCA TCAACCCACC ACCTGCCTCC ATTTATCAG AATTTATCAG AATTTATCAG	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAA ACACCCAACA GCCCCTTATT TCAACCGTAC GCAACTTTAT CATGCCCAG ACGGTTCCTG GTTCTAAACG GTCTAAACG GTACTAAACG GTACTAAACG GTACTAAACG GTACTAAACG GTACTAAACG GTACTAAACG	CAGAACCTCG CCTCCCTGCC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACTCACACCAC CACTGCAACAC CACTGCAACAC GCCACACAAC GGATAGCACT GAACCACACAC GGACCACACAC GGACCACACAC GGACCACACAC GGACCACACAC GGACCACACAC GGACCACACAC GGACCACACAC GGACCACACAC GGACCACACT GAAGCAGACT	CCCAGGGCCC CGTAATTTTG TTCTCAACCT TAAGCAAGCACA AACAGCGCCA AGCTCCTCCA CACCATCACC GCACCAACACC GCACAAAAGC AGCTGCCCAC TGCAACTCACC TGCAACTCACC TGCAACTCACC TGCAACTCAGC TGCACCTCAG CTGTATAAAA ACCTCGGAGA	120 180 240 300 360 420 480 540 600 660 720 780 840
55 60	Nucleic Ac: Coding sequing seq	Id Accession Hence: 64 11	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCTTATT TCAACCGTCA GCAACTTTAT CATGCCCCAG ACGGTTCCTG GTTCTAAACG GACAAGGAGT GCCACAGGAGT	CAGAACCTCG CGTCCCTGGC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACCTGCAAC ACTCACACAC GCCACACAAC GGATAGCACT GAACAGGC GGCCCACCCC GAAGCAGAC GGTTTTTTC GGTTTTTTC ACTGTGCAC	CCCAGGGCCC CGTAATTTTG TTCTCAACCT TAAGCAAGCA AACAGGGCC CACCAGCCCA CACCATCACC TGGGAACACC GCACAAAAAC TGCACCTCAG CTGTATAAAA ACCTCGGAAA ACCTCGGAAAA	120 180 240 300 360 420 480 540 600 720 780 840 900
55 60	Nucleic Ac: Coding sequing seq	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTTAGCAGC TTACAGTCAG TTACAGTCAG GTAACAGTAGA GTAACAGTAGA GTAACAGTAGA GTAACAGTAGA GTAACAGCTGA GCACAGCTGG TCAAGACTGG GGATACAGCT TCAGACCCCAA TGAACTTTACAGTTGG	#: NM_014 1314 21 CCGGACTTCG CGCGGGGCC AGCAAAAGCA AAGCATCATGCA AACCCAGGCA AACCCAGGCA CCCTAGCTTA CACCCTCCA TCAACCCACC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCCA CGCAACGCAC GGATGTTAACAA CGCAACGCAA	31 CCGCACGCTG GCGCTCTTCG GTTCCAGAAA AAACCTGTCCT AATACAAAAA ACACCCAACA GCCCCTTATT TCAACCGTCA GCAACTTTAT CATGCCCAG ACGGTCCTG GTTCTAAACG GTCATCAGACA GCCCTCTGGG GCCAAGGAGT GCCTCTGGG GCCAAGGAGT GCCTCTGGG GCTAATCTCA	CAGAACCTCG CCTCCCTGCC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACCTGCAACC ACTGCCACC ACTGCCACC GCCACCACACA GGCACACACAC GGATAGCACT GAACCACACC GAACCACACAC GGCTTTTTTC GAACCACACAC CGTTTTTTC CAACCACACAC CATTTACCAA CATTTACCAA	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC GCACAAAAGC AGCTGCCCAC TGCACCTCAG CTGTATAAAA ACCTCGGAGA ACCTCGGAGA CCGAAAATGC GGAAAATGC	120 180 240 300 420 480 540 600 660 720 780 840 900 960
556065	Nucleic Ac: Coding sequitoring	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC CCCTGGTCAG ATACAGCTGG ATACAGCTGG GTAACCAGG ATACAGCTGG GCACAGCTGC TCAAGACTGG GGATACAGCT TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGAGT TCAAGACTGAGT TCAAGACTAGAGT TCAAGTGAGGT TCAAGTGAGGT TCAGTGAAGT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCTTATT TCAACCGTAC GCACTTAT CATGCCCAG ACGGTTCCTG GTTCTAAACG GCACATCTAACG GTTCTAAACG GCACATCTAACG TCAAACG GCACAGGAGT GCCTCTGGGA TTGACCGTCT CAGACAGCAG	CAGAACCTCG CCTGCCCCCGCGCACAGC CCACAGCTTTA AGCAACCACC CCCTCTCA ACTCACACAC CACTGCAAC CCCACACAC CGATAGCACC GAACAACGC GACCACACAC CGGTTATTTC CACTGCCAC CACTTTTACCAC CACTTTACCAC CAGTTTACCAC CAGTTTACCAC CAGTTTACCAC CAGTTTACCAC CAGTTCACAC CAGTTCACAC CTGCGCATTC	CCCAGGGCCC CGTAATTTTG TTCTCAACCT TAAGCAAGCA AACAGCGCC CACCAGCCCA AGCTCCTCCA CACCATCACC TGGGAACACC TGCACCATCACC TGCACCTCAG CTGCACTCAG CTGTATAAAA ACCTTGGAGA CCGAAAATCC GGATGAACAC GGATGAACAC CTGAAGTTAC CTTCAAGTGC CTTCAAGTGC	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020
55 60	Nucleic Ac: Coding sequing seq	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTACAGCAGC TTCCAACAAC CCCTGGTCAC TTACAGTCGG ATACAGCTGG ATACAGCTGG CAAGACCTGA GGAAGCCTGA TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTAGAGT TCAAGACTGAAGT TCAAGACTGAAGT AACATGCGGT AACATGCGGT AACATGCGGT AACATGCGGT AACATGCGGT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCACA GCCCTTATT TCAACCGTCA GCACTTTAT CATGCCCAG ACGTTCATA GCAACTTAT GTTCTAAACG GTCAAGGAGT GCTCTGGGA GTGAATCTCA TTGACCGTCA TTGACCGTCA CTGACAGCAG CACCTTGCAGG CACCTGCAGG	CAGAACCTCG CCTGGCCCCAGAGATTA AGCAACCAGC CCAGAGATTA AGCAACCAGCACCACCACCACCACCACCACCACCACCACC	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC GCACAAAAGC AGCTGCCCAC TGGAACACC GCACAAAAGC AGCTGCCCAC CTGTATAAAA ACCTCAGGAGA ACCTGAGAAATCC GGAAAATCC GGATGAACAC GGATTTAC CTTCAAGTGC CGATGTCCAA	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080
556065	Nucleic Ac: Coding sequing sequing sequing sequing sequing accordance accorda	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTTCAACAAC CCCTGGTCAC TTACAGTCGG GTAACCAGAC AGAAGCTTGA GCACAGCTGG GGATACAGCT TCCAGCCCAA TCAACAGCT TCAGTCAGC TCAGCCCAA TCAACTGG AGATTTTCA TCAGTGAGT AACATGCGT AACATGCGT AACATGCGT AACATGCGT AACATGCGT AACATGCGT AACATGTTTAGA	#: NM_014 1314 21 CCGGACTTCG CGCGGGGCC AGCAAAAGCA AGCATAAAA AAGATTCATG TACCCCAGCA AACCCAGGCA AACCCAGGCA CCCTTCCA TCAACCCACC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCC ACTGCCTCC CGCTGCCTCC CGCTGCCTCC CGTGCTCCA CGCAGCCACCCAC CGTGCTTCAA CGCAACCCAC CGTGCTTCAA CGCAACCCAC CGTGATTTTCAC CGTGATCGTCC AGATGACCAC AGATGACCACC	31 CCGCACGCTG GCGCTCTTCG GTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGGTCA GCAACTTTAT CATGCCCAG GTTCTAAACG GTTCTAAACG GTCATCAGA ACGACTCTGGA TTGACCGTCT CAGAACGCAG CTCAGCAG TTGACCGTCT CAGAACGCAG TTTGAAATT	CAGAACCTCG CCTCCCTGCC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACCTGCAACC ACTGCCACC ACTGCCACC GCACACACAC GGATAGCACT GAACACGGC GACACACAC GGATAGCACT GAAGCAGACT CCGTTTTTTC ACTGTGCACC CATTTACCAA CAGATCCAGA TCGGACT TCGGACT TCGAAACAAC	CCCAGGGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGGGCC AGCTCCTCCA AGCTCCTCCA CACCATCACC GCACAAAAGC GCACAAAAGC AGCTGCCCAC TGCACCTCAG CTGTATAAAA ACCTOGGAGA ACCTGGAGA ACCTGAGAGAC GGATAAAGC CGAAAATC CGAAAATC CGATGAAGAC CGATGAACAC CGATGAACAC CTCCAGTCC CGATGTCCAC CTCCAGTCC CGATGTCCAAC CTCGCACC CCATGTCCCAC CTCCAGTCCAC CTCCAGTCCAC CTCCTCAACTCC CCATGTCCCAC CTCGTCTCAAC CTCTCTCAAC CTCTCTCT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1200
556065	Nucleic Ac: Coding sequitoring	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC TTACAGTCAG ATACAGCTGG ATACAGCTGG ATACAGCTGG GCAACAGCTGG TCAAGACTGG GCACAGCTGC TCAAGACTGG TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTGC TCAAGACTTTTCA TCATGCAGT ACATGCGGT ACAGCCTCCA TTGATTTTGA TTGCTTCCTGT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACCGTAC GCACTTATC CATGCCCAG ACGGTTCCTG GTTCTAAACG GTTCTAAACG GTTCTAAACG TTGAATCTC CAGACGCGC CTGAATCTC CAGACGCGC CTCGCAG CACTGCAG CACTGCAG CACTGCAG CACTGCAG CACTGCAGG CACTGCAGG ATCGTGGTTG ATCGTAGTTG ATCGTGGTTG ATCGTGGTTG ATCGTGGTTG ATCTGGTTG	CAGAACCTCG CCTCCCTGCC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACTCACACCAC CACTGCACACAC GCCACAACAC GGATAGCACT GAACCAGCAC GGCCCACCAC GGCTTTTTC ACTGTGCAC CAGTTTACCAA TCGGGCATTACCAC TCGATTACCAC TGAACCAGAT TGGATGAGT TG	CCCAGGGCCC CGTAATTTTG TTCTCAACCT TAAGCAAGCA AACAGCGGCC AGCTCCTCCA CACCAGCCCA AGCTCCTCCA CACCATCACC TGGGAACACC GCACAAAAGC AGCTGCCCAC TGCACCTCAG CTGTATAAAA ACCTCGGAGA CCGAAAATCC GGATGAACAC GGATGAACAC GGATGAAGAC ACCGAAAATCA CTCTCAAGTGC CTTCAAGTGC CTTCAAGTGC CTTCAAGTGC CTATGACTATGA CTCGTCTGAC TATGGGTATG	120 180 240 300 360 420 550 600 660 720 780 840 900 1020 1080 1140 1200 1260
55606570	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTACAGCAGC TTCCAACAAC CCCTGGTCAC TTACAGTCAG AGAAGCCTGA AGAAGCCTGA TCAAGACTGG GGATACAGCTG TCAAGACTGG TACAGCTGA TCAAGACTGG TACAGCTAA TCAGTGAGT TCAGTGAGT TACAGTGAGT ACAGTGCGT ACAGTCCCTA TGATTTTGA TGCTCCCTCT TGATTTTGA TGCTCCCTCT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCTTATT TCAACCGTCA GCAACTTAT GCATCCTGCA GTTCTAAACG GTCATAGACAGCAC GCACATCAG GTCATAGACAGCAC GCACAGCAGCAC TTGACCGTCT CAGACAGCAG TTGCACAGCAG TTTGCAAATG ACCTGCTGCAGG TTTGGAAATG ATCGTGGTA TCATCTGGGA	CAGAACCTCG CCTGGCCCCAGAGATTA AGCAACCAGC CCAGAGATTA AGCACCACCACCACCACCACCACCACCACCACCACCACCA	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGCGGCC AGCTCCCA AGCTCCCCA AGCTCCCCA CACCATCACC GCACAAAAGC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC CGCACAAAAGC AGCTGCCCAC CGACAAAAACC GCACAAAAACC GCATAAAAA ACCTCAGGAGA ACCTCAGGAGA ACCTCAGGAGA ACCTAGAGTTTAC GGATGAAGAA GACAGTTTAC CTTCAAGTGC CATAGGGTATG TATGGGTATG TAAGGTATG TTAATTGGTTTG	120 180 240 300 360 480 540 600 720 780 900 960 1020 1140 1200 1200
556065	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTACAGCTGG TTACAGCTGG ATACAGCTGG AGAAGCTGG GTAACCAGA AGAAGCTGA GCACAGCTGC TCAAGACTGG GCATACAGCTGA AGAAGCTGA TCAGTGAGT TCGACCCAA TCAGTTTTCA TCGACCCCAA TCAGTTTTTCA TCGACTCCTGT AACATTCGGT AAGACTTCGAT TTGATTTTGA TTGCTTCCTGT AATACCGCT AATACCGCT AATACCCCTAA ACCATCCCTGT AATACCCCTAA ACCTCCAGAGT CCCTCAGAGT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACCGTCA GCAACTTTAT CATGCCCAG ACGGTTCTTA GTTCTAAACG GTTCTAAACG GTTCTAACG GTTCTAACG GTTCTAACG GTCCTCGGA GTGAATCTCA TTGACCGTCT CAGACAGCAG CACCTGCAGG TTTGGAAATG ATCGTGGTTG TTAGAAATG ATCGTGGTTG TCAACCATGGTT CAAACCATGTT CAAACCATGTT CAAACCATGTT	CAGAACCTCG CCTCCCTGCC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACTCACACCAC CACTGCCACC GCCACACAAC CGATAGCACT GAACCAGCAC GATAGCACT GAACCAGCAC CACTTTCCAAC CACTTCCACC CGATTACCAA ACTCACCAC CATTTCCAA CAGATCCAGA TCGGGCATTC TGAAACCAAC TGGATGAGTG GTCTCTGCCT ACCAGAGAAT CATCCCTTCC ACCAGAGAAT CATCCCTCC	CCCAGGGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGGGCC AGCTCCTCCA CACCAGCCCA AGCTCCTCCA CACCATCACC TGGAACACC GGCACAAAAGC AGCTGCCCAC TGCACCTCAG CTGAACATC GGATGACAC GGATGACAC GGATGACAC GGATGACAC TTCAAGTGC CTTCAAGTGC CGATGTCCAA TTTCAAGTGC TATGGGTATG CTAATTGTTG AGGATGGTATG AGGATGGTATC AGGATGGTATG CTAATTGTTTC AGGATGGTATG CTAATTGTTTC AGGATGGATG CTTCTAATTGTTTC AGGATGGATG CTTCTAATTGTTTC AGGATGGATG CTTCTAATTGTTTC	120 180 240 300 360 420 660 660 720 780 840 900 1020 1080 1140 1200 1260 1380 1380
55606570	Nucleic Ac: Coding sequitoring	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTTCAACAAC CTTTAGCAGC TTACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGA AGAAGCTTGA TCAAGATGG TCAAGATTTCA TCAGTGAGT ACATGCGGT AACATGCGT TAGATTTTGA TGCTTCCTGT ATACAGAGT ATACAGCTCAA TGATTTCGA TGCTTCCTGT ATACAGAGT CCTCAGAGT CCTCAGAGT CCTCAGAGT CCTCAGAGT CCTCAGAGT CCTCAGAGT CTCAGAGT CGTCATGTGTG	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACTACAAAAA ACACCCAACA GCCCTTATT TCAACCGTCA GCAACTTAT CATGCCCCAG GACAGTTAT CATGCCCCAG GTCAACAGGAGT GCTCTGGGA GTGAATCTCA TTGACGGTCA CACTGCAGG TTTGACAGTCT AGACAGCAG ATCTTGGAAATGT ACGCTCTT CAAACAATGT AGACAGCAG ATCTTGGAAATGT AGACACTCTT CAAACAATGT AGACAGCAC ACCTGCAGA TTTGAAATGT AGGCAGCACA	CAGAACCTCG CCACAGATTA AGCAACCACC CCACAGATTA AGCAACCACC CCACTACCA ACTCACACCA CACTGCAACA CCACACACC CGATAGCACC GACACACAC GGACACACAC GGACACACAC GGACACACAC	CCCAGGGCCC CGTAATTTG CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGCGCC AGCTCTCCA CACCAGCCCA AGCTCTCCC CGCACAAAAGC AGCTGCCCAC TGGAACACC TGCACCTCAG CTGTATAAAA ACCTTGGAGA CCGAAAATCC GGATGAACAC CTTCAAGTGC CTTCAAGTGC CGATGTCCAA CTGTCTCAAC CTGTCTGAC CTATGGGTATG CTATTGTTG AGGATGGATG CTTCTATTTT	120 180 240 360 420 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500
55606570	Nucleic Ac: Coding sequence of the coding seq	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTACAGCAGC TTCCAACAAC CCCTGGTCAC TTACAGTCGG ATACAGCTGG GTAACAGCTGG GCACAGCTGG TCAAGACTGG GCACAGCTGC TCAAGACTGC TCAGCCCCAA TCAGTGAGT ACAGTGCGT ACAGTCCCCA TGATTTTGA TGATTTTGA TGCTTCCTGT AATACCGCT AATACAGCT ATGAATTTTGA TGCTTCCTGT TGATTTTGA TGCTCCAGAGT TGTCATGTGTG TGTCATGTGTGT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGGTCA GCAACTTAT CATGCCCAG ACGGTCCTGGA GCAACTTAT CATGCCCAG ACGTTCTGGA GCAACAGCAG GTCAACGCAC TTGACGCTC TGACCGCAG TTTGGAAAT ATCGTGGTT CAAACAGCAG TCATCTGGAT ATCGTGGTT TCAACAGCAG TTATCTGGATA ATCATGGTTG TCATCTGGAT AGACACTTT CAAACAACTA TTATTTTCTA	CAGAACCTCG CCTGGCCCCCAGAGATTA AGCAACCAGCCCCCCCCCC	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC GCACAAAAGC AGCTGCCCCA TGGAACACC GCACAAAAGC CGACAAAAGC CGACTACACC CGATGACCAC CTGTATAAAA ACCTCAGGGAA ACCTCAGGCTATCAAGTC CGATGTCCAA CTCTAAGTGC CATTGTGCTAA CTCTCAAGTGC CATTGTGCTAAC CTCTAAGTGC CATTGTGCTAA CTCTTAAGTTC AGATATTTTA AGATATTTTTT AGATATTTTTA	120 180 240 300 360 480 540 600 780 900 960 1020 1080 1140 1200 1320 1380 1440 1500
5560657075	Nucleic Ac: Coding sequitoring	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTACAGTCAG ATACAGTCAG GTAACAGTAG ATACAGCTGA GCACAGCTGA GCACAGCTGA TCAAGCTGG GGATACAGCT TCAGACCCCAA TCAACAGCT TCAGACCTGA TCAGCTGAGT ACATTTTCA TCAGTGAGT ACATTTTGA TGATTTTGA TGCTTCCTGT AAATCCGCT AAATCCGCT ATGAAATTTTGA TGCTTCCTGT AAATCCGCT ATGAAATTTTGA TGCTTCCTGT AAATCCGCT ATGAAATTTTGA TGCTTCCTGT AAATCCGCT ATGAAATTTTGA TGCTTCCTGT TGAAAAGATTT TGAAAAGATTT TGAAAAGATTT TGAAAAGATTT TGAAACATTT	#: NM_014 1314 21 CCGGACTTCG CGCGGGCC AGCAAAAGCA AGCATAAAA AAGATTCATG TACCCCAGCA AACCCAGCC ACCTGCCTCA ACCCTTCCA TCAACCCACC ACTGCCTCC ACTGCTTCA CGCTTCTCA CGCTGCCTCC ACTTGCTTCA CGCTGCTCC ACTTGCTCA CGTTGTCAGC CGTTGTCAGC AGATGACCAC CATTGGGGCC AAGTTTACAC CGTTGTCAGC CATTGGGGCC AAGTGTCAA CGCAGCCAACCCAC CATTGGGGCC AAGTGACCAC CATTGGGGCC AAGTGTCAA CGCAGTCAA CGCAGTCAA CGCAGTCAA CGCAGTCAA CGTGGGTCTT ATTTAAGTTC AGTGGGCTGT CAGTGAGCTGT CAGTGAGCTGT	31 CCGCACGCTG GCGCTCTTCG GTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGTCAT GCAACTTTAT CATGCCCAG ACGGTTCTTA GTTCTAAACG GTCTTAAACG GTCTTAAACG GTCTTAAACG GTCTCTGGAA GTGAATCTCAGACAGCAG CACCTGCAG CACCTGCAG CACCTGCAG ATCGTGGTTG TCAACAGTAG ATCGTGGTTG TCAGAACTGTTACAGAATGT AGAACTCTTT CAAACAATGT AGGACTCTTT AAACAATGT AGGACTCTTT AGAATTTTCTAA AGAATTTAACAT	CAGAACCTCG CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCAACCAGC TCACCTTTCA ACCTGCAACC ACTGCCACC GCACCACACAC CGATAGCACT GAACCACGC GACACACC GATGCCACC GAGCACACA CGATTCCACC GAGCACACAC CGATTCCACC GAGCACACT CCAGTTTTTC ACTGTGCACC CGATTCCACA CAGATCCAGA CGGCATTC TGAAACCACC GCACCACT CCAGAGAGAT CCACCACT CCACCTTCC AAACCACCAT CCAATTTCTA GTTTCCTTTCA AATATTCTA AATATATGTA	CCCAGGGCCC CGTAATTTG TTCTCAACCT TTAGCAAGCA AACAGGGGCC AGCTCCTCCA CACCAGCCCA AGCTCCTCCA CACCATCACC TGGGAACACC GCACAAAAGC AGCTGCCCAC TGCACTCAC TGGAACACC GGATATAAAA ACCTCGGAGA ACCTCTCAAGTGC CGATGAAGACA CTCAATGTCCA CTTCAATGTCC TATGGGTATG CTAATTGTTC AATACTTTTC AATACTTTTA AATACTTTTT GAATATTTTA AAGTATGAATA	120 180 240 300 360 420 6600 6600 720 780 840 900 960 1020 1140 1200 1260 1320 1380 1440 1560 1560
55606570	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTACAGCAGC TTCCAACAAC CCCTGGTCAC TTACAGTCAG ATACAGCTGG ATACAGCTGG ATACAGCTGG GCACAGCTGC TCAAGACTGG GCACAGCTGC TCAAGACTGG TCAACACC TCAAGACTGG TCAAGACTGG TCAAGACTGC TCATGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TGATTTTGA TGCTCCTGT ATGATTTTGA TGCTCCTGT TGATTTTGA TGCTCCAGAGT TGTCATGTGTG TCAAGAGTAT TTATAAACCA ACCCTTGATT TTATAAACCATTT TTATAAACCATT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGGTCA GCAACTTAT CATGCCCAG ACGCTCCTGGT GTTCTAAACG GCCAGGTCTCAG GCACAGGAGT GCTCTGGGA GTGAATCTCA TTGACCGTCT CAGACAGCAG TTTGGAAATG ATCGTGGTTG TCATCTGGAT AGACACTTT CAAACAACTA ATCATGGTTG TCATCTGGAT AGACACTAT AGACAGCAG TTATTTTCTA AGATTAACAT GTAACTAATT CAAATTAACAT CTTATTTTCTTTG CTTTTGCTTTG CTTTTTGCTTTG TTTTTTTT	CAGAACCTCG CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCACCACCACCACCACCACCACCACCACCACCACCACCA	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC GCACAAAAGC AGCTGCCCAC TGGAACACC GCACAAAAGC AGCTGCCCAC TGCACCTCAG CTGTATAAAA ACCTGGGGA ACCTGAGCTAAAAC CGAAAATCC GGATGAACAC CTTCAAGTGC CGATGTCCAA CTCTCAGTTCAA CTCTCAGTTCAA CTCTTCAGTTC AGGATGACAA ATACTTTTT AGGATGATT AATACTTTTT AAGTAGATTA TGCATTTAAA TGCATTTAAA TGCATTTAAATTTTA AAGTAGAATA TGCATTTCAGTTC GATATTTTA AAGTAGAATA TGCATTTCAGT	120 180 240 300 360 480 540 600 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1680 1680 1740
5560657075	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTAGCAGC TTACAGTCAG TTACAGTCAG GTAACAGCTGA GTAACAGCTGA GCACAGCTGG TCAAGACTGG GTAACCAGAC TCAGCCTCA TCAGCCCCA TCAGCCTCA TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TCAGTGAAGT TGATTTTGA TCAGTGAAGT TGATTTTGA TGCTCCTGT TAGAAATTAA CCCTCAGAGT TGAAAATTA TTATAAACCA ACCCTTGATT TTATAAACCA ACCCTTGATT TCTTGTTTT	#: NM_014 1314 21 CCGGACTTCG CGCGGCCC AGCAAAAGCA GGACATAAAA AAGATTCATG TACCCCAGCA AACCCAGCC CCCTAGCTTA AACCAGTCC ACTICACCACC ACTICACCAC GATTATCAG GGAGCCTAT GGGAGCCTAT GGGAGCCTAT GGTAGTGTCC AAGTGACCAC GATTGAGCCA CATTTAAGGCC AAGGTGCCA AGGTGCCAT ATTTAAGTTC AGTGAGCTGT GAGATATGTT AGGGTCAATT TTAACAAAGC ATGGTTCAT TTAACAAAGC ATGGTTTCAT	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGGTCA GCACTTAT CATGCCCAG ACGGTCCTG GTACTTAT CATGCCCAG ACGGTCCTG GTCTTAACG ACGGTCCTC GGAACAGGAG TTGACCGTC TCAGACAGCAG TTGACGGTC TCAGACAGCAG TTCTGGATT CAACAGCAG TTCTGGAT ACGACTTTTC CAACAGCAG TTCTGGAT ACGACTTTTC CAACAACGT TCATCTGGTTG TCATCTGGTT CAACAACGT TTATTTTCT GTTACTTTC GTTACCATACA	CAGAACCTCG CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCACCACCACCACCACCACCACCACCACCACCACCACCA	CCCAGGGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGGGGCC AGCTCCTCCA AGCTCCTCCA CACCATCACC TGGGAACACC GCACAAAAGC AGCTGCCCAC TGCACTCAG CTGTATAAAA ACCTOGGAGA ACCTGAGCCAC GGAAAATC CGTAGAAGAC GAAAATC TTCAAGTGC CGATGTCCAA CTTCAAGTGC CTATGTCCAA CTTCAAGTGC CTATGTCCAA CTTCAATTTTC AGTATGTTGA AGGATGGATG CTTATTTTA AAGTAGAATA TGCATTTTA AAGTAGAATA TGCATTTTAAAG GACTTTCAAGT CTATTTTAAAGTAGTTTAAAGTTTTTA AAGTAGAATA TGCATTTTAAAGTAGATTA TGCATTTTAAAGTAGATTA TGCATTTTAAAGTAGATTA TGCATTTTAAAGTAGATTA TGCATTTCAAGT GTAGCACTTTA	120 180 240 300 360 420 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1620 1680 1740 1800
5560657075	Nucleic Ac: Coding sequitoring	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTCCAACAAC TTACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG GGATACAGCTGG GGATACAGCTGC TCAAGATGG GGATACAGCT TCAAGATTTCA TCAGTGAAGT AACATGCGGT AACATGCGGT AACATGCGGT AACATGCGT AACATGCGGT AACATGCGGT AACATGCGGT TGAATTTTGA CCCTCAGAGT GTCATGTGTGT TGAAAGTAT TTATAAACCA ACCCTTGATC TCTGTGTTTT TTATAAACCA ACCCTTGATC TCTGTGTTTTT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACCGTCA GCACTTATT CATGCCCAG ACGGTTCCTG GTTCTAAACG GCTCTGGAA GTGAATCTA CAGCAGCAG TTGACCGTCA CACCTGCAGG TTGGAAATG ACTGCTCAGGAA ACTGCTCAGGAA ACTGCTCAGGAA ACTGCTCAGGAA ACTGCTGGAA ACTGCTTC CAGACAGCAG TTTTGGAATG TCAACCAGCAC TTATTTTCTAA GAATTAACAT GTAACTAATA CTTTGCTTTG	CAGAACCTCG CCTCCCTGCC CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCAACACC CCTTCCACC CACTGCACC CACTGCACC CGCTGCACC CGCTAGCACC CGATAGCACT GAACCACACAC CGATAGCACT CAACCACACAC CACTTCCACC CATTCCACAC CACTACCACAC CGCTTTTTC CAATTACCAA TCGGGCATTC TCGAATAGCAC TCGATTCACCAC ACCAGAGAAT CATCCTCCC ACCAGAGAAT CATCCTTCC TTACCTTCC TTACCTAC TCAATTTCTA TTACTATAC CTTCTCTTCT TTACCAAT CTTCCTTTC TTACCAAT CTTCCTTC	CCCAGGGCCC CGTAATTTTG CCCAGGCCA AACAGCGCCA AACAGCGCCA AGCTCCTCCA CACCAGCCCA AGCTCCTCCA CACCATCACC CGGAACACC GCACAAAAGC AGCTGCCCAC TGCAACTCAG ACTGCCCAC TGCAACTCAG ACTGCCCAC TGCAACTCAG CTGATAAAA ACCTCGGAGA ACCTCGGAGA CCGATGACCAC CTTCAAGTGC CGATGTCCAC CTATGGGTAG CTAATGTTG AGGATGATG CTAATTTTA AGGATGTTCA AATACTTTT GAATATTTTA AAGTAGAATA TGCATTGAAG GACTTTCAGT GTAGCACTTA TGCATTGAAG GACTTTCAGT TGCATTGAAG GACTTTCAGT TGCATTGAAG TGCATTGAAG TGCATTGAAG TGCATTTCAC TTCTTCACC TTCTTTTTCACC TTCTTCACC	120 180 240 360 420 480 540 660 720 780 840 900 960 1080 1140 1260 1380 1560 1560 1680 1740 1860
5560657075	Nucleic Ac: Coding sequitoring	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTACAGCAGC TTCCAACAAC CCCTGGTCAC CTTACAGTCAG GTAACAGCTGG ATACAGCTGG ATACAGCTGG AGAAGCTTGA GCACAGCTGC TCAAGACTGG GGATACAGCTG TCAAGACTGG TACAGCCCA TGAATTTTCA TCAGTGAAGT TACAGTGAGT TGCACCCCA TGAATTTTGA TCCCCCTAGAGT TGTACTTGTGT TGTAACAGCT TTGAAAATAA CCCTCAGAGT TGTAAAGATAT TTAAAACTCT TTAAAACTCT TCAGTGTGTTT TTAAAACTCT TCAGTGTTTT TAAAACTCT TCACTTTAAACT TCACTTTAATTT TACAACTCT TCACTTTAAATTT TACAACTCT TACAACTCT TCACTTAAATTT TACAACTCT TCACTTTAAATTT TACAACTCT TACAACTCT TCACTTTAAATTT TACAACTCT TCACTTTAAATT TACAACTCT TCACTTTAAATTT TACAACTCT TCACTTTAAATTT TACAACTCT TCACTTTAAATTT TACAACTCT TCACTTAAATTT TACAACTCT TCACTTAAATT TACAACTCT TCACTTAAATT TACAACTCT TCACTTAAATT TACAACTCT TCACTT TCACTT TCACTT TCACTT TCACTT TCACTT TCACTT TCACT TCACTT TCACT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCTTATT TCAACCGTCA GCACTTATT TCAACCGTCA GCACTTATA CATGCCCAG ACGTCATG GTTCTAAACG GCACAGGAGT GCTCTGGGA GTGAATCTCA TTGACGTCT CAGACAGCAG TTCGGAAAT ACACTGTGT AGACATCTT CAAACAATG TCATCTGGAT AGAACTCTTT CAAACAATG TTATTTTCTA GAATTAACAT CTTATCTTTG GTAACTAATA CTTTTGCTTTTG GTAACTACAC TTTTTTGAGAA TTTTTTGAGAA TTTTTTGAGAA TTTTTTTGAGAA TTTTTTGAGAA TTTTTTTGAGAA TTTTTTTGAGAA TTTTTTGAGAA TTTTTTGAGAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAAA TTTTTTGAGAAAA TTTTTTGAGAAA TTTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTGAGAAA TTTTTTTT	CAGAACCTCG CCAGAGATTA AGCAACCAGC CCAGAGATTA AGCAACCAGC CCACACACC CACTGCACC CACTTCCACC CATTACCAA CAGATCCAGA TCGAGACAGAC TCGAAACAGGC CTCTCCCCT CAACCACCAT CATTTCCTTCACT CAATTCCTAC CTTCCCTTTA AATATATGTA CTACTGTGTG CTACTCTGCT TTATCCAAATG TATTCCTGTT CAGATTCCTGCT CACTCTCGCT CACTCTCGCT CACTCTCGCT CACTCTCCCCCCCCCC	CCCAGGGCCC CCTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA CACCATCACC GCACAAAAGC AGCTGCCCAC GCACAAAAGC GCACAAAAGC TGCACCTCAG CTGATATAAAA ACCTCAGGCTA ACCTCAGGCTAAAACC GCACAAAACC GCACAAAACC GCACAAAACC GCACAAAACC GCATGACCAA CCTGAGACA CCGAAATCC GCATGACAAA CCTTCAAGTGC TATGGGTATTA CGATGTCCAA CTCGTCTCAC TATGGGTATT AGGATGGATG CTTAATTTT AAGTATATTTT AAGTATATTTT AAGTATATTTT AAGTAGAAT TGCATTGAAG GACTTTCAGT GTAGCACTTA TCTTGTCACC CGGGTTCAAG	120 180 240 300 360 420 540 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500 1560 1680 1740 1800 1860 1920
556065707580	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CAACAGTACA CTTTAGCAGC TTACAGTCAG TTACAGTCAG TTACAGTCAG GTAACAGCTGA ACAGCTGA TCAAGCTGG TCAAGACTGG GTAACAGCTA TCAGTGAGT TCAGTGAGCT TCAGTGAGTTTTAAATCAG TCATTTTGA TCATTTTTAAACCA ACCCTTGATT TTATAAACCA ACCCTTGATT TCACTTGGTTT CACTTTGACT TACATTGGCT TACATTTGAT TACATTGGCT TCATTTGATTT CACTTTGACT TTACATTGGTTT CACTTTGACT TTACATTGGCT TACATTGGCT TACATTGGCT TCATTTGGCT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTTCG GTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCCTTATT TCAACGGTCA GCACTTAT CATGCCCAG ACGGTCCTG GTACTTAT CATGCCCAG ACGGTCCTG GTCTTAACG ACGGTCCTC GGAACGAGT TCAACGGCAG TTGACGGTC TCAGACAGCAG TTGACGTCT CAGACAGCAG TTCTGGAT ACGACTTTT CAAACAATGT ACGACTACAG TTATTTTCTA GAATTAACAT GTAACTAACA TTTTTGAGAC TTGGATTAC	CAGAACCTCG CCCAGAGATTA AGCAACCAGC CCCAGAGATTA AGCAACCAGC CCCAGAGATTA AGCACCACCACCACCACCACCACCACCACCACCACCACCA	CCCAGGGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGGGCC AGCTCCTCA AGCTCCTCA AGCTCCTCA CACCATCAC TGGGAACACC GCACAAAAGC AGCTGCCCAC TGCACTCAG CTGTATAAAA ACCTOGGAGA ACCATCAGC CGATGACGAC TGAAATTTC CTTCAAGTGC CGATGTCCAA CTGTCTGAC TATGGGTAT CTAATTTTC AGGATGGATG CTAATTTTA AGGATGGATG CTTCTATTCA AATACTTTTT AAGTAGAATA TGCATTTAAAT TGCATTTAATTTTA AAGTAGAATA TGCATTTCAGT GTTAGACT CTTTTAATTTTA AAGTAGAATA TGCATTTCAGT GTTAGCACTTTA TCTTGTCACC CGGGTTTCAGC CGGGTTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGGTTCACC CGGGGTTCACC CGGGGTTCACC CGGGCTTCACC CGCGCCTG	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1240 1320 1380 1440 1560 1620 1680 1740 1800 1860 1980
5560657075	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTTCAACAAC TTCCAACAAC TTACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGA GCACAGCTGC TCAAGACTGG GGATACAGCT TCAAGACTGG TCAAGACTGC TCAAGACTCA TGAATTTTGA TCCTCTGT ATACAGCTT ATACACATTTTAAACCCTT ATACACATTT TTATAAACTT TCATTTAAT TCACTTGATT TCACTTTAAT TCACTTGATT TTACAGTGGCA GCTTCAGCTT GTATTTTAT TACAGTGGCA GCTTCAGCTT GTATTTTAT TACAGTGGCA GCTTCAGCTT GTATTTTAT TACAGTGGCA GCTTCAGCTT CACTTTAAT TACAGTGGCA GCTTCAGCTT CACTTTAAT TACAGTGGCA GCTTCAGCTT CACTTTAAT TACAGTGGCA GCTTCAGCTT CACTTTAAT CACGTGGCA GCTTCAGCTT CACTTTAAT CACGTGGCA CACTTCAGCTT CACTTCAGCTT CACTTCAGCTT CACTTCAGCTT CACTTCAGCTT CACTTCAGTT CACTTCAGCT CACTTCAGTT CACTTCAGT CACTT CACTTCAGT CACTT CACTT CACTT CACTT CACTT CACTT CACTT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACTT CACTT CACT CACTT CACTT CACTT CACT CACTT CACT CACT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCTTATT TCAACCGTCA GCACTTAT TCAACCGTCA GCACTTAT GCACTGCAG ACGGTCATA GCACTTAT TCAACCGTCA GCACAGGAGT GCCTCTGGGA GTGAATCTCA TTGACAGTCT CAGACAGCAG ATCGTGGTA ATCTGGAA ATCTTGGAAT AGAACATTT CAAACAATGT TCATCTGGAT TCATCTTGGAT AGGACGCAG ATCTTTTCACATG TTATTTTCTA GAATTAACA TTTTTTTGACAT TTTTACCATAT TTTTACCATAT TTTTACCATAT TTTTACCATAT TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC	CAGAACCTCG CCTCCCTCCCCCCCCCCCCCCCCCCCCCC	CCCAGGGCCC CGTAATTTIG TTCTCAACCT TAAGCAAGCA AACAGGGGCC CACCAGCCCA AGCTCCTCCA AGCTCCTCCA CACCATCACC GCACAAAAGC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC AGCTGCCCAC CGCACAAAAGC AGCTGCCCAC CGATGAAGAA ACCTCAGGAGA ACCTCAGGAGA ACCTTCAAGTAC CTTCAAGTGC CTAATTGTTG AGGATGGATG CTAATTGTTT AAGTAGTATTTT AAATACTTTTT GAATATTTTT AAATACTTTTT AAATACTTTTT AAATACTTTTT AAATACTTTTT AAATACTTTTT AAATACTTTTT AAATACTTTTT AAATACTTTTT CAATATTATA TCCATTGAAG GACTTTCACC CGGGTTCAAG ACCACGCCTG TGGTCTGAA TCGTGTCTGAA TCCTGGAATG ACCACGCCTG TGGTCTTGAA TACCAGGCCTG TGGTCTTGAA	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1500 1680 1740 1880 1740 1880 1920 1980 2040
556065707580	Nucleic Ac: Coding sequitorial	Id Accession lence: 64 11 CGGGGCCTGC GGCAGCTCAG GTCAAATGAG CTTCAACAAC TTCCAACAAC TTACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGG ATACAGCTGA GCACAGCTGC TCAAGACTGG GGATACAGCT TCAAGACTGG TCAAGACTGC TCAAGACTCA TGAATTTTGA TCCTCTGT ATACAGCTT ATACACATTTTAAACCCTT ATACACATTT TTATAAACTT TCATTTAAT TCACTTGATT TCACTTTAAT TCACTTGATT TTACAGTGGCA GCTTCAGCTT GTATTTTAT TACAGTGGCA GCTTCAGCTT GTATTTTAT TACAGTGGCA GCTTCAGCTT GTATTTTAT TACAGTGGCA GCTTCAGCTT CACTTTAAT TACAGTGGCA GCTTCAGCTT CACTTTAAT TACAGTGGCA GCTTCAGCTT CACTTTAAT TACAGTGGCA GCTTCAGCTT CACTTTAAT CACGTGGCA GCTTCAGCTT CACTTTAAT CACGTGGCA CACTTCAGCTT CACTTCAGCTT CACTTCAGCTT CACTTCAGCTT CACTTCAGCTT CACTTCAGTT CACTTCAGCT CACTTCAGTT CACTTCAGT CACTT CACTTCAGT CACTT CACTT CACTT CACTT CACTT CACTT CACTT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACT CACTT CACTT CACTT CACT CACTT CACTT CACTT CACT CACTT CACT CACT	#: NM_014 1314 21	31 CCGCACGCTG GCGCTCTCG TTTCCAGAAA AAACCTGTCC GATGGTCATA ACACCCAACA GCCCTTATT TCAACCGTCA GCACTTAT TCAACCGTCA GCACTTAT GCACTGCAG ACGGTCATA GCACTTAT TCAACCGTCA GCACAGGAGT GCCTCTGGGA GTGAATCTCA TTGACAGTCT CAGACAGCAG ATCGTGGTA ATCTGGAA ATCTTGGAAT AGAACATTT CAAACAATGT TCATCTGGAT TCATCTTGGAT AGGACGCAG ATCTTTTCACATG TTATTTTCTA GAATTAACA TTTTTTTGACAT TTTTACCATAT TTTTACCATAT TTTTACCATAT TTTTACCATAT TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC TTTTCACCATC	CAGAACCTCG CCTCCCTCCCCCCCCCCCCCCCCCCCCCC	CCCAGGGCCC CGTAATTTG TTCTCAACCT TAAGCAAGCA AACAGGGCC AGCTCCTCA AGCTCCTCA AGCTCCTCA CACCATCAC TGGGAACACC GCACAAAAGC AGCTGCCCAC TGCACTCAG CTGTATAAAA ACCTOGGAGA ACCATCAGC CGATGACGAC TGAAATTTC CTTCAAGTGC CGATGTCCAA CTGTCTGAC TATGGGTAT CTAATTTTC AGGATGGATG CTAATTTTA AGGATGGATG CTTCTATTCA AATACTTTTT AAGTAGAATA TGCATTTAAAT TGCATTTAATTTTA AAGTAGAATA TGCATTTCAGT GTTAGACT CTTTTAATTTTA AAGTAGAATA TGCATTTCAGT GTTAGCACTTTA TCTTGTCACC CGGGTTTCAGC CGGGTTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGTTCACC CGGGGTTCACC CGGGGTTCACC CGGGGTTCACC CGGGCTTCACC CGCGCCTG	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1200 1320 1380 1440 1500 1680 1740 1880 1740 1880 1920 1980 2040

CCGACCCTCT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAACCA

GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAATGT

CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT

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GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT

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2160

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85

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Seq ID NO: 540 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..672

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Seq ID NO: 542 DNA sequence Nucleic Acid Accession #: XM_035292.2 Coding sequence: 53..1576

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WO 02/086443

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PCT/US02/12476

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	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA	CTCCCCTCC TCTGGAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG	CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG	TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATG GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT	120 180 240 300 360 420 480 540
	CAAAAAAAC CGGCGAGGGG CAGCTCCTT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAAAA	ATTTCCTTCS CCGCAGACCG GTGTTTGCCTG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAG TGTCATCTGA TCTACTGCTT	CTCCCCTCC TCTGGAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGGATCAGAG TGATGCGGAC	CTCTCCACTC CGAATCCTAA GCTAATCGAG GCAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CCATAGTTTAG CGATTTTCAA	TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAA ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCACTT AGCAGTCAAA	120 180 240 300 360 420 480 540 600
	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GGGATGCAAAA GGGAAAAGGGA	ATTTCCTTCS CCGCAGACCG GTGTTTGCCTG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGGTT AGTTAAGAGC	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT	CTCTCCACTC CGAATCCTAA GCTAATCGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAA CGATTTTCAA TTGTTTGAGG	TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA AGTTTGAGGA TTGGGACAGA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGGAAATTTG	120 180 240 300 360 420 480 540 600 660 720
50	CAAAAAAAC CGGCAAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAATA GAGATGCAAAGGGA GAATTCAAAG	ATTTCCTTCG CCGCAGACCC CCGCTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA	CTCCCCTCC TCTGGAATGC CCTGGATTGG GTCCTATACA CCCAAAACAA CGAAACTTAAA ATGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCCGAC TTTATCCATT TGGAGTCGAA	CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTAG CGATTTTGAG AGTGTTAGTC	TGAGAAGCAG AGCGTTTCCT ACTACAGACA ACTCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGGGAA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT	120 180 240 300 360 420 480 540 660 720 780
	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTCTTGAAG AAATATCCAA CAACTAAATG ACACATTCA GTCAGCGGAG AAATGCAATA GGAAAAGGGA GGATACAAAG TTAGATCCAT	ATTTCCTTCG CCGCAGACCG AGGTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTAATGA TCATACTGTT	CTCCCCTCC TCTGGAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG	CTCTCCACTC CGAATCCTAA GCTAATGGAT GCGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTTCAGG AGTTTTCAGA TGTTTTCAGA ATGTTTTCAC CCAAACTCAA	TGAGAAGCAG AGCGTTTCCT AGCGAT ATCAAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA CTTGGGACAGA CTTGACAAGTA CTTGACAAGTA CTGACAAGTA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TCACTACGGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC	120 180 240 300 360 420 480 540 600 720 780 840
50	CAAAAAAAC CGGCAAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGAATGCAATA GGAAAAGGGA GATTTCAAAG GTTAGATCCAT AATGGCTCAT	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGGTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCC	CTCCCCTCC TCTGGAATGC CCTGGATTGC GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGA TGATGCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCACA	CTCTCCACTC CGAATCCTAA GCTAATGGAT GCAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTTAA CGATTTTCAA TTGTTTGAGG AGTGTTAGTC CCAAACTCAA GACACGATTG	TGAGAAGCAG AGGGTTTCCT ACTTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGAGGA CTTGAGAA CTGACAAGTA ACTGGATTGT	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACACTTTAC TTTACACTTTAC	120 180 240 300 360 420 480 540 600 660 720 780 840 900
50	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAGTAAATG AACACTATCA GTCAGCGGAG AAATGCAATA GAGATGCAAA GGAAAAGGGA GATTTCAAAG TTAGATCCAT AATGCTCAT ACAGTTAGCA	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCT TGACATCTCC TCTCTGAAAG	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TTTATCCATT TGGAGTCGAA GAACCTTCTG GAACCTTCTG CCCTGCACA CCAGTTGGCT	CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TCTCCTATCA TCTCAGGAT AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAGG AGTGTTAGTC CCAAACTCAA GACACAGTTG GCTTTTTTTTG	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGGGAA CTGACAGAGTA ACTGCACAGTA ACTGCACAGTA ACTGCACAGTA ACTGCACTTAC	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCACTGGGA ATTTCCACTT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTACATTTACA TTACATTTACA AATGCAACAA	120 180 240 300 360 420 480 540 660 720 780 840 900 960
50	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTAAATG ACCACTTCA GTCAGCGGAG AAATGCAATA GGAAAAGGA GGAAAAGGGA GATTTCAAAG TTAGATCCAT AATGCCTCAT ACAGTTAGCA TCTGGTTATG	ATTTCCTTCG CCGCAGACCC AGATTGCCTG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTGT TGACATCTGT TCATACTGTT TGACATCTGT TCATACTGTT TGACATCTGAAAG TCATGCTGAT	CTCCCCTCC TCTGGAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA ATGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCAC CCAGTTGGCT GGACTACTTA	CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTAG AGTGTTAGCG AGTGTTAGTC CCAAACTCAA GACACACTCA GATAACCAATT CAAAACAATT	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA CTGACAAGTA ACTGCACAGTA ACTGCACAGTA ACTGCACAGTA ACTGCACAGTA ACTGCACTTCTAC TTCGAGAGGCA TTCGAGAGGCA TTCGAGAGGCA TTCGAGAGGCA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCACTGGGA ATTTCCACTT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GGGAAAGGGA GGATATCAAAG GTTACAAC TTTAGAAC TTAGATCAT ACAGTTAGCA TCTGGTTATG TTTCTTAGAC	ATTTCCTTCG CCGCAGACCG GRGTTTGCCG AGATTGGCTG CATGTAATAG TCGATTAATAG GAGTTTCAGA TCTACTGCT AGTTAAGAGC CGATTATTGA TCTACTGCT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCC TCTCTGAAAG TCATACTGTAT AGGTGTTTTC AGGTGTTTTC	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGATCAGA TGATGCGGAC TTTATCCATT TGGAGTCGAG GAACCTCTG TCCCTGCACA CCAGTTGGCT GGACTACACT CTCATACACT	CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CGATTTTCAA GTGTTTTTGAG AGTGTTATCAA TTGTTTGAG AGTGTTAGTC CCAAACTCAA GACACGTTG GTTTTTTTTTGTG GTAAACAATT GGAAACGAAG	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGATAACTT AAGGACAAAAA GTTTTGAGGA CTTTTGAGGA CTTATGAGA CTTATGAGTA ACTGATTTTGAGA ACTGACAGTT ACTGATTTTCACAA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTACAATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGT	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAGCTAAATG AACACTTCA GTCAGCGGAG AAATGCAATA GGGATAGCAAA GGAATAGCAAA GGAATAGCAAA GGAATAGCAA TTAGATCCAT AACAGTTAGCA TCTGGTTTATG TTCTCTAGAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC	ATTTCCTTCG CCGCAGACCC AGATTGCCTG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTGT TGACATCTGT TCATACTGTT TGACATCTGT TCATACTGTT TGACATCTGAAAG TCATGCTGAT	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA ATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACTTA TCAGGCTGAC CTCAGCACA CTCATACACT TCAGGCTGAC	CTCTCCACTC CGAATCCTAA GCAATCGAT GCAGCACTGA TCTCCTATCA TCTCCTATCA TCTCAGGGTT GTGGAAATTAA AAGCAAGCA CGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTTGAG AGTGTTAGTC CCAAACTCAA GCACAGTTG GTTTTTTGTG CAAAACAATT GGAAACAATT GGAAAGGAAT CCAGAGAATT	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAACC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTTGAGGA CTGACAGGA CTGACAAGTA ACTGGATTGTTAC ACTGACAGTA AAGTTCTTAC TAGAGAGCA AAGATTCATCA AGATTCATCA ATACCAGCCT	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGGAAAATTTG GCAGGCTGCT TTACATTTACA TTACATTTACA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020
50	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTAAATG GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAATA AGGATAAAGGA TTAGATCCAT AATGCCTCAT ACAGTTAGCA TCTCGTTATG TCTCTCTAGAC TGGGAAAGAC TGGGAAAGAC	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TCAATAACAC GAGTTTCAGA TGTCATCTGA AGTTAACAGC CGATTATTGA TCATACTGCTT TGACATCTGT TGACATCTCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATGCTGAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT	CTCCCCTCC TCTGGAATGC CCTGGATTGG GTCCTATACA CCCAAAACAA CGAAAACAA AATGGTGTTT TGGATCAGAG TTATCCATT TGGAGTCGAA GAACCTTCTG GACCTTCTG GACTACTCT GGACTACTTA CCAGTTGGCT TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TTATGATACCT	CTCTCCACTC CGAATCCTAA GCAAACGAT GCAGCACTGA TCTCCTATCA TCTCCTATCA TCTCCAACTTAG CGATTTTAG CGATTTTAG CGATTTTAG CGATTTTAG ACACACTCAA GCACACTCAA GCACACTTG GCAAACCACTT GGAAACGAAT GCAAACCAATT GCAAACGAAT CCAGAGGAAT ATGATTGAGA	TGAGAAGCAG AGGGTTTCTT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACT ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGGGAA CTGACAGGTA ACTGTACAGTA ACTGTACAGTA ACTGTACTTAC TTCGAGAGCA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCCAAA AGGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGTTACA TTTGTTACA TTTGTTACA TTTGTTACAG	120 180 240 360 420 480 540 660 720 780 840 900 960 1020 1080 1140
50	CAAAAAAAC CGGCAAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GGGAAAAGGGA GTTTCCAAG TTTAGATCCAT AATGCCTCAT AATGCTCAT ACAGTTAGAC TCTCTTAGAC AGTTCAGAAC CGGAAAGAC TGGGAAAGAC CAGTTAGGAT	ATTTCCTTCS CCGCAGACCG GRGTTTGCCG AGATTGGCTG CATGTAATAG TCGATAACAC GAGTTTCAGA TCTACTGCTT AGTTAAGAC CGATTATAGGC CGATTATCGT TCTACTGCTT TGACATCTCT TCTACTGTT TGACATCTCC TCTCTGAAAG TCATACTGTAT AGGTGTTTTC CAGAAAATGT CTCAGATCCC AGAGAGACCCA	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGAC CCAGTTGGCT GGACTACACT CGACTACACT CTCATACACT TCAGGCTGAC TCATACACT TCAGGCTGAC TCATACACT TCAGGCTGAC TATGATACC	CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTAA CGATTTTCAA GTTTTTGAG AGTGTTAGTCAA TTGTTTGAG AGTGTTAGTC CCAAACTCAA GACACGTTG GTTTTTTTTTT	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCCCACTAA AGGATAACTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGAGGA CTGACAAGTA ACTGGATTGT AAGTTCTTCTAC AGATTCATGA ATACCAGCCT AGATTCATGA ATACCAGCCT AGTTTGCAGT	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTCAT TTACATTTAC TTTACAATTAC TTTTAAAGAT AATGCAACAA AGCAGTTTGT TCTTGTTACA TTTGTACCAG TCAAGACTTG	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1200
50 55 60	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GGAAAAGGGA TTAGATCCAT AATGCTCAT ACAGTTAACA TCTGGTTTATG TTCTCTTAGAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGATC AGGTTGGATTC CGGGAAAAGAC CGGGAAAAGAC GGTGCTTTTC	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG AGATTGGCTG CATGTAAATAG TCAATAAACAC GAGTTTCAGA TGTCATCTGA TCTAATAGAGC CGATTATTGA TCAATCTGTT TGACATCTCC TCTCTGAAAG TCATGCTTGT TGACATCTCC TCTCTGAAAG TCATGCTTGT AGGTGTTTTC CAGAAAATGT CTGGAGTCCT TCAGAGGACCA TCAATAATTT	CTCCCCTCC TCTGGAAATG CCTGGAATGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACTT TCAGGCTGAC TCAGTACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC TATGATACCAAGCAAGCAAGCAACCAACCAAT	CTCTCCACTC CGAATCCTAA GCAAATCGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTAA AAGCAAGCA CGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTCAG GGATTTTCAG GGATTTTGTG GTTTTTGTG CCAAACTCAA GACACAGTTG GTTTTTGTG CAAAACCAATT GGAAAGGAAG CCAGAGAATT ATGATTGACG AATTTTTGAG AATTTTTGAG AATTTTTGAG AATTTTTGAG AATTTTTGAG AATGAGTTATG	TGAGAAGCAG AGGGTTTCCT ACTACAGAAAAAA ATTATGATGA GGGATAAAAC ATCCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGAA CTGACAGGA CTGACAAGTA ACTGGATTGTAA ACTGGATTGTAA ACTGATTGAAAGCA ACTGCACAGAA ATTCTTAC AGATTCATGA ATTACCAGCCT AGTTTGCAGT AGTTGCAGT ATTCCAGAT ATTCCAGAT ATTCCAGAT ATTCCAGAT ATTCCAGAT ATTCTCAGAT ATTCTTACAGAT ATTCTTACAGAT ATTCTTCAGAT	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTACATTTAC TTTTACATTTAC AGTAGCAAA ACAGTACAAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTTGTACCAG TTGTTACAAGACTACAAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTGTTACCAG TGTAGCCATA	120 180 240 300 360 420 540 660 720 780 840 960 1020 1080 1140 1200 1260 1320
50	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAGCTAAATG AACACTTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAATA AATGCTAAAA TTAGATCCAT AATAGCTCAT ACAGCTCAT ACAGCTCAT ACAGCTCAT TCTCTAGGA TCTCTAGGAC TCTCAGAAC TCTGGTATG TCTCTAGGAC TGGGAAAGAC CAGTTGGATG CAGTTGGATG TGCCACTAATG	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TCATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGATCATTCA TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGCT TCATACTGT TCATACTGCT TCATGCTGAT AGGTGTTTTC CCAGAAAATGT CAGAAGAAATGT CTCAGAGAGACA TCAATAATTT GCTATATAGG	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGATCAGAG TTTATCCATT TGGAGTCGAA CAACCTTCTG GAACCTTCTG GAACCTTCTG GGACTACTC TCCATGCACA CCAGTTGGCT TCAGGCTGAC TTATGATAC TCAGGCTGAC TATGATAC AACAAGCAT AAAATACAGC	CTCTCCACTC CGAATCCTAA GCAAACCTGA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA AAAGCAAGCA CGATTTTCAG CGATTTTCAG GGATTTTCAG AGTGTTTCAA TTGTTTGAGG AGTGTTAGTC CCAAACTCAA GCACACGTTG GCAAACCAAT GGAAAGCAAT AGAAACAATT ATGATTGAGA GAATTTTTGAG GAAATTTTTGAG AAATTTTTGAG AAACAACTGA	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAACC ATCCCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA CTGACAGGA GTTTTGAGGA CTGACAGGT ACTGCACAGTA ACTGCACAGTA ACTGCACAGTA ACTGCACAGTA ACTGCATCT ACTTCCACAGT AGATGCCACAGTA ATACCAGCCT AGTTTGCAGT CACATGCACAT TTCTCCACAT TTCTCCACAT	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTCAT TTACATTTAC TTTACAATTAC TTTTAAAGAT AATGCAACAA AGCAGTTTGT TCTTGTTACA TTTGTACCAG TCAAGACTTG	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1080 1240 1250 1320 1380
50 55 60	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTAAATG GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAATA AGGATACCAT AATGCTCAT ACAGTTAGCA TCTCGTTATG TCTCTTAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC CAGTTGGATG ATCCCTAATG AATCCCTGAAC AATCCCTGAAC	ATTTCCTTCG CCGCAGACCC CCGCAGACCC AGATTGGCTG CATGTAATAG TGAATCTTAA TGATACAC GAGTTTCAGA TGTCATCTGA TGTCATCTGA TGTAATAGAC CGATTATTGA TCATACTGCT TGACATCTCT TGACATCTCC TCTCTGAAAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT CTCAGAGGCCA TCAATAATTT GAGAGGACCA TCAATAATTT GCTTATATGG TTGATCTTT	CTCCCCTCC TCTGGAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA ATGGGAAAACA AATGGTGTTT TGGATCAGAG TTATCCATT TGGAGTCGAA GAACCTTCTG GAACCTTCTG GGACTACTCA CCAGTTGGCT TCAGCCTGCAC TCAGCCTGCAC TCAGCCTGAC TCAGCCAAC AACAAGCAT AAAATACAGC CCCTGAATTA	CTCTCCACTC CGAATCCTAA GCAAACGAT GCAGCACTCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCAACTTAG CGATTTTAG CGATTTTAG CGATTTTAG CGATTTTAG CCAAACTCAA GACACACTTC GCAAACTCAA GCACAGATT GGAAAGGAAT ATGATTTAG GCAGAATT ATGATTAGA ATGACTTAGA ATGACTTAGA ATGACTTAGA ATGACTTAGA ATGACTTAGA ATTGGAACTG ATTGGAACTG	TGAGAAGCAG AGGGTTTCTT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAACT AGGACAAAA GGTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGAT ACTGACAGTA ACTGACAGTA ACTGACAGTA ACTGACAGTA ACTGACAGTA ACTGACAGCA AGATTCATGA AGATTCATGA AGTTCATGA TCGAGCA AGATTCATGA TTCTCAGT TTCTCAGAT TTCTTCAGAT AGAATGACTA AAGAAATAAT	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATCGGGA ATTTCCACTT TCACTGGGGA ATTTCCACTT AGCAGTCCAAA AGAAAATTTG GCAGGCTGCT TTACAATTACA TTACAATTACA AATGCAACAA ACAGTACAAA ACAGTACAAA ACAGTACAAG TCTTTTACA TTTTTTACA TTTTTTACA TTTTTTTACA TCTTGTTACA TCTTGTACCAG TCAAGACTTTG AGTAGCCATA GCCTACTGAT	120 180 240 300 360 420 480 540 660 660 720 780 840 900 960 1020 1020 1140 1200 1260 1320 1380 1440
50 55 60	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA GACAATCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GGAAAAGGGA TTAGATCCAT AATGCCATT ACAGTTAACA TTCTGGATCAT TTCTTAGAC AGTTCAGAAC GAAGAGGAA	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCCG AGATTGCTG AGATTGATAG TCAATAACAC GAGTTTCAGA TCTAATCTGT AGTTAAGAC CGATTATTGA TCAACTGTT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT CTGAGTGCTCA TCAGAGTACTTT CCGAGTCCT TCAGAGTACTTT CCGAGTCCT TCAGAGTACT TCAGAGTACT TCAGAGTACT TCAGAGTACT TCAATAATTT GCTTATATGG TTGATCTTT AAGACATTGA	CTCCCCTCC TCTGGAATG CCTGGAATGG GTCCTATACA CCCAAAACAA AAGGAACATAAA TGGGAAAACA AATGGTGTTT TGGATCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACTT TCAGGCTGAC TTATGATACACT TCAGGCTGAC TTATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC GCTACCCAAT AAAATACAGC CCCTGAATTA AGAAGGCGCT	CTCTCCACTC CGAATCCTAA GCAATCGAT GCAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CGATTTTCAA GTTTTGAGG AGTGTTTAGTC CCAAACTCAA GACACAGTTG GTTTTTTTTTT	TGAGAAGCAG AGGGTTTCCT ACTTACAGACA ATCAAGACA ATCAAGACA ATCACACTA ATCACACTA AGGACAAAA AGGACACATA AGGACAAAA CTGACAGAC ATCGGACAGA GTTTTGAGGA CTGACAGAC ACTGACAGT ACTGACAGT ACTGACAGT ACTGACAGT ACTTCACAGT ACTTCACAGT ATTCCAGCCT AGTTTTCAGT TTCTTCAGT TTCTTCAGAT AGGAAAAAAAT CTGGTAGAGAA CTGGTAGAGAA CTGGTAGAGAA ACTGGTAGAGAA CTGGTAGAGAA ACTGATAGAAAAAA CTGGTAGAGAA ACTGATAGAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAA CTGGTAGAGAA ACTGAAAAAAAA CTGGTAGAGAA CTGGTAGAGAA ACTGAAAAAAAA CTGGTAGAGAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAA CTGGTAGAAAA CTGGTAGAAAA CTGGTAGAAAAA CTGGTAGAAAAA CTGGTAGAAAAA CTGGTAGAAAAA CTGGTAGAAAAA CTGGTAGAAAAA CTGGTAGAAAAAA CTGGTAGAAAAAA CTGGTAGAAAAAAAA CTGGTAGAAAAAAAAAA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATGGGGA ATTTCCACTT AGCAGTCCAAA AGGAAAATTTG GCAGGCTGCT TTACATTTAC TTTACATTTAC ATTTAAAGAT AATGCACAAA ACAGTACAAG AGCAGTTTGTTACA TTTGTTACA TTTGTTACA TTTGTTACAG TCAAGACTTG AGTAGCCATA AGCACATA AGCAGATTGAGCCATA CCAAGACTTG	120 180 240 300 360 420 540 660 720 780 840 900 960 1020 1080 1140 1260 1320 1380 1440 1500
50 55 60	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAGTAAATG AACACTTCA GTCAGCGGAG AAATGCAATA GGGAAAGGGA GATTTCAAAG TTAGATCCAT AACAGTTAGCA TCTGGTTATG TTCTTAGAC TGGGAAAGAC CAGTTGGATC TGGGAAAGAC CAGTTGGATT TGGATTAGAC TGGGAAAGAC CAGTTGGATT TGGATTAGAAC TGGGAAAGAC CAGTTGGATT TGGATTAGAAC AGTTCAGAAC CAGTTGGATT CAGAAATCA AACCAAATCA AACCAAAATCA	ATTTCCTTCG CCGCAGACCG CGCAGACCG AGATTGCTG AGATTGGCTG CATGTAATAG TCAATACAC GAGTTTCAGA TCTACTGCTT AGATCATTAA TCTACTGCTT TGACATCTCC TCTCTGAAAG TCATGCTGAT TGACATCTCC TCTCTGAAAG TCATGCTGAT TCAGAGTCTTTC CCGAGTCGT CAGAAAATGT CCAGAAAATGT CCAGAAAATGT TCAATACTTTT GCTTATATGG TCAATTTATGG TCAATTTATGG TTAATAGG AGAACATTTA GGGAAAAAGGA GGGACAATGA GGAAAAAGGA	CTCCCCTCC TCTGGAATG CCTGGATTGG GTCCTATACA CCCAAACTA ATGGGAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT TGGAGTCGAA CCAGTTGCT GGACTACTT TCCGGCAC CCAGTTGCT TCAGGCTGAC TTATGATACACT TCAGGCTGAC TTATGATACACT TCAGGCTGAC ACCAAGCAT AAATACAC CCTGAATA AAATACAC CCTGAATT AAATACAC CCTGAATT AAATACAC CCTGAATT AAATACAC CCTGAATT AAATACAC CCTGAATT ACCCCAGATT ACCCCAGATT	CTCTCCACTC CGAATCCTAA GCAATCCTAA GCAGCACTGA TCTCCTATCA TCTCAGGGTT GTGGAAATTAA AAGCAAGCA CGATTTTCAG GGTTTTGAGG AGTGTTTGAG AGTGTTTGAG GCACAGTTG GTTTTTGTG CAAAACCAA TGGAAAGCAA TGGATTTTGTG CAAAACAATT AGAAACAATT AGAAACAATT AGAATTGAGA AGAATTTTGAG AAATTTTGAG AATTTTTGAG AATTTTTGAG ATTGGAAACTGA ATTGGAAACCAA ATTGGAAACCAA ATTGGAAACCAA ATTGGAAACCAA ATTGGAAACCAA	TGAGAAGCAG AGGGTTTCTT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACA ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTTGAGGA CTGACAGGA CTGACAGGTA AAGTTCTTAC TAGGACAGAT AAGTTCTTAC TAGGACAGT TTCAGAGACA ATACCAGCCT AGTTTGCAGT TTCTTCAGT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTCACAT AAGAATAAT CTGTAGAGAATAAAC CACACTACAA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTGTTACCAG TCAAGACTTG TCAAGACTTG AGTAGCCATA GCCTACTGAT CAAGGAGGAG CAGTGCTACAC CAGGAGGAG CAGTGCTACAC CACGACTAC	120 180 240 300 360 420 660 720 780 840 960 1020 1080 1140 1260 1320 1380 1440 1500 1500
50 55 60 65	CAAAAAAAC CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAAT AATGCTCAT AATGCTCAT ACAGTTAGCA TCTGGTTATG TTCTCTAGAAC TCTGGTATG TTCTCTAGAAC TGGGAAAGAC CAGTTCAGAAC CAGTTCAGAAC TGGCAAATAC AACCAAATCA AACCAAAATCA ACGAAAATCA	ATTTCCTTCG CCGCAGACCG GGGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TGTCATCTGAT TGTCATCTGT AGTTAATAGAC CGATTATTGA TCATACTGTT TGACATCTGT TGACATCTCT TCATACTGTT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTTC CCGAGTCGT GAGAGGACCA TCAATAATTT GCTTATATGG TTGATCTTTT AAGACATTTT AAGACATTTT AAGACATTAGA TGAATACGA ATGAAAGCA ATGAAGCAA	CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGATCAGAG TTTATCCATT TGGAGTCGAA GAACCTTCTG GAACCATCTCTG GACTACTCTG GACTACTTCTG GACTACTTA CTCATCACCC TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TCAGCCAAT ACAACAAGCAT ACAAAGCCTC ACCAATTA AGAAGGCCGAT AGCAAGCATT AGCAAGCTTA AGCAAGCATT AGCAAGCTTA AGCAAGCATT AGCACGATT ACCCAGATT ACCCAGATT ACCCAGATT ACCCAGATT ACCCAGATT ACCTAACCGA	CTCTCCACTC CGAATCCTAA GCAATCCTAA GCAGCACTCA TCTCCTATCA TCTCCTATCA TCTCCTATCA CATAGTTTAG CGAATTTTAG CGATTTTCAA CGTTTTCAA TTGTTTCAA TTGTTTCAA GACACTCA GACACTCA GAAACCAAT CCAGAGAAT ATGATTCAC CAAACTTAG GAAACCAAT ATGATTCACA ATTGTGAATC ATTGGAACT ATTGGAACT ATTGGAACT ATTGTGAACT TCTCACCACAA TCCCCAACAA TCCCCAACAA	TGAGAAGCAG AGGGTTTCTT ACTACAGACA ATCAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA GTTTTGGGAACTATAA AGATATTATGATA ACTGAATTA ACTGATTATCAGA AGATTCATGA AATACCAGCT AGTTTTCAGGT CAGATGGCTA TTCTTCAGAT CTGGTAGAGA AAGAAATAAT CTGGTAGAGA CACACTACAA GAGGAAGTGA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGGAAAATTTG GCAGGCTGCT TTACATTTACA TTACATTTACA TTACATTTACA ACAGTACAAA ACAGTACAAA ACAGTACAAG TCTTGTTACA TTTGTACCAG TCTTGTTACA TCTTGTACCAG TCAAGACTTGT AGCAGCATAG GCCTACTGAT CAAGGAGCAGA CAGTGCTACA CAGTACTGAT CAAGGACTGAT CAAGGACCATA GCCTACTGAT CAAGGACCAGA CCAGTTACAG TCGCATTACAG TCGCATTACGG	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1140 1200 1320 1380 1440 1560 1560
50 55 60	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA GACAATCCAAT GTCAGCGGAG GAAATGCAATA GAGAATGCAATA GAGAATGCAATA AATGCATAAAG GAAAAGGGA TTAGAATCCAT ACAGTTAAGCA TCTGGTTATG TTCTTAGAC AGTTCAGAAC TCGGAAAGAC CAGTTGGATG GGGAACAC GAGAGGGAA AACCAAATCA AAGGAGGGAA AACCAAATCA AAGGAGGGAA AACCAAATCA AAGGAGGGAA AACCAAATCA AAGGAGAGTGAT	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCCG AGATTGCCG AGATTGCCG AGATTTAATAG CGAGTTCATCAG TCTACTGCTT AGTTAAGAGC CGATTATTGA TCTACTGCTT AGTTAAGAGC CGATTATTCA TCATACTGCT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT CCGAGTCGT TCAGAGTCCT TCAGATACTT GCTTATATAG TCAGATCTTT AAGACATTGA GGAAAAAGGA ATGAAGCCAA TTCCCAATAC TTCCCAATAC	CTCCCCTCC TCTGGAATG CCTGGAATGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGAATCAGT TGGATCAGA TATGCGGAC TTTATCCATT TGGAGTCGGAC TCCTGCACA CCAGTTGGCT GGACTACACT TCAGGCTGAC TCAGGCTGAC TTATGATACC TCAGGCTGAC CCAGTTGGCT GGACTACACT CCAGGTTGAC TCAGGCTGAC TCAGGCTGAC TATGATACACT TCAGGCTGAC CCAGATTA AAAATACAGC CCCTGAATTA AGAAGGCGCT ACCCCAGATT AGAAGGCGCT ACCCCAGATT AGAAGGCGCT ACCCCAGATT AGAAGCCGA ATCTTTAAAT	CTCTCCACTC CGAATCCTAC GGAATCCTAC GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTTCAG GACACACTTA GACACACTTA GGAAACAATT GGAAAGGAAG CCAGAGAATT ATGATTTTCAG ATGATTTTCAG ATGATTTTCAG ATGATTTTCAG ATGATTCACA ATTGACACAA TCCCCAACAA TCCCCAACAA TCCCCAACAA TCCCCAACAA	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAGACA ATCAAGACA ATCAAGACA ATCACACTACA AGGATAAAACA AGGATAACACT AGGGACAGA GTTTTGAGGA CTGACAAGTA ACTGGATGT AAGTTCTACA AGATTCATAA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA ATACCAGCCT ACGATTGCGAT TTCTTCAGAT AGGAAATAAT CTGGTAGAGA ACCAGTTCACA AGGAGTACAA AGCAATTCACA	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATCGGGA ATTTCCACTT TCACTGGGGA ATTTCCACTT AGCAGTCCAAA AGGAAAATTTG GCAGGCTGCT TTTACATTTACA TTTTAAAGAT ACAGTACAAA ACAGTACAAA ACAGTACAAG TCTTTTACA TTTGTACCAG TCAAGACTTGT TCATGTTACA TCTTGTTACA TCTTGTTACA TCAGGAGCATA GCCTACTGAT CAAGGAGGAG CAGTTGCTACA TCGCATAGGG ATTCTTGGA	120 180 240 300 360 420 540 650 720 780 960 1020 1080 1140 1260 1320 1320 1320 1350 1560 1560 1620 1620
50 55 60 65	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA GACAATCA GTCAGCGGAG AAATGCAATA GGAAAAGGGA GATTACAAG GGAAAAGGGA TTAGATCCAT AATGCTCAT ACAGTTAGCA TCTGGTTATG TTCTCTAGAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGGAAAAGAC CGAGTAGATC AATCCTGAAC AATCCTGAAC AACCAAATCA AACCAAATCA ACCAAAATCA ACCAAAATCA ACCAAAAAAAA	ATTTCCTTCG CCGCAGACCG CGCAGACCG AGATTGCCG AGATTGCCG AGATTGCCG AGATTGCTG TCAATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAGC CGATTATTGA TCAACTGCTT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT CTGAGAGCCA TCAATACTGTT GCTATATTG AGGAGACCT TCAATACTGT TCAGAGGACCA TCAATACTTT GCTTATATGG TTGAACATTT GCTTATATGG TTGAACATTTAAGAGCATTGA GGAAAAAGGA ATGAACATTCA ATGAAGCCAA ATGAAGCCAA ATGAAGACATTCA ATATTTCCTT	CTCCCCTCC TCTGGAAATG CCTGGAATGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGAGTCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT GGACTACCTT TCAGGCTGAC TCAGGCTGAC TATGATACCT TCAGGCTGAC TATGATACCT TCAGGCTGAC TATGATACCT TCAGGCTGAC TACCAAGCAT GCTACCCAAT AAAATACAGC CCTGAATT AGAAGGCGTC ACCCAGATT GCCTAACTT AGAAGGCGTC ACCCAGATT GACTAACCCA ACCTAACCAA AGAAGCCTC TCCCAGATT GACTAACCCA ACCTAACCAA ACCTTAAAT GACTTCACAG	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTTAG CGATTTTGAG GGATTTTGAG AGTGTTTGAG AGTGTTTGTT	TGAGAAGCAG AGGGTTTCCT ACTACAAAAAA ATTATGATGA GGGATAAAAC ATCCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA CTTGAGGACAAAA ACTATCTCACTAA AGATCACAGA ACTGACAGAA ACTGACTTCAC AGTTTTGAGAA ATTACCAGCCT AGTTTGCAGT AGATCACTACAGT ACTGCACATAA ACTGCACAT ACACACACAC ACACTACAA AACCAGCCACC ACTTCCACA AACCAGTCAC AACTCACCAC AACTGCCACC	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTACAATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTTGTACCAG TCAAGAACTTG AGTAGCCATA GCCTACTGAT AGCAGTTGAT CCAGGGCCATA GCCTACTGAT CAAGGAGCAG CAGTGCTACA TCAGGAGCAG CAGTGCTACA TCAGGATAGGG ATTCTCTGGA TAAATTAGCC	120 180 240 300 360 420 660 720 780 840 960 1020 1080 1140 1200 1320 1320 1340 1450 1560 1650 1680 1740
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50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG GAATGCAATA GGGAAAGGGA GTTACAATA AATGCATTACAT AATGCCTCAT AATGCCTCAT ACAGTTAGAC TCTCTTAGAC AGTTCAGAGAC TCGGAAAGAC CAGTTAGAT GGAAAAAC GAAGAGGAA AACCAAATAC AAGGGTGAT ACAGAAAAAC AAGGGTGAT AACTTAGTCG GAAGACTCAG CAAGTTAGTC GAAGACTCAG CAAGAAAAC AAGGGTGATT AACTTGTCGG AGTTTTTTTGAC GAAGACTCAG GAAGATTCAG GAAGATTCAC GAAGATCAC GAAGATTCAC GAAGATCAC GAAGATTCAC GAAGATTCAC GAAGATTCAC GAAGATTCAC GAAGATTCAC GAAGAT	ATTTCCTTCG CCGCAGACCG GRGTTTGCCG AGATTGCTG AGATTGGCTG AGATTGATAG TCGATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAC CGATTATAGGC CGATTATCGT TGACATCTCT TGACATCTCT TGACATCTCT TGACATCTCT TGAGAGAAATGT TCTAGAGTCCT CAGAGAAATGT TGATATATG TTGATATTT GCTTATATGG TTGATCTTT AGGAAAATGA ATGATCTTT AGGACATTCC TCAGATACTTT AGGACATTCC TCAGATACTTT AGGACATTCC TCAGCTCTT CGGCTCTTT CGGCTCTTT CGGCTCTTT CGCCTTTT CGCCTTTCATCAGC CCAGTTTCATCAGC CTAGCCATTA CAGCCTTAC AGACTAATAC CTTCATCAGC CTAGCTCTAC AGACTTACATC CTTCATCAGC CTAGCTCTAC AGACTAATTA	CTCCCCTCC TCTGGAAATG CCTGGAATGG GTCCTATACA CCCAAAACAA AGAACTTAAA TGGGAAAACA AATGTGTTT TGGATCAGAG GAACCTTCAGAG GAACCTTCAG GACACTTCAGAG TCCTGCACA CCAGTTGGCT TCAGGCTGAC CTCATACACT TCAGGCTGAC CTATACACT TCAGGCTGAC CACTACACAT AAAATACAGC CCCTGAATTA AGAAGCGCT ACCCAGATTA AGAAGCGCT ACCCCAGATTA AGAATGCCAAT CACTTCATACACT CCCTGATTA AGAAGCGCT ACCCCAGATTA AGAATGCCAAT CACTTGATACCT CACTCTGAATCAC CATCTCTGAG ATCTTTAAAT GCTTGATACT CATCTCTGAG ATATGATGCC TCAGGAGTA AGAAGAGAA AGACATAACA CACTGAGATTA CACTCTGAGATTA AGACATAACA CACTGAGATTA CACTCTGAGATTA CACTCTAGAGATA CACTCTAGATACA CACTCTAGAGATA CACTCAGAGATA CACTCAGATA CACTCAGAT	CTCTCCACTC CGAATCCTAC GGAATCCTAG GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTTTAGG AGTGTTTAGTC CCAAACTCAA GACACAGTTG GTATTTTTTTTGTG GACACAGTTA GGAAAGCAAT ATGATTTGTG GAAACGAAT ATGATTAGTG GACACACTGA ATTGTGAGA GACTTATG GACCACTGA ATTGTGAATC TCCACACAA TCCCCAACAA TCCCCACCACA TCCACTTCCC ACTGTGACTG ACTGTGACTG ACTGTGACTG ACTGTGACTG ACTGTGACTG ACTGTGACTG ACTGTGACTG ACACTTCCC CCTATTACCACAA TCCACTACAC ACTGTGACTG ACAGTTTCTA GGAGCTGAAG ACAGTTTCTA GCACTTACCAC TCACTAAAGG CCACTAAAGG CCACTAAAGG CCACTAAAGG CCACTAAAGG CCACTAAAGG CCACTACACC CGTGTTGATG CGACACCCCC CGTGTTGATG	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAGACA ATCAAGACA ATCACAGACA ATCACACTAA GGGATAAAACA GTTTTGAGGA GTTTTGAGGA GTTTTGAGGA CTGACAGAG TTGGGACAGA GTTTTGAGGA ACTGCATGA ACTGCATGA ACTGCATGA ACTGCATGA AGATTCATGA ATCCAGCCT TTGTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTCAGAT ACGATTACA ACCATCCA ACCATCA ACCATCCA ACCATCCA ACCATCCA ACCATCCA ACCATCCA ACCATCCA ACCATCA A	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTTAAAGAT AATGCAACAA AGCAGTTTGT TCTTGTTACA TCTTGTTACA TCTAGTACAG AGCAGTTGT TCACAGTGCAT AGCAGTTGT TCAGGAGCTGG TCAGGACTTG TCAGGACTTG TCAGGACTTG TCAGGACTTG TCAGGACTTG TCAGACTTG TCAGCATAGG TCACATATG TCACATA	120 180 240 360 420 480 540 660 720 780 960 1020 1080 1140 1220 1380 1440 1500 1680 1740 1560 1680 1740 1980 1980 2040 2160 22160 2220
50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA GACATACAT GTCAGCGGAG GAATGCAATA GAGATGCAATA GAGATGCAATA GAGATGCAATA AATGCATTAAAG GAAAATCCAT AATGCCTCAT AATGCCTCAT ACAGTTAGCA TCTGGTTATG TTCTTAGAC CAGTTCAGAC CAGTTGGATC GGGAAAGAC GAGAGGGAA AACCAAATCA ACGAAATCA CGAGAGGTACT CGCACTTCTG GCAACTTCTG GCAACTTCTG GCAACTTCTG GAAACTCAA GGAACTTCTG GAAACTCAA GGAACTTCTC CGAAACTCAA GGAACTTCTC GCAACCCAG GAACTTCTC CACCTTTCTCTC TCCTTTTCTCT	ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCCG AGATTGCCG AGATTGCCG AGATTGCTTAA TCTATAACAC GAGTTTCAGCAT TCTACTGCTT AGTTAAGAGC CGATTATTGA TCTACTGCTT TGACATCTCC TCTCTGAAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT CTGAGTTCTT AGACATCTC TCAATAATTT GCTTATATTG GGAAAAAGGA ATGAAGCCAA TTCCCAATAC ATATTTCCTT CAGCCTCTT CAGCTCTT CAGCCCAGT CAGGCCCAGT	CTCCCCTCC TCTGGAAATG CCTGGAATGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGAACACAT TGGGAACACAT TGGGACACAT TGGGACACACAT TGGACTCCTGCACA CCAGTTGGCT GGACTACACT TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TCAGGCTGAC TAACACT TCAGGCTGAC TAACACT TCAGGCTGAC TAACACT GCTACACAT AAAATACAGC CCCTGAATTA AGAAGACT ACCCAGATT GACTAACCGA AATCATCCCAGATT GACTAACCGA AATCATCACG AATCATCACGC AATCTTTAAAT GACTTCTCAG AATCATCTCTCAG AATCATCTCTCAG TCATCCTCTAGATACT CATCTCTTAAAT GCTTGATACT CATCTCTCAGAAAA AGACATAACA CACTGAGATA CACTGAGATA CACTGAGATA GACGTTACACG AATCTTCAGAAAA AGACATAACA CACTGAGATA GACTTCACAG CACTGAGATA	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CGATTTTCAG GGTTTTTTAGG AGTGTTTATCA GACACACTTA GACACACTTA GGAAACAATT GGAAACAATT GGAAAGGAAG ATGGAATTATCA ATGGTTATCA ATGGTTATCA ATGGATTATCA ATGGATTATCA ATGGATTATCA ATGGAACTCA ATTGGAACTCA ATTGTGAATC TCTACCACAA TCCACTACACA TCCACTACACA TCCACTACACA TCCACTACACA TCCACTACACA TCCACTACAC TCTATACACCA TCACTACACA TCCACTACAC TCACTACAC	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAGACA ATCAAGACA ATCAAGACA ATCACACTACA AGGATAAAACA AGGATAACACT AGGACAGA GTTTTGAGGA CTGACAGAG ACTGACAGAG ACTACAGA ACTCACAGA ACCACTACAG ACCACT	AGGAGCCGCA CGCTTGCATT ACAGGAAAA TTGGGGAAAG AGATCTTACA TGACTGGGA ATTATCACTT TCACTGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTACAATTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGT TCATGTTACA TTTGTACCAG TCAAGACTTG AGTAGCATA GCCTACTGAT TCAAGGAGCTACA TCAGGAGCTACA TCAGGACTTGGA TCAGGACTACA TCAGGACTACA TCAGGAGAGAG CCCACTATG TCAGGAGAGAG TCCACTATG TGAGGAGAGAG CCCACTATG TGAGGAGAGAG CCCACTACC CCACTATG TGAGGAGAGAG CCCAGTCCC AATTGCTCC GGAGGAAAT AGGCAGAGAG GGAAACCAAG GGAAACCAAG GGAAATGCC	120 180 240 360 420 540 660 720 780 960 1020 1020 1020 1320 1320 1320 1320 1340 1560 1560 1740 1860 1920 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980
50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA ACACATTCA GTCAGCGGAG GAAATGCAATA GGAAAAGGGA TTAGATCCAT ACAGTTAAAG TTAGATCCAT ACAGTTAAC TTTGGTTATG TTTCTTAGAC AGTTAGAAC AGTTAGAAC AGTTAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTCATATC AATCCTGATC GAAAAACCAAATCA ACGAAAATCA ACGAAAAAC ACGAAATCA ACGAAAACCAA CGAAACTCAG GCAACTTCTG GAAAACCCAA GGAAAACCCAA GGAAAACCCAA GGAAAACCCAA CGAAATCA ACGAAATCA ACGAACTTCTC CATTATTCTC CATTATTCTA CATTATTCTA	ATTTCCTTCG CCGCAGACCG CGCAGACCG AGATTGCCG AGATTGCCG AGATTGCCG AGATTGCCTG TCAATACAC GAGTTTCATCAG TCTACTCTGA TCTACTCTTAAGAC CGATTATTGA TCAACTCTTC TCTCTGAAAG TCATCTCC TCTCTGAAAG TCATCTCTC TCAGAGTCTTT CAGAAAATGT CTGAGTCTTT CAGAGTCCTT TGACATCTCT TCAGAGTCCTT TCAGCTCTTT TCAGCCTCTT AGACCATTCAA CTATCCCATT AGACCATTAC AGACTATAC AGACCAGT CCTTCATCAGC CTTCATCACC CCTTCACCACC CCTTCACCAC	CTCCCCTCC TCTGGAAATG CCTGGAATGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACA AATGGTGTTT TGGATCGGAC TTTATCCATT TGGAGTCGAA GAACTTATCATT TGGAGTCGAA CCAGTTGGCT GCACTACACT TCAGGCTGAC TCAGTACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC AACAAGCAT GCTACCCAAT AAAATACAGC ACCAGATT GACTACCAAT AAATACAGC CCTGAATT ACCCAGATT GACTACCAA AATGATGGC ATCCTTAAAT GACTTCTCAG AATGATGAC TCTTCAGAAGAA AGACATAACA CCTTGAAGAAA AGACATAACA CCTTGAAGAACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAAGACA CCTTGAACAC CCTTGAACAC CCTTGAACAC CCTTGAACAC CCTTGAACAC CCTTGAACAC CCTTGAACAC CCTTCCAACT CCTTCCAACT CCTTCCAACT CCTTCCAACT CCTTCCAACT CCTTCCCAACT CTTCCCAACT CCTTCCAACT CCTTCCAACT CTTCCCAACT CTTCCCAACT CTTCCCAACT CTTCCCAACT CTTCCCAACT CTTCCCAACT CTTCCCAACT CTTCCCAACT CTTCCCCAACT CTTCCCAACT CTTCCCCAACT CTTCCCCACT CTTCCCCCAACT CTTCCCCAACT CTTCCCCCAACT CTTCCCCCAACT CTTCCCCCAAC	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTTAG GGATTTTAG GGATTTTAG GGATTTTAG GGATTTTAG GGATTTTAG GGATTTTGTTTG	TGAGAAGCAG AGGGTTTCCT ACTACAAAAAA ATATTGATGA GGGATAAACC ATCCACATAA AGGACAAAA GGGATAAACT TGAGGACAAAA CTGACAGAA CTGACAGAA CTGACAGAA ACTACTCAGAC ACTTCAGACAGAA ACTACTCAGAC ACTTCAGAC ACTTCAGAC ACTTCAGAT TTCTCAGAT ACCACTCAC AACTTCACAA ACCAGTTCAC AACCAGTTCAC AACTTCACAA ATTCTTCAGA TTACAGATCA TTACAGACTA ATTCTTCAGAT TTACAGATCT TTCATGCTT TTCATGCT TTCATGC TTCATGCT TTCATGC TTCATG	AGGAGCCGCA CGCTTGCATT ACAGGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTACATTTAC TTTTACATTTAC TTTTACATTTAC AGTAGCAAA ACAGTACAAA ACAGTACAAG AGCAGTTTGT TCATGTACCAG TCAGAGACTTG AGTAGCCATA GCCTACTGAT CAAGGAGGAG CAGTGCTACA TCGCATAGGG ATTCTCTCGAA TCACATATG TCACACTATG TGAGGAGGAG CTCCAGTCCC ATTTTCCTCC AAATGCTCC AGAGGAGAG GACAACCAAG GGCAGAGAG GGCAAATGCCCA TACCCCATCCC	120 180 240 360 420 360 480 540 660 720 780 960 1020 1020 1320 1320 1340 1560 1620 1620 1740 1860 1740 1860 1920 1980 2040 2160 2220 2160 22280 2340
50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA AACAATTCA GTCAGCGGAG GAAATGCAATA GGGAAAGGGA GAAATGCAATA AAGGTAAAA GGAAATGCAT AATGCCTCAT AATGCCTCAT AATGCCTCAT ACAGTTAGCA TCTGGTTATG TTCTTAGAC CGGAAAGAC CGGAAAGAC GAAGAGGGAA AACCAAATCA AAGGGTGATT AACCAAATCA AAGGGTGATT AACTTGTCGG GAAGACTCAG CGAGGAAAAC AAGGGTAATC AACTTTGTCGG GAAAACCAA CGAAAATCA AAGGGTGATT AACTTGTCCG GAAACTCTCG GAAAACCCAA GTGTGGTTTC CCATTTCTCC CCTTTTCTC CTCTTTTCTC CTCTTTCTC CTCTTTTCTC CTCTTTCTC CTCTTTTCTC CTCTTTTCTC CTCTTTTCTC CTCTTTCTC CTTTCTC CTCTTTCTC CTTTTCTC CTCTTTCTC CTCTTTTCTC CTCTTTTCTC CTTTTTCTCTC CTTTTCTTC	ATTTCCTTCS CCGCAGACCG GRGTTTGCCG AGATTGCTG AGATTGGCTG AGATTGACTA TCTATAACAC GAGTTTCAGA TGTCATCTGA TCTACTGCTT AGTTAAGAC CGATTATCGT TGACATCTC TCTCTGAAAG TCATCTGAT AGGTGTTTTC CAGAAAATGT CTGAGTCGT CAGAAAATGT CAGATCTTT AGACATTGA TGATCTTT AAGACATTGA GGAAAAATGA TTGATCTTT AAGACATTGA GGAAAAATGA TTGATCTTT CAGCTCTTT CAGCCCAGT CTTAGCCAGT CCTTTGCCCAT CAGCCCAGT CCTTTGCCCAT CAGGCCCAGT CCTTTCCTTT	CTCCCCTCC TCTGGAATTG CCTGGAATGG GTCCTATACA CCCAAACAA AAGGAACATAA ATGGGAACAT AATGGTGTTT TGGAATGAG GAACCTCAT GGAGTCGAG TCCTGCACA CCAGTTGGCT TCAGGCTGAC CTCATACACT TCAGGCTGAC CTATACACT TAGAGTCGAC CTATACACT TAGAGTCGAC CTCATACACT AAACAAGCAT AAAATACAC CCCTGAATTA AGAAGGCGCT ACCCCAGATT ACACTTCAGA ATCTTTAAAT GACTACCCA ATCTTTAAAT GACTACCCA ATCTTTAAAT GACTACCCA ATCTTTAAAT GACTACCCA ATCTTTAAAT GACTACCCA ATCTTTAAAT GCTTGATACT CATCTCTGAG ATATGATGCC ATCTTGAGAATA CACTGAGATTA CACTGAGATTA CACTGAGATTA CACTGAGATTA CACTGAGATTA CACTGAGATTA CACTGAGATTA CACTGAGATTA CACTCCCAAGTC CTCCCAAGTC CTCCCAACTC CTCCCAAGTC CTCCCAAGTC CTCCCAAGTC CTCCCAAGTC CTCCCAAGTC CTCCCAACTC CTCCAACGTC CTCCAACTC	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTAA AAAGCAAGCA CATATTTTGAG GGATTTTTTTTGAG GACTCTATAA GACACGTTG GTTTTTTTTTT	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAGACA ATCAAGACA ATCACAGACA ATCACAGACA ATCACACTAA AGGATAACATT AGGATAACATT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA CTGACAAGTA ACTGGATGT AAGTTCTAC TTCGAGAGCA AGATTCATCA AGATTCATCA AGATTCATCA ATCCAGCCT AGGTTCTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT ATCTTCAGAT AACAGAATAA ATCTTCAGAC AACTGCACC TAACAGATA AATCTTCAGA ATCCTTCAT ATCTTTCAGAT TTCACAGATCT TCACAGATCT TCACAGATC TCACAGATCT TCACAGATCT TCACAGATCT TCACAGATCT TCACAGATCT TCACAGATC TCACAGATCT TCACAGATC TCACAGATCT TCACAGATCT TCACAGATCT TCACAGATCT TCACAGATCT TCACAGATC TCAC	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA TGACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTACATTTACA TTTTACACTT AATGCAACAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAA ACAGTACAA ACAGTACAA ACAGTACAA TCACTACTGAT CCAGTCACTACA TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTG TCACACTTTC TCACACTTTC TCACACTTTC TCACACTTTC TCACACTTTC TCACCACTTCC AATTCCTCC AATTCCTACC AATCCTACCA GGCACACCAG GGCACACCAC GGACACCCATCC AACCCCATCC	120 180 240 300 360 420 480 540 660 720 780 960 900 910 1020 1080 1140 1260 1380 1320 1380 1440 1560 1560 1680 1740 1860 1920 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 1980 19
50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA GACACATTCA GTCAGCGGAG GAAATGCAATA GAGATGCAATA GAGATGCAATA GAGATGCAATA AATGCATAAAG GAAATGCAAT AATGCCTCAT AATGCCTCAT AATGCCTCAT ACAGTTAGCA TCTGGTTATG TTCTTAGAC CGGTAAGAC CGGAAAGAC CGAGTTCAGAAC GAGAGGGAA AACCAAATCA AACGGAAATCA AACGGAAATCA AAGGGTGATG GAAGGTACT GAAAATCA AAGGGTGATG GAAGGTACT GAAAACCCAA CGAAACTCCG GAAACTCCG GAAACTCCG GAAACTCCCC CCTTTTCTCC CTTTTCTCC CTTTTCTC CTTTTCTCC CTTT	ATTTCCTTCG CCGCAGACCG GRGTTTGCCG AGATTGCTG AGATTGGCTG AGATTGATAG GRGTTTCAGATAG TCTATAACAC GAGTTTCAGAT AGTTAAGAC CGATTATGAT AGTTAAGAC CGATTATTGA TCTACTGCTT TGACATCTCC TCTCTGAAAG TCATACTGAT TCAGATCTTC CAGAAAATGT CTGAGTCTGAT AGGAGACCA TCAATAATTT GCTTATATGG GGAAAAAGGCA TTGATCTTT AAGACATTGA TGACTCTT CAGCTCTTT CAGCTCTTCAT CAGCTCTTTCCTTA CAGGCCCAGT CCTTTTGCTTA CAGGCCCAGT CCTTTTGCTTA CAGGCCCAGT CCTTTGCTTA CAGGCCCAGT CCTTTTGCTTA CAGGCCCAGT CCTTTTGCTTA CAGGCCCAGT CCTTTTGCTTA CAGCTCTTA CAGCCCAGT CCTTTA CAGCTCTTA	CTCCCCTCC TCTGGAAATG CCTGGAATGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGAACACAT TGGGAAACAT AATGGTGTT TGGACTACACT TCAGGTCGAC CCAGTTGGCT GGACTACACT TCAGGCTGAC TTATCCATT AGACTCACA CCAGTTGGCT GGACTACACT TCAGGCTGAC TTATGATACC TATGATACC TATGATACC TATGATACC TATGATACAC TATGATACC AACCAAGCAT ACACCAGATT AGAATACAGC ATCTTTAAAT GACTACCGAGATT CACTCTCAGA ATCTTTAAAT GACTACCT CATCTCTAACT CATCTCTAGA TCATCTCTAGA TATGATACT CATCTCTGAGATA CACTCTGAGATA CACTCTGAGATA CACTCTGAGATA CACTCTGAGATA CACTCTGAGATA CACTGAGATA GAGACATAACC TCCCAAGCT TCCCAACT CTCCCACGTC TCTCCACGTC TCTCCACGTC TCTCCACCT TCTCCACCT TCTCCACCT TCTCCACCT TCTCCACCT TCTCCACCT TCTCCACCT TCTCCACCT TCTCACCCT TCTCCACCT TCTCACCT TCTCCACCT TCTCACCT TCTCCACCT TCTCACCT TCTCCACCT TCTCACCT TCTCCACCT TCTCACCT TCTCCACCT TCTCA	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CGATTTTCAG GGTTTTTTAGG AGTGTTTATCA GACCACTTA GACACACTTA GACACACTA GACACACTA ATGGAAACACTA ATGGAAACACTA ATGGAACACTA ATGGAACACTA ATGGAATTAGA GAATTTTTAG GACACACTA ATGGAATTAG ACCACTTAC ATTGTGAATC ATTGTGAATC ACTGTGACTC ACGGTTTCCAC ACGGTCCCC ACTGTGACCCCC ACTGTGACCCCC ACTGTTGACC ACGCCCCC ACTGTTCACT ACGGTGATACAC AACGTGGTAT TCCTACACTAT TCCTACACTAT	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCAAGACA ATCAAGACA ATCACAGACA ATCACAGACA ATCACACTAA AGGATAACACT AGGATAACACT AGGACAGA GTTTTGAGGA GTTTTGAGGA ACTGACAGAG ACTGACAGAG ACTGACAGAG ACTGACAGAG ACTGACAGAG ACTGACAGAG ACTGACAGAG ACTGACAGAG ACTGCACC ACTGCAGAG ACACTACAA ACCAGCCA ACCAGCAC ACCAGCAC ACCAGCAC ACCAGCAC ACCAGCAC ACTGCACC TAACAGAATA ATCCTTCAGAT ATCCTCAGAT ATCCTCAGAT ACCAGCTCAC ACTGCACC TAACAGAATA ATCCTTCAGAT ACCAGCTCAC ACTGCACC TCATGCTTT ACCAGATCA ACCAGCACC ACTGCAC ACTGCACC TCATGCTTT ACTCTCAGAT ATCCTTCAT ATCTTCAGAT ATCCTTCAT ATCCTTCAT ATCCTTCAT ATCCTTCAT ATCCTTCAGATA TTCAGAGAT ATCCTCAGATA ATCCTTCAGAGAT ATCCTCAGAGAC ACTGCAGACC CTCATGCTTT ACTCGCAGAC GTGAAATCCT TCATGCTTT ACTCGCAGAC GTGAAATCCT TCATGCTT ACTCGCAGAC GTGAAATCCT TCATGCTT ACTCGCAGAC GTGAAATCCT TCATGCTT ACTCGCAGAC GTGAAATCCT TCATGCT T	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA TGACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTTACAATTTAC TTTTAAAGAT AATGCAACAA AGAAACTTG TCACTGGGA ACTTTTACACTT AATGCAACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTGACCAG TCAAGACTTG TCAAGACTTG AGTAGCCATA GCCTACTGAT CAAGGAGAG CAGTCTACA TCAGGAGAGAG CACCACTGTG TCACACTGTG TCACCACTCC AATTCCCC GGAGGAAAT AGCCAACCAG GGAAATGCCA TACCCCATCC AACCCCATCC TCCCCAACCG TCCTCCACCCC TCCTCAGTC TCCCCACCCC TCCTCTTAGTC	120 180 240 360 420 360 480 540 660 720 780 960 1020 1080 1140 1260 1380 1320 1380 1440 1560 1560 1620 1680 1740 1860 1920 1920 2040 2160 2220 2240 2240 2460
50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA GACACATTCA GTCAGCGGAG GAAATGCAATA GGAAAAGGGA TTAGATCAA GGAAAAGGGA TTAGATCCAT ACAGTTAACA TCTGGTTATGCA TCTGGTTATGCA TCTGGTATATG AGTTCAGAC CAGTTGGATG GGAAAAAC CAGTTAGAC GAAGAGGGAA ACCCAATTCA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATACA ACGAAATCA ACGAAATCA ACGAAATCA ACGAAATCA ACGAAATCA ACGAAATCA CGAAGGTACTT ACTTGTCG GAAACTCCG GAAGATCCAG GCACTTCTC CATTATTCTA CTCCAGACAAC CCCTTTCTCT CCATTATCTA ACCCCTTTCTCT CATTATCTA ACCCCTTTCTCT CATTATCTA ACCCCTTTCTT CCATTATCTA ACCCCTTTCTT CCATTATCTA ACCCCTTTCTT CCATTATCTA ACCCCTTTCTT CCATTATCTA ACCCCTTTCTT CCATTATCTA ACCCCTTTCTT CCATTATCTA ACCCCTTTCTTCTCT CATTATCTA ACCCCTTTCTTCTA ACCCCTTTCTTCTTCTA ACCCCTTTCTTCTA CCATTATCTA ACCCCTTTCTTCTTCTTCTTCTA ACCCCCTTTCTTT	ATTTCCTTCG CCGCAGACCG CGTGTTTGCCG AGATTGCCG AGATTGCTG AGATTGGCTG TGAATCTTAA TTCATATAGAC GAGTTTCATCAGA TCTACTGCTT AGTTAAGAC CGATTATTGA TCACTGTT TGACATCTCC TCTCTGAAAG TCATGCTGTT TGACATCTCC TCTCTGAAAG TCATGCTGTT TGACATCTCC TCTGAGAGCCA TCAATAATTT GCTTATATGG TTGACATTTT AGACATTATGG TTGACATTT AGACATTATG GGAAAAAGGA ATGAAGCCAA TCACATAAC ATATTTCCTT CAGCCTCTTT CAGCCTCTTT AGACCATTA CCTTCTACAG CCTTCATCAG CCTTCATCAG CCTTCATCAG CCTTCATCAG CCTTTTGCCTA AGGATTATGC TGACTGCTTA AGAGCTAAT CCTTCATCAGC CTTCATCAGC CTTCATCAGC CTTCACCAG CCTTTTGCCTA AGGATTTGCT AGGACTACC TGCTTGACCA TGTGACCAC TGCTTGACCA TGTGACCAC TGCTTGACCA TGTGTGACCAC TGCTTGACCAC TGCTTGACCAC TGCTTGACCAC TGCTTGACCAC TGCTTGACCAC TGCTTGACCAC TGCTTGACCAC TGCTTTGACCAC TGCTTGACCAC	CTCCCCTCC TCTGGAATG CCTGGAATG GTCCTATACA CCCAAACAA GAACTTAAA TGGGAAACA AATGGTGTT TGGAATCGGAC TTTATCCATT TGGAGTCGAA GAACCTTCTG TCCCTGCACA CCAGTTGGCT TCAGGCTGAC TTATGATACA CTATAGATCA CCAGTTGGCT TCAGGCTGAC TTATGATACAC TCAGGCTGAC TATGATACAC TCAGGCTGAC TATGATACAC CCCTGAATTA AAATACAGC CCCTGAATTA GACTACCCA AACTAACAC AACTAACAT GCTACCCAAT GCTTACACT TCAGGAGAA ATCTTTAAAT GCTTGATACT CTCCTGAG ATTCTCTGAG ATTCTCTGAG ATTCTCTGAG ATTCTCTGAG CTTCCACGGTC TCCCCACCT TCTCCCACGTC TCTCCACCT TCTCCACCT TCTCACCT TCTCACACT TCTTCACCT TCTCACCT TCTTCACCT TCTTCACCT TCTCACCT TCACACT TCTTCACCT TCACACT TCTTCACCT TCTTTTTTTCACCT TCTTCACCT TCTTCACCT TCTTCACCT TCTTCACCT TCTTCACCT TCTTTTTTTCACCT TCTTCACCT TCTTCACCT TCTTCACCT TCTTTCACCT TCTTCACCT TCTTTTTTTT	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTAA AAGCAAGCA CGATTTTGAG GGATTTTGAG GGATTTTGAG GGATTTTGAG GGATTTTGAG GACACAGTTG GTTTTTGAG GACACAGTTG GTTTTTGAG GAACTCAA GACACAGTTG GGAACTCAA ATGGATTGAGA CCAGAGAATT ATGATTGAGA ATGGATTATG GACCAACTGA ATTGGAACTG ATTGGAACT ATTGGAACT ATTGTAAACTG ACTGTGACTG CCTAAAACTG CCACAA TCCACCAA TCCACCAA TCCACCAA TCCACCAA TCCACCAA TCCACCAACTGA ATGGACTTCC CTTAAAACTG CTTAAAACTG CCTTAAAACTG GAGGTTAACTG GAGGTTAACTG GAGGTTAACCG CTTATACCAG GAGGTTAACG GGGCCCG CGTGTTTAACCG CGTGTTTCACAGT TCCACACAG GGGCCCAACACCC CACGTGTTACCAC AACGTGTTACACGT GAGGTTACACGT TCCTACAGTT TCCTACAGTT TCCTACAGTT AACACTACCC	TGAGAAGCAG AGGGTTTCCT ACTGACAA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCACACTAA AGGACAAAA AGGACAAAA AGGACAAAA ACTGACAGAA ACTGACAGAA AGGACAAAA ACTGACAGAA ACTGACAGAA ACTGACAGAA ACTGACAGTA ACTGACAGTA ACTGCACC AGTTTGCAGT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT ACTGCACC ACTGCACC TTCTTACATC ACTGCACC TTCTTACATC ACTGCACC TTCTTACATC ACTGCACC TTCTTACATC ACTGCACC TTCTTACATC ACTGCACC TTCTTAGAT ATTCTTCAGA ATCCTTCTAGAA ATCCTTCTAGAA ATCCTTCAGAT ATTCTTCAGA ATCCTTCAGAT ATTCTTCAGAA ATCCTTCAGAT ATTCTTCAGAC ACTGCACC TTCTTAGATC TTCAGGAAC ACTGCACC TTCTTAGATC TTCAGGAAC ACTGCAGC ACTGCAGC TTCCTTGAGAA TTCAGGAAC ACTGCAGC TTCCTTGAGAA ATCCTTCAGAA ATCCTTCAGAA ATCCTTCAGAA ATCCTTCAGAAC ACTGCAGC TTCAGCAGAC TTCAGCAC TTCAGCAGAC TTCAGCAGAC TTCAGCAC TTCA	AGGAGCCGCA CGCTTGCATT ACAGGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT TCACTGGGGA ATTTCCACTT TTACATTTGA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTTGTACCAG TCAGAGCATTG TCAGAGCATTG CAGTACTAGG ATTCTCTGGA ATTCTCTGGA TTACATTTGCCACATTGG TCACACTGTG TCACACTGTC AATTCCTCC AATTCCTC AATTCCTC AACTCCAACCG TCCCCATCC AACCCAACCG TCCCCATCC AACTCCCATCC AACTCCAACCG TCCCCATCC AACTCCAACCG TCCCCATCC AACTCCAACCG TCCCCATCC AACTCCATCC AACTCCATCC AACTCCTAGTC AACTCCTAGTC AACTCCTAGTC AAGTAGTGAT	120 180 240 300 360 420 660 720 780 840 900 960 1020 1320 1320 1380 1440 1500 1560 1620 1680 1740 1890 2040 2220 2340 24460 2450
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50 55 60 65 70	CAAAAAAAC CGGCGAGGGG CAGCTICCTCT CTTGTTGAAG AAATATCCAA GACACATTCA GTCAGCGGAG GAATGCAATA GAGATGCAATA GAGATGCAATA GAGATGCAATA AATGCATTAAGCA TCTGGTTATG TTCTTAGAC TCTGGTTATG TTCTTAGAC AGTTCAGAC CGGAAAGC CAGTTGGATG GGAAAGC GAAGAGC CAGTTGGAT AACCCAATAC AACCCAATC AACCCAATC GAAGAGC GAAGAGC GAAGATCA ACGAAATCA ACGAAATCA ACGAAATCA ACGAAATCA AACCCAATC GAAGAGC GAAGGTGAT GCACTTCTG GAAACCCAG GAAGATTCAC GTATACTCTC TCCCTTTCTC TCCCGTTTCT TCCGGCCTTGC TCCTTCCT	ATTTCCTTCG CCGCAGACCG GRGTTTGCCG AGATTGCTG AGATTGGCTG AGATTGGCTG AGATTGATAG GRGTTTCAGA TCTATAACAC GAGTTTCAGA TCTATATGGTT AGTTAAGAC CCGATTATCGTT TGACATCTCC TCTCTGAAAG TCATACTGTT CCGAGTCTTC CAGAAAATGT CTGAGTCCT CAGAAAATGT CAGATATTG TGAGAAAATGT TGAGATCTTT AAGACATTGA GGAAAAATGT TCGATTCTT AAGACATTGA GGAAAAATGT TCGATTCTT AAGACATTGA CTATATTTCC TGACTCTTT CAGCTCTTT CAGCTCTTT CAGCTCTTT CAGCTCTTT CAGCTCTTT CTAGCTCTTT CTAGCTCTTT CTAGCTCTTT CTTAGTCCTTT CTAGCTCTTT CTTAGTCCTTT CTTAGTCCTTT CTTAGTCCTTT CTTAGTCCTTT CTTAGTCCTTT CTTAGTCCTTT CTTAGTCCTT CCTTTTCCCTT CCTTTTCCCTT CTTTTCCCTT CTTTTCCCTC TCTTTTCCCT TCTTTTCCCT TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTTCCC TCTTTCCCC ATGGTTCCC ATGGTTCCC ATGGTTCCC ATGGTTCCC ATGGTTCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCC ATGGTTCCCC ATGGTTCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCCC ATGGTTCCC ATGCTCC ATGGTTCCC ATGGTTCCC ATGGTTCC ATGGTTCC ATGGTTCC ATGGTTCC ATGCT	CTCCCCTCC TCTGGAATTG CCTGGAATGG GTCCTATACA CCCAAAACAA AAGAACATAAA TGGGAAACAA AATGGTGTTT TGGATCAGT TGAGATCGGAC TTTATCCATT TGGACACCTTCGCACA CCAGTTGGCT TCATACACT TCAGGCTGAC TTATACATT AGAATCACAT ACACTACACT	CTCTCCACTC CGAATCCTAC GGAATCCTAA GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTAA AAAGCAAGCA CATATTTTGAG GGATTTTTTTTGAG GACACAGTTA GGACACTCA GACACAGTT GGAAACTCAA GACACAGTT GGAAACACTA ATGATTTTGAG GACACAGTT GGAAACACTA ATGATTAGA GACTTATAG GACCACTGA ATTGTGAAT TCCACACAA TCCACACAA TCCACACAA TCCACACAA TCCACTCCC ACTGTGACTG ACTGTGACTG ACTGTGACTG ACAGTTTCTA GGAGCTGAAA TCCACTACAC CCTTATACCAC CCTTATACCAC CCTTATACCAC ACTGTGACTG ACAGTTTCTA GGAGCTGAAA TCCACTACAC ACTGTGACTG ACAGTTTCCA CCTTATACCAC ACTGTGACTG ACAGTTTCCA CTTATACCAG TCACACACAC CCTGTTGACTG ACAGTTACCAC ACTGTGATT TCCTACAGTA AACACTACCC AGTGTTCATA ACACTTACCTG AGTGTCACTG AGTGTCACTG AGTGTCACTT TCCTACAGTA AACACTACCC AGTGTTCATCT TCCTACAGTA AACACTACCC AGTGTCCATCT TCTTACCAGTA AACACTACCC AGTGTTCATCT TCCTACAGTA ACACTTACCTC TCTTCCTCTT TTTCCTCTT TTTTCCTCTT TTTCCTCTT TTTCCTTCTT	TGAGAAGCAG AGGGTTTCCT ACTACAGACA ATCACAGACA ATCACAGACA ATCACAGACA ATCACAGACA ATCACAGACA ATCACACTAA AGGATAACATT AGGATAACATT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA CTGACAGAGT TTCGAGAGCACA AGATTCATCA AGATTCATCA AGATTCATCA AGATTCATCA ATCCAGCCT AGCTTCAGAT ATCCTCAGAT ATCCTCACACT ACCACCT ACCACC ACCACC ACCACC ACCACC ACCACC ACCACC	AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGTCAAA AGAAAATTTG 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		CGTTAATAAC					3120
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		IQLLCVCRLD	WANGYYRQQR	KLVERIGWSY	TGALNOKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLKKL	KFQGWDKTSL	ENTFIHMTGK	TVBINLTNDY	RVSGGVSEMV	120
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		CSSEPENVQA					360
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		SENPETITYD					660
		ESFLQTNYTE					720
		SSRQQDLVST					780
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		ADTNEKDADG					1620
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		TLRNTKIKKG					1920
		VECSAGVGRT					1980
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		WDHNAQLVVM					2160
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50	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AAATAATCA	574 DNA sec id Accession lence: 148-4 11 CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC	nuence 1 #: Eos sec 1518 21 1 CTCACTTCGA CTCCCCCTCC CTCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAACTTAAA TGGGAAACA	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT	120 180 240 300 360 420 480
50 55	Seq ID NO: Nucleic Aci Coding sequ CACACATACG CAAAAAAAC CAGGAGGGG CAGCTCCTG CTTGTTGAAG AAATATCCAA CAAGTAAAT CAAGTAAAT CAAGTAATG AACACATTCA GTCAGCGGAG	574 DNA sec id Accession ience: 148-4 11 CACGCACGAT ATTTCCTTCG CGCAGACCG AGATTGCCG AGATTGCCG AGATTGCCG AGATTGCTG CATGTAATAG TGAATCTTA TTCATAACAC GAGTTTCAGA	uence u #: Eos sec 1518 21 CTCACTTCGA CTCCCCTCC TCTGGAATGG GTCCTATACA CCCAAAACAA CGAAACTTAAA TGGGAAACA AATGGTGTTT	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTCAATGGAT GCAGCACTGA TCTCCTATCA TTTCAGGGTT TTTCAGGGTT AAAGCAACTA AAAGCAAGCA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT	ACCAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA	120 180 240 300 360 420 480 540
50 55	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAAAAAAAC CGGGAGGGG CAGCTCCTCT CTTGTTGAAG CAAGTAAATG AACACATTCA ACCACATTCA GTCAGGGGG AAATGCAATA	574 DNA Becoded Accession sence: 148-4 11 CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG AGATTGGTA TTCATAACAC GAGTTCAGA TGTCATCAGA TGTCATCTGA	nuence 1 #: Eos sec 1518 21	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA GTAGGAAGCA CATAGTTTAG	GAGGATTAA TGAGAAGCAG ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAT TGACTACCGT TCACTGGGGA ATTTCCACTT	120 180 240 300 360 420 480 540
50 55 60	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AAATATCCAA AACACATTCA GTCAGCGGAG AAATGCAAAT GAGATGCAAAA	574 DNA Sec 574 DNA Sec 10 Accession 11 CACGCACGAT ATTICCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGA TCTCATCTGT	nuence 1 #: Eos sec 1518 21 CTCACTTCGA CTCCCCCTCC CTCAGAATG GTCCTATACA CCCAAAACA GAAACTTAAA TGGGAAACA AATGGTGTTT TGGATCAGAG TGATCAGAG TGATCAGAG TGATCAGAG	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAA	GAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA	120 180 240 300 360 420 480 540 600 660
50 55 60	Seq ID NO: Nucleic Aci Coding sequ 1	574 DNA section and section an	quence 1 #: Eos sec 1518 21 CTCACTTCGA CTCCCCTCC CCTGGAAATG GTCCTATACA CCCAAAACAA AAACATTAAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TGATGCGGAC TTTATCCATT	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTTCAG TTTCTAGTTTAGAGTTTTAG	GGAGGATTAA TGAGAAGCAG AGCCTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA GTTTTGAGGA TTTGGGACAGA	I AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG ATCATTTGGAA TGACTACCGT TCACTGGGGA ATTTTCCACTT AGCAGTCAAA AGGAGTCAAA AGGAGAAATTTG	120 180 240 300 360 420 480 540 600 660 720
50 55	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CASAAAAAAC CAGCAGGGG CAGCTCCTCT CTTGTTGAAG CAAGTAAATG AACACATTCAA GTCAGCGAG AAATGCAATA GAGATGCAATA GAGATGCAATA GAGATGCAATA GAGATGCAATA GAGAAAAGGGA GAATTCCAAAGGGA GAATTCCAAAGGGA GAATTCCAAAGGGA GAATTCCAAAAG	574 DNA Becode Accession a	puence 1 #: Eos sec 1518 21	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTCAG	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGGAAATTTG GCAGGCTGCT	120 180 240 300 360 420 480 540 600 660
50 55 60	Seq ID NO: Nucleic Aci Coding sequ CACACATACG CAAAAAAAA CGGGAAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATATCCAATGCAAAAGGGA AAATGCAATAAATGCAATTCAAGGAAAAGGGA GTATTCAAAGGTAAAAGGGAAAAGGGA GTTTAGATCCAT	11 11 CACGCACGAT ATTICCTTCG CGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TTCATAACAC GAGTTTCAGA TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TGTCATCTGAT TCTACTGTT AGTTAAGAGC CGATTATGGA TCATACTGTT	nuence 1 #: Eos sec 1518 21 CTCACTTCGA CTCCCCTCTC TCTGGAATG GTCCTATACA CCCAAACAA GAAACTTAAA TGGGAAACA TGGGATCGGTGTTT TGGATCAGAG TGATCAGAG TGATCAGAG TGATCAGAG TGATGCGGAC TTTATCCATT TGGATCAGA GAACCTTCTG	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTCAA TTGTTTGAGG AGTGTTAGGC CCAAACTCAA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGAGGA CTGACAAGTA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGGAAATTTG GCAGGCTGCT	120 180 240 300 360 420 480 540 600 660 720 780
50 55 60	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAARAARAAAC CGGCGGGGG CAGCTCCTCT CTTGTTGAAG ARATATCCAA ARATATCCAA GACATGCGAAG GAAAAGGGA GAATGCAATA GGAAAAGGGA GATTCAAAG GTTAGATCCAT AATGCCAT AATGCCTCAT	11 CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCCG AGATTGGCTG CTGAATCATAACAC GAGTTCAGA TCTCATCAGA TCTACTCGA TCTACTGA TCTACTGA TCTACTGA TCTACTGA TCTACTGT AGTTAAGAGC CGATTATGA TCATACTGTT AGTTAAGACC TGAATCTTTAACACTGTT TGACATCTCC	quence 1 #: Eos sec 1518 21 CTCACTTCGA CTCCCCCTCC CCGANACGA GAACTTAGA GGGAAACA AATGGTGTT TGGATCGGG TGATGCGGAC TTATCCATT TGGATCAGA TGTGATCAGAG TGATGCGGAC TTATCCATT TGGAGTCGAG TGATGCGGAC TTATCCATT TGGAGTCTAGA TGCCTGCACA	Juence 31 TCTATACACT CTCTCCACTAC GCAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAGG AGTGTTAGTCCAACCCAAACTCAA GCACACTCAA	GGAGGATTAA TGAGAAGCAG AGCOTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA GTTTTGAGGA CTGACAGATA ACTGGATTGT	ACAAACAAA AGGAGCOGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAB AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC	120 180 240 300 360 420 480 540 660 720 780 840
50 55 60 65	Seq ID NO: Nucleic Aci Coding sequ Cacacatacg Caaaaaaaa Cagcgaggg Cagctcctct CTTGTTGAAG AAATACCAA CAAGTAAATG AACACATTCA GTCAGCGGAG GAATGCAAA GGAAAAGGGA GAATGCAAA GGATGCAAA TTAGATCAAA TTAGATCAT AATGGCTCAT AATGGCTCAT ACAGTTAGCA	574 DNA BEG 1d Accession zence: 148-4 11 CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG CATGTAATAG TGAATCTTAA TCTCATAACAC GAGTTTCAG TCTCATCATCT AGTTAAGAGC CGATTATTGA TCATACTGTT TGACATCTCT TGACATCTCT TGACATCTCT TGACATCTCT TGACATCTCT TCATCTGAAAG TCATGCTGAT TCATGCTGAT TCATGCTGAT TCATGCTGAT	PUENCE 1 #: EOS BEC 1518 21	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCAGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG GGATTTCAG GGATTTCAG GGATTTCAA TGTTTGAG AGTGTTAGTC CCAAACTCAA GACACGTTG GACACAGTTG CAAAACAATT	GGAGGATTAA TGAGAAGCAG AGCOTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACTT AAGGACAAAA GTTTTGAGGA TTGGGACAGA CTGACAAGT ACTGACAAGT ACTGGATGT ACTGGATGT ACTGGATGT TCGAGAGCA TTCGAAAGCA	ACAAACAAA AGGAGCOGCA GGCTTGCATT ACAGAGAAAA TTGGGGAAAA ATCATTGGAA TGACTACCGT TCACTGGGA ATTTCACTGGGA ATTTCACTT AGCAGTCAAA AGAAAATTTC TTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA	120 180 240 300 360 480 540 660 720 780 840 900 960 1020
50 55 60	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAAAAAAAA CGGCAGGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AAATATCCAA GACACATTCA GTCAGCGGAG AAATGCAATA GGAAAAGGGA GATTCCAAG GATTCAAG TTTGATCAT AATGGCTCAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG TTTCTAGAGC	11	quence 1 #: Eos sec 1518 21 CTCACTTCGA CTCCCCCTCC CTCAGAATG GTCCTATACA GAAACTTAAA TGGGAAACA AATGGTGTT TGGATCAGAG TGATCAGAG TGATGCGGAC CTTATCCATT TGGAGTCGAG GAACCTCTG CCCTGCACA CCAGTTGGCT CCAGTTGGCTT CCCTGCACA CCAGTTGGCTT CTCATACACT	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATACA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAG AGTGTTAGTCAA TTGTTTGAG AGTGTTAGT CCAAACTCAA GACACGTTG GTTTTTTTGTG GTATATCAATT	GGAGGATTAA TGAGAAGCAG AGCATTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTTGAGGA GTTTTGAGGA GTTTTGAGAA ACTGACAGATA ACTGGATTGT AAGTTCTTAC TTCCAGAGCA AGATTCATAA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA ATCATTGGAA ATCATTGGAA ATCATTGGAA ATCATTGGAA ATCATTGGAA AGATCAACA AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG AGCAGTTTGT	120 180 240 300 360 420 540 660 720 780 840 900 960 1020
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50 55 60 65	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAAAAAAAC CAGGGAGGGG CAGCTCCTCT CTTGTTGAAG AAATACCAA CAAGTAAATG AACACATTCAA GTCAGCGGAG AAATGCAAT GAGATGCAAT GAGATGCAAT AATGCTCAT AATGCTCAT AATGCTCAT AATGGCTCAT AATGGCTCAT AATGGCTCAT TCTGGTTATG TTCTCTAGAC TCTGGTAAGAC TGGGAAAGAC	11	puence 1 #: Eos sec 1518 21	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AGAAGCAAGCA AAACAAGTA AGTTTTCAGG GACACTTGAG GACACAGTTG GCAAACCAATT GGAAACAATT GGAAACAATT GGAAAGGAAG CCAGAGAATT ATGATTGAGA	GGAGGATTAA TGAGAAAGAA ATCAAAAAAA ATATTGATGA GGGATAAACT AGGACAATTTGAGGA ATTTTGAGGA GTTTTGAGGA CTGACAAGA ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT ACTGACAAGT TTGGAGATGT ACTGATTGT AGGATTGT AGGATTGT AGGATGT AGTTTCTAC AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA AGATTCATGA	ACAAACAAA AGGAGCOGCA CGCTTGCATT ACAGAGAAAA ATTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAAAGAT AATGCAACAA ACAGTACAA ACAGTACAAG AGCAGTTTTAC TCTTGTACAGTTACA TCTTGTTACAGTTTACA TCTTGTTACAGTTACA TCTTGTTACAGTTACA TCTTGTTACAGTTACA	120 180 240 360 420 480 540 660 720 780 960 1020 1020 1140 1200
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50 55 60 65 70	Seq ID NO: Nucleic Aci Coding sequ 1 CACACATACG CAAAAAAAA CGGCAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA AACACATTCA GTCAGCGGAG GAAAAGGGA GAAAAGGGA GATTCAAAG TTAGATCCAT ACAGTTAGCA TCTGGTTAGCA TCTGGTTAGCA AGTTCAGAAC TCGGAAAGAC CGGGAAAGAC CGGGAAAGAC GGTTCAGTTC GGTTCAGTC GGTTCAGAC TCGGAAAGAC TGGGAAAGAC TGGGAAAGAC CGGGAAAGAC GGTTCATTC	574 DNA BEG 11 CACGCACGAT ATTTCCTTCG CCGCAGACCG AGATTGCCC AGATTAACAC AGATTCACT AGTTAAGAGC CGATTATCA TCTACTGTT TGACATCTCC TCTCTGAAAG TCATGCTGTT AGGTGTTTTC CAGAAAATGT CTCGAGTCGT GAGAGGACCA TCAATAATTT	THE EOS BEC 1#: EOS BEC 1518 21 1 CTCACTTCGA CTCCCCTCC CTCTGGAATG CCTGGATTGG GTCCTATACA CCCAAAACAA AATGGTGTTT TGGATCAGA GAACTTAAA GAACTTCAT TGGGGTCGAA GAACTTCTG TCCCTGCACA CCAGTTGGCT GGACTACTTA CTCATACACT TCAGGCTGAC TTATGATACACT TCAGGCTGAC TTATGATACACT TCAGGCTGAC TATGATACACT TCAGGCTGAC	Juence 31 TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GGAGCACTGA TTTCCAGGTT GTGGAAATTA AAAGCAAGCA CGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTTCAG GGATTTTCAG GCACACTCA GCACACTCA GCACACTCA GCACACTCA GCACACAGTTG GTTTTTTGTG CAAAACCAATT GGAAAGGAAG CCAGAGAAT ATGATTGAGA ATGATTTTGAG AATTTTTGA	GGAGGATTAA TGAGAAGCAG AGCSTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAACT AGGACACTTTAAGGA GTTTTGAGGA GTTTTGAGAGTA ACTGATTGT AAGTTCTTAC TGCAGAGCA AGTTCTTAC AGTTCATCA ATACCAGCT AGTTTGCAGT CAGATGGCT AGTTTGCAGT CAGATGGCTA TTCTTCAGAT	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATCACA ATCATTGGAA ATCATTGGAA ATTACTGGGA ATTTCCACTT AGCAGTCAAA AGGAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA TCTTTGTACCATTGTTACA TTGTACCAGT TCTTGTACCATTGTACAAAAACAAAAAAAAAA	120 180 240 300 360 420 480 660 720 840 900 960 1020 1140 1200 1260 1320
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20	Nucleic Ac	612 DNA se id Accession Lence: 14	n.#: XM_098	151			
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45	Coding sequ	nence: 771	21 	31 	41	51	
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50 55 60	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTTCAGC CATAATTACT CTAAAGCCGC TCTCCTCCAG ATTATTGCGG GTGATCAGCG GTGATCAGCG CTGGGTCGCT CTCAGAGATCC CTGAAGATCC CTGAAGATCC CTGAAGATCC TGCTGCCT TGCAGC TGCAAGATCC TGCAAGA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAGAATTAAA GAGAATTCAA GAGGATTCA CAGGCCTGT CCACACCTG CAAGGCTTAA ACAAGGACTA GTTCCAAGGA ACAAGGACTA ACTTCCAAGGA ACAAGGACTA ACTTCCAAGGA ACACGGAGTG ACCGGGAGTG ACCGGGAGTG ACCGGGAGTG	31 GCAGGCCACC GGCGGCGCTG TCAAGTTCCA TCAAGTTCCA CTCCAACATT TAAGTCAAAA AGACAACCGG GTGCATGGTG ATTTCAGTGT CACCATCGAG ACCTACATGGT CTCCAACACG CTCCAACACG CTCCAACACG CTCCAACACG CTGCAACACG CTGCAACACG CTGCAACACG CTGCAACACG CTGCAACACG CTGCAACACG CTGCAACACG CTACTCTCATT CAGCAGCTCAT TCAGCAGCC CTATCTCAT TCAGCAGCC CTATCTCAT TCAGCAGCC CTATCTCAT TCAGCAGCCC	GAGGCCGCCG TCGAACTGTGCA ACCTGGTGCA ACCTGGTGCA ACCTGGTGCC TCTGATGCTC CATGACTGCCC CATGACTGCC TGTGATGCCC TGTGATGCCC TGTGAGGCA AACCAGCCCT TGTGGAGGCA TACCCAAAGA AAGGGGGAGCA TACCCAAAGA CAGGGGCAC TTTTGGCACAA CCGGAGCAGC CACTACTACC	CCGTCTAGCG TCCTGGTGST ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTCATCAG AGGAGGACTA TGAAAGTTTGA ACCACAACGA CCCGGACTAT GCTGTGAGGT TGAAAATGAC GCTCTGAAGT	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140
50 55 60 65	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTTCAGC CATAATTACT TCTAAAGCCGC TCTCCTCCAG ATTATTGGGG AGGCACCAGG AGGCACCGGG GTGATCAGCC CTCATCCTAC CTGATCCTAC TGCCTGCCCT GGAAAAGAGA ATTATTCCC ATGCTTTCCC ATGCTTTCCC ATGCTTTCCC ATGCTTTCCC ATGCTTTCCC ATGCTTTCCC ATGCTTTTCCC ATGCTTTTTCC	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAGATTAAA GAGAATTCAC GGGGCTCTGT CCACACACTG CAAGGACTTAA ACAAGGACTTAA ACAAGGACTTAA ACAAGGACTTAA ACAAGGACTTAA ACTTCCAAGGA ATTCTACCGA ATTCTACCGG ACGGGGTGTCCTGCCCCC CTGCTGCCCCC	31 GCAGGCCACC GGCGCGCTG TCAAGTTCCA CTCCAACATT TAAGTCAACA AGACAACCAG GTGCATGGTG ATTTCAGTGT CACCATCAGA CACCATGAGA CACCATGAGA CACCATCAGA CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATCAGTG CACCATGAGT CTCCAACAG CAGGCTGAC CAGGCGGGTGT CGATCCCCAG CTATCTCTAT TCAGCAGCAC CCAATGGAAA	GAGGCOGCOG CTTCTCTGCG CTGAACTGTGCA ACCTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT TCTGATGCTC AGGCGACCCT TGTGGAGGCA TACCCAAAGA AACCAGCCT TACTGAGGCA CAAGGGGAGCA TTTTGGCACAA CCGGAGCAGC CACTACTACG ACAGATTCCT	CCGTCTAGCG CCGTCTAGCG TCCTGGTOST ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA TCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTCATCAG AGGAGGACTAT GAAGTTTGA CCCGGACTAT GCTGTGAGAT GCTGTGAGAT GCTGTGAGAT GCTCTGAGAGT GCCTCGAGAGT	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020 1080 1040 1140 1200
50 55 60	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TOTGTGTCCA GGGCAGCACT CGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC ATTATTGGG AGGCACCGG GTGATCAGC CTGAGCACCGG CTGGGTCGCT CTCATCCTAC CTGAAGATC CTGAAGATC CTGAAGATC GGAAAAGAGA CTGATTTCCC GGAAAAGAGA CTGATTTCCC CTGATCTATCTAC CTGCTGCCCT CGCATCTATCTAC CTGCTGCCCT CGCAAAAGAGA CTGATTTCCC CTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	21 CCCTCCTGCC GAGCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA ACAGCATGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAGATTCAC GGGGCTCTGT CCACACACTG CCACACACTG CCACACACTG ACAGGCTTAA ACAAGGACTA GTTCCAAGGA ACTTCCAAGGA ACTTCCAAGGA ACTTCCAAGGA CCACGGGAGTTC CTGCTGACCC CTTCCCTCCC	31 GCAGGCCACC GGCGGCCACC TCAAGTTCCA CTCCAACATT TAAGTTCAAA AGACAACCGG GTGCATGGGC ATTTCAGTGT CACCATCAGG CACCATCAGG CACCATCAGG CACCATCAGG CACCATCAGG CACCATCAGG CACCACAGA CAGGCTGAC CAGGCTGAC CAGGCTGAC CAGGCTGAC CAGAGGGTT CAGACCCCAG CTATCTCAT TCAGCACCC CCAATGGAACA AGGCCCCAT	GAGGCOGCOG CTTCTCTGCG CTTCTCTGCG CTGCATGCTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGATGCTC AGGCGACCCT TGTGGAGGCA AACCAGCCCT TGTGGAGGCA AACCAGCCCT TGTGGAGCAA ACGCTTGCTC GCGCAGCAGA CCGGAGCAGC CACTACTACA CCGGAGCAGC ACAGATTCCT ACTTTGACTG	CCGTCTAGCG TCCTGGTGST ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTCATCAG AGGAGGACTA TGAAAGTTTGA ACCACAACGA CCCGGACTAT GCTGTGAGGT TGAAAATGAC GCTCTGAAGT	120 180 240 300 360 420 480 540 660 720 780 960 960 1020 1080 1140 1200
50 55 60 65	Coding sequilibrium sequilibriu	11 GCCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCAGGAAAGG GTCCTTCAGC CATAATTACT TCTAAAGCCGC TCTCCTCCAG ATTATTGGGG GTGATCAGCCC CTGAGCACCGC GTGATCAGCC CTGAGCCCT CTCATCCTAC GGAAAAGAGA CTGATTTCCC ATGCTATGTG CCCCTCGTCT GGATGTGCCC ATGCTATGTG CCCCTCGTCT GGATGTGCCC ATCCGCAGTC ATCCGCAGTC ATCCGCAGTC	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGGAACCA TGAGGAACTCA AAACGTACCA AAACGTACCA AAACGTACCA GCAGGAACCC TGTCCCAAGA AAGATTCAC GAGGCTCTGT CCACACACTG CAAGGCTTAA GTTCCAAGGA CGATGTATAA ATTCTACCGA ACCGGGAGTG CTGCTGACCC GTTCCCTCCA ACACGCACACACA ACACACAGGA ACACACAGGA ACACACAGGA ACACACAGGA ACACCAAGGA ACACCAAGGA ACACCAAGGA ACACCAAGGA	31 GCAGGCCACC GGCGCGCTG TCAAGTTCCA CTCCAACATT TAAGTCAACA AGACAACCGG GTGCATGGTG ATTTCAGTGT CACCATCGAG ATTTCAGTGT CACCATCGAG CACCTACAGG CACCTACAGG CACCTACAGG CACCTACACG CACCTACACG CACCTACACG CACCTACACG CACCTACACG CACCTACACG CACCTACACG CACCTACACG CACCTACACACG CAATCGAAA AGGCCGCATG AGAGAATGGC AGAGAATGGC AAGAAATGGC	GAGGCCGCCG CTTCTCTGCG CTGAACTGTGCA ACCTGGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT TCTGATGCTC AGGCGACCAAAGA AACCAGCCT TGTGGAGGCA TACCCAAAGA ACGGCTTGCTC GCGCAGCCAT TTTGGCACAA CCGGAGCACG CACTACTACG ACAGATTCCT ACTTTGACTC ACTTGACTG CTGGCGAGCAG CTGGCCCTCT	CCGTCTAGCG CCGTCTAGCG TCCTGGTOST ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA TCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTCATCAG AGGAGGACTA TGAAGTTTGA ACCACAACGA CCCGGACTAT GCTGTGAGAT GCTGTGAGT GCTCTGAAGT GCTCTGAAGT GCTCTGAAGT GCTCTGAAGT GCTCTGAAGT GCCAGGGAGA GAATTGTGAG TCTCACACTT GAGGGTCCCC	120 180 240 300 360 420 600 660 720 780 840 900 960 1020 1080 1240 1250 1320
50 55 60 65	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TOTGTGTCCA GGGCAGCACT CTGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC ATTATTGGG AGGCACCACG ATTATTGGG AGGCACCACG CTGGGTCGCT CTCATCCTAC CTGAAGATC CTGATCTAC CTGATCTAC GGAAAAGAGA CTGATTTCCT GGAAAAGAGA CTGATTTCCT GGAAAAGAGA CTGATTTCCT GGATTTCCT GGATTTCCT CCCTCGCCT GGATTTCCC CGGCACCAC ATCGCACCAC CGGGCACCAC	21 CCCTCCTGCC GAGCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGC ACAGGAACCA ACACGTACCA ACAGGAACTCA ACAAGTACTA CAGGAACTCA ACAAGTACTA CAAGGATTCAC GGGGCTCTGT CCACACACTG CAAGGCTTAA ACAAGGACTA ACTTCCAAGGA ACTTCCAAGGA ACTTCCACGGAGTT CTGCTGCCC GTTCCCTCCA TGAAGGACAC CGTTCCCTCCA TGAAGGACAC CGCTTTCTT	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTTCAAA AGACAACGGG TGCCCACAGA AGACAACGGG GTGCATAGTG ATTTCAGTGT CACCATCAGG CACCTAGGTG CACCCAG CAATCTCAT TCAGCACCC CCAATGGAACG CCAATGGAACG CCCAATGGAACG GCTGGTTGTC	GAGGCOGCOG CTTCTCTGCG CTGAACTGTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGACTGCA ACCTGCTATG AGGCGACCCT CATGACTGCG GCCAAAAGA AACCAGCCT TGTGGAGCAA ACCAGACCAT TTTGGACCAA CCGGAGCCAT TTTGGCACAA CCGGAGCAGC CACTACTACC ACTACTACC ACTACTACC ACTTTGACTG TACACGAGAGCAG CTGCCCCTCT ACTTTTGCACA	CCGTCTAGCG TCCTGGTOGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAG TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTCATCAG ACGACAACGA ACCACAACGA CCCGGACTAT TGAAAATTAC GCTCTGAAGT TGCCGGACTAT TGAAAATTAC GCTCTGAAGT TGCCGGACAA GAATTGTGAG GCAGGGAGA GAATTGTGAG GCAGGGAGA GAATTGTGAG TCTCACACTT GAAGGTCACC TAGAGTCACC	120 180 240 300 360 420 480 540 660 660 720 780 840 900 1020 1080 1140 1260 1320 1320 1440
50 55 60 65 70	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT TGTGTGTCCA GGGCAGCACT TCAAGGCACCT CTAAAGCCGC CATAATTACT CTAAAGCCGC ATTATTGGGG AGGCACCGGG GTGATCAGCG CTGGGTCGCCT CTCATCCTAC CGGAAAAGAAGA CTGATTTCCC GGAAAAGAAGA CTGATTTCCC ATCCTACC ATCCTACC TGCCTGCCCT GGAAAAGAAGA CTGATTTCCC CTGCCTCTCC CCGGCACCAC GGAAAAGAGA	21	31 GCAGGCCACC GGCGCCTG TCAAGTTCAAA CACCATGGGC TGCCACAGA AGACAACGG GTGCATGGGC ACTACGTG CACCATGGGC CACCATGGGC CACCATGGGC CACCATGGGG CACCATGGGG CACCATGGGG CACCATGGGG CACCATGGGG CAGTGGT TCAGCACGG CTATCTCTAT TCAGCACCG CTATCTCTAT TCAGCACCG CCAATGGAAA AGGCCGCATG GCCAGGGGT AGAGAATGGAA AGGCCGCATGGAC GCCAGGGGT AGAGAATGGC CCAATGGAAA AGGCCGCATGGT GCCAGGGGTT AGAGAATGGC CCAGTGGTT TAGGCTCTGC	GAGGCCGCCC CTTCTCTGCG CTTCTCTGCG CTCGATGCT CACTGCTATG CGGCCCTGCC TCTGATGCT CATGATGCT CATGACTGCT GAGCAAAGA AACCAGCCCT TGTGGAGGCA TACCCAAAGA CAGGGGAGCAG CACTACTACT CAGGAGCAGCAG CACTACTACA ACCAGAGAG CACTACTACA ACTTGCAGAGA TCCGAGCAGC ACTACTACAG ACAGATTCCT ACACGAGAG ACTTGCTC TACACGAGAG ACTTTGCAG ACAGATTCAT ACTTTGCAG ACAGATTGCAA ACTTGCACAA	CCGTCTAGCG CCGTCTAGCG TCCTGGTOST ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA TCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTCATCAG AGGAGGACTA TGAAGTTTGA ACCACAACGA CCCGGACTAT GCTGTGAGAT GCTGTGAGT GCTCTGAAGT GCTCTGAAGT GCTCTGAAGT GCTCTGAAGT GCTCTGAAGT GCCAGGGAGA GAATTGTGAG TCTCACACTT GAGGGTCCCC	120 180 240 300 360 420 480 540 660 720 780 960 1020 1080 1140 1260 1320 1380 1440 1500
50 55 60 65	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACT TGTGTGTCCA GGCAGCACT TTAAAGCAC TCTCTCCAG ATTATTACT CTAAAGCAC ATTATTGGGG AGGCACCAC CTGATCATC CTCATCCTAC GAAAAAGAGA ATTATTGGGG CTGGTTCGCT GGAAAAGAGA ATTATTCCC GGAAAAGAGA CTGATTTCCC GGAAAAGAGA CTGATTTCCC CGGAATTGCCC CGGGCACCAC GTAAGAAGAG GTGAACGACA GTGAACGACA GGCCAGGATT	21 CCCTCCTGCC GAGCCCTGCT GAGCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAGATTAAA GAGATTCAC GGGGTCTTGT CCACACACTG CAAGGACTTAA ACTACACACTG CAAGGACTAA ATTCTACCGA ACTGCAAGA CCGGGAGTG CTGCTGACCC GTTCCTCCA TGAAGGACAA ACACCAAGGA CCGCTTTCTT ACTGGGAAGA CCGCTTTCTT ACTGGGAAGA ATAGCTTTAC GAGGGTTGTT CAGGGAGGTGC CGGGGGTGTT CTGGGAAGA CCGCTTTCTT ACTGGGAAGA ATAGCTTTAC CAGGGGTTGTT	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTTCAAAA AGACAACCGG GTGCATGGTG ATTTCAGTGT CACCATCGTG CACCACCGGTTAC CTAATCTCTAT TCAGCAGCCTC CCAATGGAAA AGGCAGATGAC GCCAGCGGTTG GCCAGTGGTGC CCTCACTGCC CCTCACTGCC CCTCACTGCC CCTCACTGCC CCTCACTGCC CCTCACTGCC CCTCACTCAC CCTCACTGCC CCTCACTCAC CCTCACTCAC CCTCACTCAC CCTCACTCA	GAGGCCGCCG CTTCTCTGCG CTGAACTGTGCA ACCTGCTATG CGCCCTGCCATGCATGCCC TCTGATGCTC AGGCGACCCT CATGACTGCC GGCCAAAGA AACCAGCCT TGTGGAGCAT TGTGGAGCAA ACCTGCTAT TGTGGAGCAT TTTGGCACAA CCGGAGCAGT TTTGGCACAA CCGGAGCAGT CACTACTACG ACAGATGCT ACTTTGACTG ACTTTGACTG ACTTTTTTTTTCAG ACAGATGGAT ACGGGTGCAT ACTTTTTTTTTT	CCGTCTAGCG TCCTGGTOST ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTCATCAG AGGAGGACTAT GCACAAACGA CCCGGACTAT GCTGTGAGAT GCTCTGAGGT GCTCTGAAGT GCTCTGAAGT TGAAAATGAC GCTCTGAAGT TGAAAATGAC GCTCTGAAGT TGCTCTGAGT TCTCACACTT TGAGGTCCCC TAGAGTCATC TTGCCTTGAG TCTCCCCTAGAGT CACACACAC TGCCTCACACT TGCCTGTAGGT TGCCTGTAGG TCTCACACT TGGCTGCCC CAGAGTCACC ACCAGCAACT	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1140 1200 1250 1320 1440 1500 1560
50 55 60 65 70	Coding sequilibrium sequilibriu	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TOTGTGTCCA GGGCAGCACTCAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC ATTATTGGG AGGCACCGG GTGATCAGC CTGAGTAGCC CTGAGTAGC CTGAGTAGC CTGATCCTC GGAAAAGAGA CTGATTTCC GGAAAAGAGA CTGATTTCC GGATTTCC GGATTTCC GGATTTCC GGATTCC GGGCACCAC GTAAGAAGAG GTGAACGACA GTAAGAAGAG GTGAACGACA GGCCAGGATG TGGACTGAAC	21	31 GCAGGCCACC GGGCGCACC CTCAACATT TAAGTCAAAA AGACAACCG GTGCACAGA AGACAACCG GTGCATGGGC CACCATGGGC CACCATGGGC CACCATGGGC CACCATGGGC CACCATGGGC CACCATGGGC CACCATGGGC CACCATGGGC CACCACGGGCTGAC GGGCAGGTGT CAGCACCCCG CTATCTCAT TCAGCACCCC CCAATGGAGCC CCAATGGAATGG	GAGGCCGCCC CTTCTCTGCG CTTCTCTGCG CTGCATGCTGCA ACCTGCTATG CGGCCCTGCC TCTGATGCTC AGGCGACCCT CATGATGCTC AGGCGACCCT TGTGGAGGCA AACCAGCCCT TGTGGAGGCA AACCAGCCCT TGTGGAGCAA ACGCTTGCTC GCGCAGCAGT CTTGGCACCAA CCGGAGCAGC CACTACTACCA ACAGATTCCT ACATGCACCA ACTTCTCACCA ACTTCTCACCA ACTTCTCACCA ACTTCTCACCA ACTTCTCACCA ACTTCTCACCA ACTTCTCACCA ACAGATGCAT ACGCCTCT CACGCCTCT CACGCTCGCT CATGTTACTC CAGGGCCTCT CAGGGCCATCT	CCGTCTAGCG TCCTGGTOGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTGCGGC GCTTCATCAG ACCACAACGA ACCACAACGA CCGGACTAT TGAAATTGAGTCTGAGGT CCTGTGAGGT TGAAATTGAGC TCTACACTT GAGGTCCAC TGAGGTCCTC TAGAGTCACT TGAGGTCCAC TTGCCTGTGG CCTGGCTGCC CCTGTGCATG	120 180 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1320 1320 1350 1560 1620 1620
50 55 60 65 70	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCAGGCACACT TCAGGGAAAGG GTCCTTCAGC CATAATTACT TCAAAGCCGC TCTCCTCCAG ATTATTGGGG AGGCACCACT CTCATCCTAC TGCTGCCT TGCATCCTAC TGCATGCTAC TGCATGCAGT TGCATGCCC ATCAGCAGT TGCAGCAGAC TGAAAAGAGAA TGCAAGACAA TGAAAGAGAA TGCAAGACAA TGGAACGACA TGCAAGCAAG TGCAAGACAA TGGAAGCCAAG TTCCCAATTA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA ACAGGACTCA AAACGTACCA AAACGTACCA CAGGAACTCC TTGTCCAAGA AAGAATTAAA GAGAATTCAC GGGGCTCTGT CCACACACTG CAAGGACTAA ACAACAGGACTA ATTCTACCGA ACTGCACACGG GTTCCCTCCA TGAAGGACTA ACACGACTG CTGCTGACCC GTTCCTTCT ACTGGGAAGA CCGCTTTCTT ACTGGGAAGA CAGCGTTTCCT CAGGGACGACC CGGAGGTGTT CCTGCAGGAC CGGAGGTGT CCTCCCCCCAC CGGAAGTGTAAA	31 GCAGGCCACC GGCGCGCCTG TCAAGTTCAA CTCCAACATT TAAGTCAAAA AGACAACCGG GTGCATGGG ATTTCAGTGT CACCATCGGC CACCATCGGC CACCATCGGG CACCACCGG CAATCGTGT TCAGCACCAG GCAGGCGTAG GCCAGGCGTAG GCCAGGCGTAG GCCAGGCGTC TAGGCTTGT TAGGCACCAG CCTCACCGGAT CCTCACCGGAT CCTCACGGAT CCTGACTCAA TTAAAAAGGG GGTGGGCATG GCTGGCTTCA TTAAAAAGGG GGTGGGCATCA CTGACTCAA GGAGCATCAA TGAAAAAGGG GGTGGGCATG GCAGGCCTCAC CCTGACTCAA GGAGCATCAA TTAAAAAGGG GGTGGGCATT GCAGCTCAAGGCATCAA TTAAAAAGGG GGTGGGCATT GCAGCTCAAGG	GAGGCCGCCC CTTCTCTGCG TCGAACTGTGCA ACCTGCTATG CGCCCTGCCC TCTGATGCTC AGGCGACCCT CATGACTGCC TCTGATGCTC AGGCGACCCT TGTGGAGCAC TACCCAAAGA AACCAGCCCT TGTGGAGGCA CAAGGCAGCAT TTTGGCACAA CCGGAGCAGC ACTACTACG ACAGATTCCT ACTTTGACTG TACACGAGAG ACAGATTCCT ACTTTGACTG TACACGAGAG ACAGATTCCT ACTTTGACTG TACACGAGAG ACAGATTCCT ACTTTGACTG TACACGAGAG ACAGATTGGAT CTGGCCCTCT TTTTTTTTTT	CCGTCTAGCG CCGTCTAGCG TCCTGGTOST ACTGTCTAAA ACTGCCCAAA AGGGGAATGG TGCCCTGGAA TTCAGCTGGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTCATCAG AGGAGGACTAT GCACAACGA CCCGGACTAT GCTGTGAGT GCTCTGAGT GCTCTGAGT TGAAAATGAC GCTCTGAAGT GCTCTGAGT TCCACACTT GAGGGTCCCC TAGAGTCCCC TAGAGTCCCC TCGCCTGTGCA ACCAGCAACT CCTGTGCATG AGGGTCCCC CTGGCTGCC ACCAGCAACT CCTGTGCATG ATGGTTGAGA CATGTTGAGA CATGTGAGA CATGTTGAGA	120 180 240 300 360 420 600 660 720 780 840 960 1020 1080 1140 1200 1320 1380 1440 1560 1620 1680 1740 1740 1860 1860
50 55 60 65 70	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TOTGTGTCCA GGGCAGCACT CTGAGGAAAGG GTCCTTCAGC CATAATTACT CTAAAGCCGC ATTATTGGG AGGCACCATG ATTATTGGG AGGACCACGG CTGGGTCGCT CTCATCCTAC CATGATTACT GGAAAAGAGA CTGATTTCCT GGAAAAGAGA CTGATTTCCT GGAATTTCT GCCCTGCCCT	21 CCCTCCTGCC GAGCCTGCT GAGCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGC ACAGGAACTACA ACACGTACCA GCAGGAACCC ATGTCCAAGA AAAGATTCAC GGGGTCTTGT CCACACACTG CAAGGCTTAA ACAAGGACTAA ACTTCCAAGGA ACTTCCACGGAGTTAA ACTTCCAAGGA ACCGGGAGTTAA ACTCCACGGAGTTAA ACTCCACACGGAGTTAA ACTCCACACGGAGTTAA ACTCCACACGGAGTTAA ACTCCACACGGAGTTAA ACACCAAGGA CCGCTTTCTT ACTGGGAAGA ACACCAAGGA CCGCTTTCTT ACTGGGAAGA ATAGCTTTAC GGAGGGTGGT CCTCCCCGACGGAG CCCCCCGACGGAG GCGCACACGGAG	31 GCAGGCCACC GGGGGGGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA AGACAACGGG TGCCCACAGA AGACAACGGG GTGCATGGGG ATTTCAGTGT CACCATCAGG CACCATCAGG CACCATCAGG CACCATCAGG CACCATCAGG CACCACCAGA CACCACCAG CAACCAGC CAATCAGTG GCCAGGGCTC AGAGCACCC CCAATGGAACG CCAATGGAACG CCAATGGAACG CCAATGGAACG CCAATGGAACG CCAATGGAACG CCTAACTGAC CCTACACGAT TAGGCTCAG CCTGACTCAC TAAAAAGGG GGTGGGCATTGC CCTGACTCAGG CTTAATCAACG TAAAAAGGG GGTGGGCATTGC CCTGACTCAACGAT CCACACTCAACGAT CCACACTCAACGAACCACCAACGAACCACCAACGAACGAA	GAGGCOGCOG CTTCTCTGCG CTGAACTGTGCA ACCTGCTATGC CGGCCCTGCC TCTGATGCTC AGGGGACCCT CATGACTGCA ACCTGCTATGCT CATGACTGCA AGCCACACAGA AACCAGCCCT TGTGGAGGCA AACCAGCCAT TTTGGCACAA CCGGAGCCAT TTTGGCACAA CCGGAGCCAT ACTTTTGACTC ACTTTTGACTC ACTTTTGACTG ACAGATGGAT AGGCCTGCT CATGTTACTG CAGGCCTCT CATGTTACTG CAGGCCTCT CATGTTACTG CAGGCAGCATCT TGTGAGGCCC CATGTTACTG CAGGCCACT TGTGAGGCCC CTTCTTTGAGGCCC CTTCTTTGAGGCCC CTTCTTTGAGGCCC CTTCAGGGCA CTTCAGGGCA	CCGTCTAGCG CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAGAA TTCAGCTGGG GGTGCTATGT CAGATGCAAA CTCTGAGGCC GCTTGCGGC GCTTCATCAG ACCACAACAA CCCGGACTAT TGAAAATTAAC GCTCTGAAGT TGAAAATTGAA GCTCTGAAGT TCTCACACTT TGCCTGTAGG GCTAGCGCACAC TTGCCTGTGC TTGCCTGTGC CTGCTGCC CTGGACTAT CCTGTGCATG ACCAGCAACT CCTGTGCATG ATGGTTGAGA ATGGTTGAGA ATGGTTGAGA ATGGTTGAGA CAGCTTGAACT CCTGTGCATG ATGGTTGAGA GAGCTTAGCC GGGCTCTGAT	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1260 1380 1560 1560 1560 1740 1800 1800 1800
50 55 60 65 70	Coding sequence of the control of th	11 GCCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCAGGAAAAGG GTCCTTCAGC CATAATTACT CTCACCAGGATAATTACT CTCACCAGGATACACC TCTCCTCCAG ATTATTGCGG GTGATCACC CTGAAGATCC CTGAAGATCC CTGAAGATCC CTGAAGATCC TGCATGCT GGAAAAGAGA CTGATTTCCC ATCCTACTC GGAAAGAGA CTGATTTCCC ATCCTACTC GGAAAGAGA CTGATTTCCC ATCCTACTAC GGCACCAGTC CGGGCACCAG TTCCACCATTA CAGCGGTTTC TGGATGAAC GGCAGTTC TGGATGAAC GGCAGCACC TTCCCAATTA CAGCGGTTTC TGTATCAGGA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAGATTCAA GAGAATTCAC GAGGATTCAA GAGAATTCAC CACACACTG CAACACTG CTCCCAACAC GTTCCTTCCTCCC GTTCCTTCCCTCCC GAACTGTATA ACTGGAAGA ATACTTTAC GAGGGGTGGT CCTCCAGGAG CCCCCCGACC GGAAGTGTAAA GGGAGCAGAG AATATATATTG	31 GCAGGCCACC GGCGGCGCCTG TCAAGTTCCA CTCCAACATT TAAGTCAAAA AGACAACCGG GTGCATGGTG GTCATGGTG ATTTCAGTGT CACCATCAGG AGACCAGG CTACATCAGG CTCCAACACGG CTCCAACACGG CTCCAACACGG CTACATCAGG CTACTCTCAT TCAGCAGG CTATCTCAT TCAGCAGG GGCAGGTGT GGAGCGCTCAG AGGCAGTGTGC CCAATGGAA AGGCCGCAT GCAGGCGTT TCAGCTGAG GCTGGTTGTC CCTCACGGAT CCTCACGGAT CCTCACGGAT CCTCACGGAT CCTCACGGAT GCAGCTGAGG ACCTAACGA ACACTAACGA TGTGTGTTATG CAGCTTAACGA TGTGTGTTATG	GAGGCCGCCC TCGAACTGTGCA ACCTGGTGCA ACCTGGTGCA ACCTGGTGCC TCTGATGCTC CATGATGCTC AGGCGACCCT CATGACTGCC GCCAAAGA AACCAGCCCT TGTGGAGGCA TACCCAAAGA ACGGAGCAT TTTGGCACAA CCGGAGCAGT TTTTGACACA ACGATTCCT ACTTTGACTC ACTTTTGACTC ACTTTTTTCCACAC ATTTTTTTCCACAC TAGGCCATCTTTTTTTTTCCCCCCCT TCTTGAGGCC TCTCTTGAGGC CTTCTGAGGC CTTCAGGCACT TTTGAGCCC TCTCTTGAGGC CTTCAGGCACT TTTGCACACT TTTGCACACT TTTGCACACT	CCGTCTAGCG CCGTCTAGCG TCCTGGTGTT ACTGCCAAA ACTGCCAAA ACTGCCAAA ACTGCCAAA ACTGCCAAA ACTGCCAAA ACTGCCAAA TCAGCTGGG GGTGCTATGT CAGATGGAAA CCTGAGGCC GGTTTGCGCC GGTTTGCGCC GGTTTGCGCC ACCAGCACTAT GAGAGTCAC GCCCGACTAT GAGAGTCAC GCTCGAGGAG GAATTGTAGA GCTCTGAAGT TCTCACACTT GAGGGTCACC TCGCCTGCG GCTCGCTGCAGCACT ACCACCAACT CCTGCCTGCAGCAACT CCTGCCATGCATG ATGGTTGAGA ATGGTTGAGA GAGCTTAGCC GGGCTCCATG AGGGTTAGCC GGGCTCCATG TGTTGTTGTGG	120 180 240 360 420 540 660 720 780 840 960 1020 1140 1200 1320 1380 1440 1500 1560 1620 1740 1860 1740
50 55 60 65 70	Coding sequilibrium sequilibriu	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCAGG ATGTGTCCCA GGGCAGCACT TCAAGGCACCT TCAAGGCACC TCTCCTCCAG ATTATTATTGGGG GTGATCAGCC TCTCATCCTAC CTGACTAC TCTCATCCTAC GGAAAAGAGAC TGGCTGCCT GGAAAAGAGAC TGATTTTCC GGAAAAGAGAC CTGATGTTCC CCGCCTGTCT GGATGTGCCC TGCATGTAGTAGACAGAC GTAAGAAGAC GTAAGAAGAC GTAAGAAGAC GTAAGAAGAC TGGCAGTC TGGATGTACCAC TGGCAGTC TGGATGTACAC TGGCAGTC TGGATGACAC TGGCAGTC TGGATGACAC TGGCAGTC TGGATGACAC TGGCAGTC TGGACGACT TGGATGACAC TGCAATTA CAGCGTTTT TCAGGATTACAGGA TTACAGGA TTACAGGA TTATCAGGA TTATCAGGA TAAGTGTACA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA ACAGGACTCA AAACGTACCA AAACGTACCA CAGGAACCC CTGTCCAAGA AAGAATTAAA GAGAATTCAC GGGGCTCTGT CCACACACTG CAAGGCTTAA ACAAGGACTA ACTTCCAAGGA CTTCCCTCCA GTTCCCTCCA ACACACGG GTTCCTTCCTCCA ACACGACGAC CGGTTCCTTC CAGGGACAC CGGTTCCTTCC CTCCACCC GTTCCTCCA CTCCCACCC GTTCCTCCA CGGGGCTGTCC CGGAGGTGTAA ACACCAGGGA CCGCTTTCTT CCTGCAGGGA CCGCTTCCTCA CGGGGCTGTC CCGGACTCCAC CGGAGTTTAA CGGGGGTGGT CCTCCACC CGAAGTTTAA CGGGAGCAGAC ATATATATTG CTAGGGACA AATATATATTG CTAGGGACC CGAAGTTTAA	31 GCAGGCCACC GGGCGCACC GGGCGCACAT TCAAGTTCAA AGACAACCAG AGACAACCAG AGACAACCAG AGACAACCAG ATTTCAGTGT CACCATGAG CAGCAG CAATGAAA AGGCGCATG GCCAGCGCT CAATGAAA AGGCGCATG GCCAGCGCT TAGGCTCAC CTAATGAAA GGCCGCATG GCCAGCGCT CCTCACCGAT CCTGACTCAA TTAAAAAGGG GGTGGGCATT GCAGCTGAG ACACTAACGA ACACTAACGA TGTGTGTTATG TGTGTGTATTG	GAGGCOGCG CTTCTCTGCG TCGAACTGTG CACTGGTGCA ACCTGCTATG CGCCCTGCC TCTGATGCTC AGGCGACCCT TCTGATGCTC AGGCGACCCT TGTGGAGCAC TACCCAAAGA AACCAGCCT TGTGGAGGA CAAGGGAGCAT TTTGGCACAA CCGGAGCAGC ACACTACTTC ACTTTGACTG TACACGAGAG CTGGCCTCT ATTTTTGCAG ACAGATTACT ACTTTTTTCAG ACAGATGAT CAGGGCATC TTGGGCCCTCT TGTGAGGCCC TCTCTTGAGGCC TCTCTTGAGGCC TTTCAGGGCA TTTCAGCGCC TTTAAGTCTA	CCGTCTAGCG CCGTCTAGCG TCCTGGTCGT ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAGAA TTCAGCTGGG GGTGCTATGT CAGATGCAAA CTCTGAGGCC GCTTGCGGC GCTTCATCAG ACCACAACAA CCCGGACTAT TGAAAATTAAC GCTCTGAAGT TGAAAATTGAA GCTCTGAAGT TCTCACACTT TGCCTGTAGG GCTAGCGCACAC TTGCCTGTGC TTGCCTGTGC CTGCTGCC CTGGACTAT CCTGTGCATG ACCAGCAACT CCTGTGCATG ATGGTTGAGA ATGGTTGAGA ATGGTTGAGA ATGGTTGAGA CAGCTTGAACT CCTGTGCATG ATGGTTGAGA GAGCTTAGCC GGGCTCTGAT	120 180 240 300 360 420 540 660 660 720 780 840 900 960 1020 1140 1200 1260 1320 1380 1440 1560 1620 1680 1680 1740 1860 1920 1980
50 55 60 65 70	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCGGGAGAAAGG GTCCTTCAGC CTAAATTACT CTAAAGCCGC TCTCCTCCAG ATTATTGGG AGGCACCACGG GTGATCAGCC CTGAGGATCCCCACCCC CTGAAGATCC CTGAAGATCC CTGAAGATCC CTGCATGCCT GGAAAAGAGA CTGATTTCCC ATGCTATTCC ATGCTATGTG GCCCTCCGTC GGATGTGCCC GGATGTGCCC GGAGGACCAGGT CCGGCACCAC GGCCACGATC CGGCACCAC GGCCAGGAT CGAAGGAGAC GGCCAGGAT CGAAGGAGAC CTGATTACAGA TAAGTGTGAG TTGTATCAGA TAAGTGTGAG TTGGATTGAG TTGGATTGAG TTGGATTGAG TTGTATCAGA TAAGTGTGAG TTGGATTGAG TTGGGTCCC TTGGGTCCC	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAAGTTCAA GGAGCTTCAAGA AAGATTCAC GGGGCTCTGT CCACACACTG CAAGGATTAAA ACTCACACTG CAAGGATTAAA ACTCACAGGA CCGTTCCAAGGA ACCGGGAGTG CTGCTGACCC GTTCCCTCCA TGAAGGACAA ACACCAAGGA ACACCAAGGA ACACCAAGGA ACACCAAGGA ACACCAAGGA ATAGTTTAC CAGGGGTTGTT CCTGCAGGAG TCCCCCGACC GGAAGTGTAAA GGAGGCAGAG CCCCCCGACC CGAAGTGTACT TAAGAGCTGG CCACCACAGGA CCACCACAGGA CCACCACAGGA CACGTGACAC	31 GCAGGCCACC GGCGGCGCCTG TCAAGTTCAA TCAAGTTCAA CACCATGGGC TGCCACAGA AGACAGG GTGCATGGTG ATTTCAGTGT CACCATCAGG CTCCAACAGG CTCCAACAGG CTCCAACAGG CTCCAACAGG CTCCAACAGG CTCCAACAGG CTCCAACAGG CTCCAACAGG CTACTCTAA TCAGCAGCCC CCAATGGAA AGGCCGCATG GCCAGGGGTT TCAGCAGCCC CCAATGGAAA AGGCCGCTATC GCTAGTTGAT GCAGCGCTAC GCTGGTTGTC CTCAACAGGA TCTCAACAGA TGTGTGTATC TGAGCTGAAG TGTGTGTATC TGGCTTGATTCA TGGCTGGGAA TGGTGTTATT TGGCTGTGTTATT TGGCTGTGGAA	I GAGGCOGCOG CTTCTCTGCG CTTCTCTGCG CTGATGCTC ACCTGCTATG CGGCCCTGCC TCTGATGCT CATGATGCT AGGCGACCCT CATGACTGCG GGCCAAAAGA AACCAGCCCT TGTGGAGCA AACCAGCCCT TTTGGAGCAA ACGCTTGCTC CGGCAGCAT TTTGGACAA CCGGAGCAGC ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA ACTACTACCA CTGGCCCTCT ACTTTTGACTG CAGGTCACT TTTTGACTGC CAGGGCATCT TGTGAGGCC CTTCTTGAGGC CTTCTTGAGGC CTTCTTGAGGC TTTTGCACACT TTTTGCACACT TTTTGCACACT TTTTGCACACT TTTTTTTTCACT TTTTTTTTTT	CCGTCTAGCG TCCTGGTOGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTGCGGC GCTTGCGGC GCTTGCAGAT TGAAGTTTGA ACCACAACGA ACCACAACGA CCACAACGA GCATTGCGGC GCTTGAGGT TGAAATTGAG CCTGTAAGT TGAAATTGAG CCTGTAAGT CCTGTAAGT CCTGTAAGT AGGGTCCCC TAGAGTCATC TTGCCTGTGG CTGCTGCTGC CTGTGCTGC CTGTGCTGC ATGTTTAGA ATGTTTAGA AGGCTTAGC CTGTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGTTGTGAG ATGTTTGTTGC TTGCTTGCAT TGTTGTTGCG TTAGGTTCACT TGTTGTTGTGC TTGCTGCACT CCTGCACCATC	120 180 240 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1440 1500 1560 1620 1620 1740 1860 1920 1980 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050 2050
50 55 60 65 70 75	Coding sequilibrium sequilibriu	11 GCCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCAGG GTCCTCAGC CTAAATTACT CTAAAGCCC TCTCCTCCAG ATTATTGGGG GTGATCAGCC TCTCATCCTAC CTGATCATC CTCATCCTAC CTGATCATC CTGATCATC CTGATCTTC CCATCCTAC GGAAAAGAGA CTGATTTCCC ATGCTATCTC GGAAAAGAGA CTGATTTCCC ATCCTACCTAC GGAAAGGAC GCCTGCCT GGAAAGGAC CTGCTGTCT GGAAGGCCAGC TTCCCAATTA CAGCGTTTC CAGCGGTTC CAGCGTTTC CAGCGGTTC CAGCGGTTC CAGCGTTTC CAGCGGTTTC CAGCGGTTTC CAGCGTTTC CAGCTCTCC AGCACTGTCC AGCACTGTCT CAGCACTGTCC CAGCACTAC CAGCACTCC CAGCACTAC CAGCACTACTC CAGCACTA	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA GCAGGAACCC TTGTCCAAGA AAGATTCAA GAGAATTCAC CAGGATTCAA GAGAATTCAC CACACACTG CAACACTG CAACACTG CAACACTG CAACACTG CAACACTG CAACACTG CTTCCTCAA ACTTCCAAGGA ACACGAGGTG CTGCTGACCC GTTCCTTCA CAGGGCTTGT ACTGGGAAGA ACACCAAGGA CCGCTTTCTT CCTCAGGA ACACCAAGGA CCGCTTTCTT CCTCAGGAC CAGGGTTGACCC GAAGTGTAA GGGAGCAGAC CGGAGCACAGAC CGGAGCACAC CGAACTGACC CCACACAGGA CCACTGACCA CCACACAGGA CCACCACAGGA CCACTGACCA CCACCACAGGA CCACTGACCA CCACTGACCA CAGTTGTCAC CCACACAGGA CCACTGACCA CCACACAGAG CCACTGACCA CCACTTCACT CCACTGACCA CCACTGACCA CCACTTCACT CCACTGACCA CCACTTCACT CCACTGACCA CCACTTCACT CCACTGACCA CCACTTCACT CCACTGACCA CCACTTCACT CCACTGACCA CCACTGACCA CCACTGACCA CCACTTCACT CCCTCTCACCA CAGTGTACAC CCACTGACCA CCACTTCACT CAGTGTACAC CCACTGACCA CCACTGAC CCACTGACCA CCACTGAC CC	31 GCAGGCCACC GGCGGCCACC GGCGGCCACAT TCAGTTCAA AGACACCAG AGACACCAG AGACACCAG AGACACCAG AGACACCAG AGACACCAG ATTTCAGTGT CACCATCAGG CACCTACAGA CACCATCAGG CACCTACAGA CACCATCAGG CACCTACAGA CACCAGC CACTCACACAG CAGCAGGTGT CGACCAGA AGACAGGC CTATCCTAT TCAGCAGC CCAATGGAA AGGCCGCATG AGAGAATGC GCCAGCGCT AGAGAATGC CCTACCGA TCAGCAGAT CCTGACTCAA TTAGACAGG GGTGGGCATT GCACTAACG ACACTAACGA ACACTAACGA TGTGTGTATT TGGCTGGTTT TGCTCGGTTT TGCTCGGTT TGCTCGGTT TGCTCGGTT TGCTCGGTT TGCTCGGTT TGCTCGGTT TGCTCGGTT TGCTCGGGTAT TTCACCTAGG TTCACTAATGA TTCACATAGA TT	GAGGCCGCCC TCGAACTGTGCA ACCTGCTATG CGCCCTGCCC TCTGATGCTC AGGGGCACCTGCCC TCTGATGCTC AGGGGACCCT GCCAAAGA AACCAGCCT TGTGAGGCA TACCCAAAGA AACCAGCCT TGTGAGGCA TACCCAAAGA CAAGGGGAGCAT TTTGGCACAA CCGGAGCACT TTTTGACTG ACAGTTTGCTC ACTTTTTTTTTT	CCGTCTAGCG CCGTCTAGCG TCCTGGTGST ACTGTCTAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA ACTGCCCAAA TCAGCTGGG GGTGCTATGT CAGATGGGAAA CTCTGAGGCC GGTTTGCGGC GCTTATCAG AGGAGGACTA TGAAAGTTTGA ACCACAAACGA CCCGGACTAT GCTGTGAGAT GCTCTGAAGT GCAGGGAGA GAATTGTGA GCAGGGAGA GAATTGTGA GCAGGGAGA GAATTGTGA GCAGGGAGA GAGTTACC TCTGCCTGTGG GCTGGCTGC ACCAGCAACT CCTGTGCATG ATGGTTGAGA GAGCTTAGCC GGGCTCTGAT CTGTGCATG ATGGTTGAGA GAGCTTAGCC GGGCTCTGAT TGTTGTGTGG ATATTTCCTT TAGGTCACTC CTGCAGCATG TTGGCCAGTT	120 180 240 300 360 420 540 660 720 780 840 960 1020 1140 1260 1320 1320 1320 1440 1560 1620 1680 1740 1860 1860 1860 1920 1980 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040 2040
50 55 60 65 70	Coding sequence of the control of th	11 CGCCGTCGCG GCCACCATGA AAAGGCAGCA TGTGTGTCCA GGGCAGCACTCAGG GTCCTTCAGC CATAATTACT TCTACCTCCAG ATTATTGGGG AGGCACCATGA ATTATTGGGG CTGATCATCCTCCAG ATTATTATTGGGG CTGATCATCCTCCT GGAAAAGAGA ATTATTCCC TGCCTGCCT TGCATCCTC TGCATCTAC TGCATGTCC TGCATGTCC TGCATGTTC CGGGCACCAC GTAAGAAGAG GTGAAGAGAG GTGAAGAGAG GTGAAGAGAG TGGATGTCC TGCATGTAG TGGATGTGCC TTCCCAATTA CAGCGTTTG TGTATCAGG GAGAGCCAGC TTAGATGTGAG GAGAGCCAGC TTAGATGTGAG GAGAGCTTTG TTAGTTGATG TTAGTTGATG TTAGTTGATG TTAGTTCACA GGCACTGTCT TTAGGTTCCAC TTTAGCCTAG TTTAGCCTAG	21 CCCTCCTGCC GAGCCCTGCT ATGAACTTCA ACAAGTACTT GTGAAATAGA CCAGCACTGA AAACGTACCA AAACGTACCA AAACGTACCA AAACGTACCA AAACGTACCA AAACGTACCA AAACGTTACA AAGAATTAAA GAGAATTAAA GAGAATTAAA GAGACTTGA CCACACACTG CAAAGGACTTA ACAAGGACTA ACTTCCAAGGA CGGTGTATAA ATTCTACCGA ACCGGAGGTG CCGCTGACCC GTCCCCCAC GGAGGTGTA ACTGGGAAGA CAGGTTTAC CGAAGGACTG CCCCCGACC GGAGGTGTA CCGGAAGTGTAA GGAGGCAGA CAGTTACAA GGAGCAGAG CACCACAGAG CACCACAGAG CACGTGACAC CCACACAGAG CACGTTCCAT TAAGAGCTGA CAGGTGACAG CACGTGACAC TAAGAGCTGACA CACGTGACAC CACACAGAG CACGTGACAC TTAAGAGCTGACA CAGGTGACAC TTAAGAGCTGACAT TTCATCCAAT	31 GCAGGCCACC GGGCGCACC GGGCGCGCTG TCAAGTTCAA CTCCAACATT TAAGTCAAAA AGACAACCGG GTGCATGGG ATTTCAGTGT CACCATCGGC CACATGGT CACCATCGGG CACCATCGGG CACCATCGGG CACCATCGGG CACCATCGGG CACCATCGGG CACCACCGG CACCACCGGG CACCACCGGG CACCACCGGG CAATCGCTAC CCAATCGACA GGCAGGCGTAC GCCAGGCGTC CCAATCGAA AGGCATCAC CCTCACCGGAT CCTGACTCAA CCTGACTCAA TTAAAAAGGG GGTGGGTTGTC TAGGCTTCA TTAAAAAGGG GGTGGGTTGTC TGGCTGAGG ACACTAACGA TGTGTGTATTG TGGTCTTGTT TGGCTCTGGGTAT TGCTCTGGTTT TGCTCTGGTTT TGCTCTGGTTT TGCTCTGGTTT TGCTCTGGTTT TGCTCTGGGTAGG CCTCACTGGGC CCTCACTGGGC TTCACTGGGA CCTCACTGGGC TTCACTGGGA TTCACATAGA CCTCACTGGG CCTCACTGG CCTCACTGC CCTCACTGG CCTCACTGG CCTCACTGG CCTCACTGC CCTCACTGC CCTCACTGC CCTCACTGG CCTCACTGG CCTCACTGG CCTCACTGC CCTCACTGG CCTCACTGC CCTCACTGC CCTCACTGG CCTCACTGG CCTCACTGG CCTCACTGG CCTCACTGG CCTCACTG	GAGGCCGCCC CTTCTCTGCG TCGAACTGTGCA ACCTGCTATG CGCCCTGCCC TCTGATGCTC AGGCGACCCT CATGACTGCC TCTGATGCTC AGGCGACCCT TGTGGAGCCCT TGTGGAGCCA AACCAGCCCT TGTGGAGGCA CAAGGGGAGCAC CACTACTACG ACCAGCACA ACCTGCTAC ACTTTTGACTG TACACGAGAC ACAGATTCCT ACTTTGACTG TACACGAGC CTGGCCCTCT TTTTTTTTTCAG ACAGATTGGAT CAGGGCATCT TTTTTTTTTT	CCGTCTAGCG TCCTGGTOGT ACTGTCTAAA ACTGCCCAAA AGGGGAATGG GGTGCTATGT CAGATGGAAA CTCTGAGGCC GGTTTGCGGC GCTTGCGGC GCTTGCGGC GCTTGCAGAT TGAAGTTTGA ACCACAACGA ACCACAACGA CCACAACGA GCATTGCGGC GCTTGAGGT TGAAATTGAG CCTGTAAGT TGAAATTGAG CCTGTAAGT CCTGTAAGT CCTGTAAGT AGGGTCCCC TAGAGTCATC TTGCCTGTGG CTGCTGCTGC CTGTGCTGC CTGTGCTGC ATGTTTAGA ATGTTTAGA AGGCTTAGC CTGTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGCTTGCAGT TCTTGTTGTGAG ATGTTTGTTGC TTGCTTGCAT TGTTGTTGCG TTAGGTTCACT TGTTGTTGTGC TTGCTGCACT CCTGCACCATC	120 180 240 300 360 420 540 660 660 6720 780 840 900 960 1020 1140 1200 1250 1320 1380 1440 1560 1620 1680 1740 1860 1920 1980 2040 2100 2210 2220

Seq ID NO: 615 Protein sequence Protein Accession #: NP_002649.1

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2100

PCT/US02/12476

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10		627 Protes					
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20	Nucleic Aci	628 DNA se id Accession Lence: 2370	1 #: M18728	.1			
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15	LLANYLDSMY AQLVLKKGFG RDCSCGAKSC LVDAGEECDC	IMLNIRIVLV GTAGMAFVGT INNSGASGSR GTPKECELDP	LRRRRAVLPQ GLEIWTNGNL VCSRSHAGGI NPSSCSAEDF CCEGSTCKLK	INIVGGAGDV NVFGQITVET EKLTLNKGGN SPAECAYGDC	LGNFVQWREK FASIVAHELG CLLNIPKPDE CKDCRFLPGG	FLITRRHDS HNLGMNHDDG AYSAPSCGNK TLCRGKTSEC	240 300 360 420 480
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10	1	11	21	31	41	51 !	•
1.5	NRVTRVAWLN NHPKTSRVHL	RSTILYAGND IVQVSPKIVE	LLPLVPTGVP KWCLDPRVVL ISSDISINEG	LSNTQTQYSI NNISLTCIAT	EIQNVDVYDE GRPEPTVTWR	GPYTCSVQTD HISPKAVGFV	60 120 180
15	LQCEASAVPS	ABPOWYKDDK	CSASNDVAAP RLIEGKKGVK NGTSRRAGCV	VENRPPLSKL	IPPNVSEHDY		240 300
20	Nucleic Ac	638 DNA se id Accession Lence: 203.	1#: NM_012	261.1			
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PCT/US02/12476

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1260

1320

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WO 02/086443 tgtatatita aattetitgt aataataata tecaaateat caaaaaaaa aaaaaaaa

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25			GATCTCTTCC				780
25			GACATCACAG CTCTCGGTGG				840 900
			CGGCACGGGC				960
	TCTTCAAGGC	CACGGAGGTC	CACTTCCGCA	GCATCCGGTC	CACGGGGAGC	AAACAGCGCA	1020
20			CCCAAGAACC				1080
30			AGGCAGGCCT TGGATCATCG				1140 1200
			CTGAACTCCT				1260
	AGACGCTGGT	CCACTTCATC	AACCCGGAAA	CGGTGCCCAA	GCCCTGCTGT	GCGCCCACGC	1320
25			CTCTACTTCG				1380
35			GCCTGTGGCT				1440
			ATCCTCCATT				1500 1560
			TTTTGATCAG				1620
40	TCCTACAAGC	TGTGCAGGCA	AAACCTAGCA	GGAAAAAAAA	ACAACGCATA	AAGAAAAATG	1680
40						CCAGAGGTAA.	
			GGCCACCCAG				1800 1860
	CAATAAAACG		GAAAGGAAAA	TIGACCCGGA	AGIICCIGIA	ATAAATGTCA	1000
45		659 Protes cession #: 1					
45				31	41	51	
	Protein Acc	cession #: 1 11	7P_001710 21 	J	1	1	
45 50	Protein Acc	cession #: 1 11 PHSFVALWAP	P_001710 21 LFLLRSALAD	 FSLDNEVHSS	 FIHRRLRSQE	 RREMQREILS	60
	Protein Acc 1 MHVRSLRAAA ILGLPHRPRP	cession #: 1 11 PHSFVALWAP HLQGKENSAP	P_001710 21 LFLLRSALAD MFMLDLYNAM	 FSLDNEVHSS AVEEGGPGG	 Fihrrlesqb QGPSYPYKAV	 RREMOREILS PSTOGPPLAS	60 120 180
	Protein Acc 1 MHVRSLRAAA ILGLPHRPRP LQDSHFLTDA	cession #: 1 11 PHSFVALWAP HLQGKHNSAP DMVMSFVNLV	P_001710 21 LFLLRSALAD	 FSLDNEVHSS AVEEGGGPGG YHHREPRFDL	 FIHRRLRSQB QGFSYPYKAV SKIPEGEAVT	 RREMOREILS PSTOGPPLAS AAEPRIYKDY	120
50	Protein Acc	11 PHSFVALWAP HLQGKHNSAP DMVMSFVNLV RISVYQVLQE TLDGQSINPR	P_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP	 FSLDNEVHSS AVEEGGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAP	 FIHRRLRSQE QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHFRS	 RREMQREILS PSTQGPPLAS AAEPRIYKDY TSNHWVVNPR IRSTGSKQRS	120 180 240 300
	Protein Acci MHVRSLRAAA ILGLPHRPRP LQDSHPLIDA IRERFDNETP HNLGLQLSVE QNRSKTPKNQ	11	P_001710 21 LFILESALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLPL LAGLIGRHGP NSSSDQRQAC	 FSLDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSFR	PIHRRLRSQE QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHPRS DLGWQDWIIA	 RREMQREILS PSTOGPPLAS AAEPRIYKDY TSNHWVVNPR IRSTGSKQRS PEGYAAYYCE	120 180 240 300 360
50	Protein Acc 1 MHVRSLRAAA ILGLPHRPRP LQDSHFLTDA IRERFDNETH HNLGLQLSVE QNRSKTPKNQ GECAFPLNSY	11	P_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP	 FSLDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSFR	PIHRRLRSQE QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHPRS DLGWQDWIIA	 RREMQREILS PSTOGPPLAS AAEPRIYKDY TSNHWVVNPR IRSTGSKQRS PEGYAAYYCE	120 180 240 300
50	Protein Acci MHVRSLRAAA ILGLPHRPRP LQDSHPLIDA IRERFDNETP HNLGLQLSVE QNRSKTPKNQ	11	P_001710 21 LFILESALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLPL LAGLIGRHGP NSSSDQRQAC	 FSLDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSFR	PIHRRLRSQE QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHPRS DLGWQDWIIA	 RREMQREILS PSTOGPPLAS AAEPRIYKDY TSNHWVVNPR IRSTGSKQRS PEGYAAYYCE	120 180 240 300 360
50	Protein Acc 1 MHVRSLRAAA ILGLPHEPRP LQDSHPLTDA IRERFDNETP HNLGLQLSVE QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Acc	11 PHSFVALWAP HLQCKHNSAP DMYMSFVNLV RISVYQVLQE TLDQQSINPK EALEMANVAE MNATNHAIVQ H 660 DNA 86	IP_001710 21 JFILRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Equence A #: Eos se	 PSLDNEVHSS AVEEGGGPGG YHREPRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSPR VPKPCCAPTQ	PIHRRLRSQE QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHPRS DLGWQDWIIA	 RREMQREILS PSTOGPPLAS AAEPRIYKDY TSNHWVVNPR IRSTGSKQRS PEGYAAYYCE	120 180 240 300 360
50 55	Protein Acc 1 MHVRSLRAAA ILGLPHEPRP LQDSHPLTDA IRERFDNETP HNLGLQLSVE QNRSKTPKNQ GECAFPLNSY RNMVVRACGC Seq ID NO: Nucleic Acc	11 PHSFVALWAP HLQCKHNSAP HLQCKHNSAP DMYMSFVNLV RISVYQVLQE TLOQQSINPK EALRMANVAE MWATMHAIVQ H 660 DNA se	IP_001710 21 JFILRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Equence A #: Eos se	 PSLDNEVHSS AVEEGGGPGG YHREPRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSPR VPKPCCAPTQ	PIHRRLRSQE QGFSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHPRS DLGWQDWIIA	 RREMQREILS PSTOGPPLAS AAEPRIYKDY TSNHWVVNPR IRSTGSKQRS PEGYAAYYCE	120 180 240 300 360
50 55 60	Protein Acc	11 PHSFVALWAP PHSFVALWAP HLQGKINSAP HLQGKINSAP DMYMSFVALW RISVYQVLQE TLDQQSINPK EALRMANVAB MMATMHAIVO H 660 DNA se d Accession ence: 211	P_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET equence 1 %: Eos se 1895	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAP KKHELYVSFR VPKPCCAPTQ quence	FIHRRLESQE GGPSYPYKAV SKIPEGEAVT EGWLVFDITA FKATEVHPRS DLGWQDWIIA LNAISVLYFD	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY	120 180 240 300 360 420
50 55	Protein Acc	11 PHSFVALWAP HLQGKRSSAP DMYMSFVNLV RISVYQVLQE TLDGQSINPK EALEMANVAE MNATNHAIVQ H 660 DNA sc d Accession eence: 211 11 GGGGCCCCAGT	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET equence 1 #: Eos se 1895 21 CACTTCCTCC	PSLDNEVHSS AVEEGGPGG YHHREPRPDL LDSRTLWASE QNKQPPMVAP KKHELYVSFR VPKPCCAPTQ quence 31 ACGTTCTCGT	 FIHRRLESQE OGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHFYS DLGMQDWIIA LNAISVLYFD	RREMQREILS PSTQGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKQRS PEGYAAYYCE DSSNVILKKY	120 180 240 300 360 420
50 55 60	Protein Acc	11 PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHOMOMSFVALWAP	IP_001710 21 LFILLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSORQAC TLVHFINPET equence 1 #: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAN KCHELYVSFR VPKPCCAPTQ quence 31 ACGTTCTCGT CCTATCCACC	 FIHRRLESQE QGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHPRS DLGMQDWIIA LNAISVLYFD	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGGTCGGA	120 180 240 300 360 420
50 55 60	Protein Acc	11 PHSFVALWAP HLQGKHNSAP HLQGKHNSAP MMWSFVNLV RISVYQVLQE TLDQQSINPR EALRMANVAE 660 DNA 66 d Accession ence: 211 11 GGCGCCCAGT GGCAGCCTCG CTGATARAAAT	IP_001710 21 LFLLRSALAD MFMLDLYNAM EMDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET equence 1 #: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAF KCHELYVSFR VPKPCCAPTQ quence 31 ACGTTCTCGT CCTATCCACC ATATTTTAA	FIHRLESQE GGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHFRS LANAISVLYFD 41 GCTGGGCGGG GCTGGGCGGG CACAGGTTTT AAACGGAGAG	RREMQREILS PSTQGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKQRS PEGYAAYYCE DSSNVILKKY	120 180 240 300 360 420
50 55 60 65	Protein Acc MHVRSLRAAA	11 PHSFVALWAP HLQGKHNSAP DMYMSFVNLV RISVYQVLQE TLDQQSINPK EALEMANVAE MNATNHAIVQ H 660 DNA se d Accession ence: 211 11 GGGGCCCAGT AGGCAGCCTG CTGATAAAAT CCCTCGAAAA	IP_001710 21 LFILLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Equence 1 #: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACCTTTTT TTTTTCTACG	PSLDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPFMVAF KCHELYVSFR VPKPCCAPTQ	 FIHRRLESQE QGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHPRS DLGWQDWIIA LNAISVLYFD 41 GCTGGGCGGG CACAGGTTTT AAACGGAGAG GCATTTCTTC	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS DSSNVILKKY 51 AGGAGCGGAT TTGGSTCGGA TTTTTAAAAA AACCAGCATA	120 180 240 300 360 420 60 120 180 240 300
50 55 60	Protein Acc MHVRSLRAAA	11 PHSFVALWAP PHSFVALWAP PHSFVALWAP LIQGKHNSAP DMYMSFVNLV RISVYQVLQE TLDQQSINPK EALEMANVAB MNATNHAIVO H 660 DNA Sc 10 Accession 10 Accession 11 GGGCGCCAGT GGGGGCCCAGT AGGCAGCCTG CTGATAAAAT CCTTCGAAAA CCTTCGAAAA CTTTCAACAGCT TTGAACAGCT	IP_001710 21 LFILIRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGF NSSSDQRQAC TLVHFINPET equence #: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACTTTTT TGACTTTTTT TATTTTCTAG GGATTCTGAT	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAB KKHELYVSFR VPKPCCAPTQ Quence 31 ACGTTCTCGT ACCTATCCACC ATATTTTTAA ATGATAAATGAAA GGCACCATTA	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHPRS DLGMQDMIIA LNAISVLYFD 41 GCTGGGCGG GCTGGGCGGG CACAGGTTTT AAACGGAGA GCAGTTTCTC CTATAGAGGA	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTTGGGTCGGA TTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC	120 180 240 300 360 420 60 120 180 240 300 360
50 55 60 65	Protein Acc	11 PHSFVALWAP HLQGKRISAP DMYMSFVNLV RISVYQVLQE EALEMANVAE MNATNHAIVO H 660 DNA 66 dd Accession dence: 211 GGGGCCCAGT AGGGAGCCTG CTGATAAAAT CCCTGATAAAAT TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGACAGAAA TTTGAACAGCT AAGGGAAAAGT	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET equence 18: Eos se 1895 21 CACTTCCTCC CTCTCCAGTTA TGACCTTTT TTTTCTACG GGATTCTGAT ACAATGTGAA	FSLDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPPMVAP KCHELYVSPR VPKPCCAPTQ	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGKLVFDITA FKATEVEFRS DLGWQDWIIA LNAISVLYFD 41 GCTGGGGGG GCACAGGTTTT GCATTTCTC GCATTTCTC GCATTTCTC GCATTTCTC GCATTTCTC GCATTTCTC GCATTTCTC GCATTTCTC GCATTTCTC CTATAGAGGA CAGGTCAACT	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGGGGAT TIGGGTCGGA TTTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC CCAGGAGGGA	120 180 240 300 360 420 60 120 180 240 300 360 420
50 55 60 65	Protein Acc I	11 PHSFVALWAP	IP_001710 21 LFILIRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGF NSSSORQAC TLVHFINPET 20 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACCTTTTT TTTTTCTACG GGATTCTGAT ACAATGTGAA ATGGGATCGA CCCTCTTAT	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAB KCHELYVSFR VPKPCCAPTQ Quence 31 ACGTTCTCGT CCTATCCACC ATATTTTAA ATGCTTCGAA ATGATATGAT	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGMUVFDITA FKATEVHPRS DLGMQDMIIA LNAISVLYFD 41 GCTGGGCGG CACAGGTTTT AAACGGAGA GCAGTTTGTC CTATAGAGGA CAGCTCAACT GGCCCAGAGG TCAACCATAA	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTTGGSTCGGA TTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC CCAGGAGGGA AACAGTGGGG AGGAGTTGCT	120 180 300 360 420 60 120 180 240 300 420 480 540
50 55 60 65 70	Protein Acc I	11 PHSFVALWAP HLQGKHNSAP HLQGKHNSAP HLQGKHNSAP HLQGKHNSAP HLQGKHNSAP RISVYQVLQE TLDQQSINPK EALRMANVAE 660 DNA 66 d Accession tence: 211 11 GGCGCCCAGT GGCGCCCAGT TTGAACAGCT TTGAACAGCT TTGAACAGCT AAGCGAAAGT GTTTCCTGA GTTTCCTGA GTTTCCTGA GTTACCCCAA	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGTATTTTTTTTTT	FSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVAF KKHELYVSFR VPKPCCAPTQ Quence 31	FIHRRLESQE	RREMQREILS PSTOGPPLAS AAEPRIYKDY TSNHWVNNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTTGGGTCGGA TTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC CCAGGAGGGA AACAGTGGGG AACAGTGGGG AACAGTGGGG AACAGTGGGG AACAGTGGGG AACAGTG	120 180 240 300 360 420 60 120 180 240 300 420 480 540 600
50 55 60 65	Protein Acc MHVRSLRAAA	11 PHSFVALMAP HLQGKRISAP DMYMSFVNLV RISVYQVLQE TLDGQSINPK EALEMANVAE MNATNHAIVO H 660 DNA sc d Accession ence: 211 GGCGCCCAGT AGGCAGCCTG CTCTATAAAAT TTTTCTCTTC TTGAACAGCT TTGAACAGCT AGGCAAAGT AAGCGAAAGT AGTTCCCTGA GTTACCCTGA CAGACTGCCT CAGACTGCCT CAGACTGCCT CAGACTGCCT CAGACTGCCT CAGACTGCCT CAGACTGCCT CAGACTGCT CAGACTGCCT CAGACTCCT CAGACTCCT CAGACTCCT CAGACTCC CAGACTC CAGACTCC CAGACTCC CAGACTCC CAGACTCC CAGACTCC CAGACTC CAGACTCC	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACATTGTT TTTTTCTACG GGATTCTGAT ACAATGGAACATGG CCCCCTTAT TGGACATGGA TCGGACATGG TCGCTTTT TGGACATGGT TCGGACATGG TCGCTTTT TGGAACATGG TCGCTTTTT TGGAACATGG TCGCTTTTT TGGAACATGG TCGCTTTTT TGGAACATGG TCGCTTTTT TGGAACATGG TCGCTTTTT TGGAACATGG TCGCTTTTTT TGGAACATGG TCGCTTTTTT TGGAACATGG TCGCTTTTTT TGGAACATGG TCGCTTTTTT TCGCTTTTT TGGAACATGG TCGCTTTTTT TCGCTTTTT TCGCTTTTT TCGCTTTTT TTGTTTTTTTT	PSLDNEVHSS AVEEGGPGG YHHREPRPDL LDSRTLWASE QNKQPPMVAP KKHELYVSFR VPKPCCAPTQ GUENCE 31 ACGTTCTCGT CCTATCCACC ATATTTTTAGACA ATACATCA CTCATTGTT ATTTTATGACT GATTTTTATGACT CAGCCAGATA	FIHRRLESQE GGESYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHPRS DLCMQDMIIA LNAISVLYFD 41 GCTGGGGGGG CACAGGTTTT AAACGGACAG GCACTTTCTC CTATAGAGGA TCAACCTAAAC GGCCCAGAG TCAACCTAAA TCAGCATAGA TCAGCATAGA	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGGTCGGA TTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC CCAGGAGGGA AACATGGGG AGGAGTTGCT TAAAACATGG AAAGCAAGAA	120 180 240 300 360 420 180 240 300 360 420 480 540 660
50 55 60 65 70	Protein Acc I	11 PHSFVALWAP	IP_001710 21 LFILIRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGF NSSSORQAC TLVHFINPET 20 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACCTTTTT TTTTTCTACG GGATTCTGAT ACAATGTGAA ACTGGATCGAT CCCCCTTAT TGGAACATGG TCGCTTTCTG TCGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVASE QNKQPFMVASE VPKPCCAPTQ Quence 31 ACGTTCTCGT CCTATCCACC ATATTTTAA ATGCTTCGAA ATGATATGTTAA CTCAACATCA CTCATTTGTT ATTTATGACT GATTTTATGACT GATTTTATGC CAGCCAGTAT GTTGGCTACT	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGKUVFDITA FKATEVHPRS DLGKQDMIIA LNAISVLYFD 41 GCTGGGCGGG CACAGGTTTT AAACGGAGAG GCATTTCTTC CTATAGAGGA CAGCTCAACT GGCCCAGAGG TCAACCTAAA ACAGCTTAAA TCAGCATAGA CCACTCTTT	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGSTCGGA TTTTTAAAAA AACCAGCATAT AAGAAAAAAGG GCAGATTGTC CCAGGAGGGA AAGAAAAAGG AGGAGTTGCT TAAAACATGGG AAAGCAAGGAA TAGGTTCCTTG TGGTTCCTTG	60 120 120 300 360 420 120 180 240 300 420 480 660 660 6720
50 55 60 65 70	Protein Acc MHVRSLRAAA	11 PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP LOWER PHONE RISVYQVLQE TLOQGINPK EALEMANVAE MNATNHAIVO H 660 DNA Sc Lot Accession Lot Accession Lot Accession Lot Accession Company Lot Accession Lot Accession Company Company	IP_001710 21 LFILIRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGF NSSSORQAC TLVHFINPET 2QUENCE 18: EOS SE 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACTTTTT TGACTTTTT TGACTTTTT TGCAATGTGAA ATGGGATGGA CCCTCCTTAT TGGAACATGG TCGCTTTCTG TCGGTTCTGT TGGAACATGG TCGCTTTCTG TCGGTTCTGT TGGAACATGG TCGCTTTCTC TCGGTTATT TGGAACATGG TCGCTTTCTC TGGTTACTTC TGGTTACTTC	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPPMVAB KKHELYVSFR VPKPCCAPTQ	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHPRS DLGMQDMIIA LNAISVLYFD 41 GCTGGGCGGG CACAGGTTTT AAACGGAGAG GCATTTCTTC CTATAGAGGA CAGCTCAACT GGCCCAGAGG TCAACCTAAA ACAGCTTAAA TCAGCATAGA ACAGCTTCATT ATTGCACTAGT ATTGCACTAGA	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTTGSTCGGA TTTTTAAAAA AACCAGCATA AAGAAAAAAGG GCAGATTGTC CCAGGAGGGA AAGAGAAAGAA TGGTTCCTT GAACATCTGG GAACTATATC	60 120 180 300 360 420 180 240 300 420 480 600 660 720 780
50 55 60 65 70	Protein Acc 1	11 PHSFVALMAP HLQGKENSAP DMYMSFVNLV RISVYQVLQE TLDGQSINPK EALEMANVAE MNATNHAIVO H 660 DNA sc d Accession ence: 211 GGCGCCCAGT AGGCAGCCTG CTGATAAAAT TTTTCTCTTC TTGAACAGCT TTGAACAGCT AGGCAACCCAA GTTTCCTTG GTAACCCCA CAGACTGCCT GCCTCTATGT TTCTTCATCT TTCTTCATCT TTCTCTTCT TTCATCTT TTCTCTTC TTGAACAGCT TTTCCTTCATCAT TTTTTTTCTTCT TTTTTTTTTT	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Quence #: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACCTTTT TTTTTCTACG GGATCTGAT ACAATGGAA ATGGAACATGG TCGCTTCTT AGGATCTGAT TGGAACATGG TCGCTTTT TGGATCTTT TGGAACATGG TCGCTTTCT AATGTATACC TGGTTACTCC TTTCATGCTG	PSLDNEVHSS AVEEGGPGG YHHREPRPDL LDSRTLWASE QNKQPPMVAE QNKQPPMVAE VPKPCCAPTQ	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGMLVFDITA FKATEVHPTS DLGMQDMIIA LNAISVLYFD 41 GCTGGGGGGG CACAGGTTTT AAACGGAAG TCAACTAGGGA TCAACTAGAGGA TCAGCTAACT GGCCCAGAGG TCAACTAGAGGA TCAGCATTAGA TCAGCATTAGT TATTGCACTAG GCATCTTTTTT	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGSTCGGA TTTTTAAAAA AACCAGCATAT AAGAAAAAAGG GCAGATTGTC CCAGGAGGGA AAGAAAAAGG AGGAGTTGCT TAAAACATGGG AAAGCAAGGAA TAGGTTCCTTG TGGTTCCTTG	120 180 240 300 360 420 60 120 180 240 300 360 420 480 540 660 720 780 840
50 55 60 65 70	Protein Acc I	11 PHSFVALWAP RISVYQVLQE TLDQQSINPK EALEMANVAE MNATNHAIVQ H 660 DNA SK d Accession ence: 211 1 GGGCCCCAGT AGGCAGCCTG CTGATAAAAT CCTCGAAAA CCTCTCATAT CTTCCCTGA CGTTCCCTGA CGTTCCCTGA CGTTCCCTGA CGTTCCCTGA CGTTCCCTGA CGTTCCTGTT TTCTCATCAT TTCTCATCAT TTTTCTATCAT TTTTCATCAT TTTTCATCAT CTTCACTGAGC TTCACGTCAGC TTCACGTCACC TTCACCCC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACGTCACC TTCACCCC T	IP_001710 21 LFILIRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGF NSSSDORQAC TLVHFINPET 20 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGATCTGAT ACAATGTGAA ACAGTGGA CCCTCTTAT TGGAACATGG TCGCTTTCT TGGATCATCC TCGGTTAT TGGAACATGG TCGCTTTCT TGGAACATGG TCGCTTTCT TGGAACATGG TCGCTTTCT TTGTACT TGGTAACTC TTGTACTC TTGTACTC TTTTACTGGGA TTCTGTGGAC TTCTGTGGAC	PSLDNEVHSS AVEEGGPGG YHHREFRFDL LDSRTLWASE QNKQPFMVASE QNKQPFMVASE QVECAPTQ QUENCE 31 ACGTTCTCGT CCTATCCACC ATATTTTAAA ATGATTCTAAA ATGATTCAAC CTCATCTTGT ATTTATGAC GATTTTGTT GATTTTATGC GATTTTATGC GAGCCAGTA GTTGGCTACT AGACGATCA AGAGCTACAA AGGCAGATCA AGAGCTACAA ACTGGAGTCCC AGAGCTCCAAA CTGGAGTCCC AGACTCACAT ACTGGAGTCCC AGACTCACAT ACTGGAGTCCC AGACTCACAT ACTGGAGTCCC AGACTCACAT ACTGGAGTCCC AGACTCACAT	FIHRRLESQE QGFSYPYKAV SKIPEGEAVT EGKLVFDITA FKATEVHPRS DLGWQDWIIA LNAISVLYFD	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGGTCGGA TTTTAAAAA AACCAGCATT AAGAAAAAGG GCAGATTGC CCAGGAGGGA AACAGTGGG AAGGCAAGAA TGGTTCCTTG GAACTATAC CAAGATTGCT CAAAGACAGA CGATTACC CAAGATTGCT CAAAGACAGA CGATGCCCA CAAGATTGCT	60 120 180 360 420 60 120 180 240 360 420 480 660 660 6720 780 840 900
50 55 60 65 70	Protein Acc MHVRSLRAAA	11 PHSFVALWAP HLQGKRSSAP DMYMSFVNLV RISVYQVLQE EALEMANVAE MNATNHAIVO H 660 DNA 66 dd Accession dence: 211 GGGGCCCAGT AGGGAGCCTG TTGAACAGCT TTTGACAGAG CTGATTCATG GTTCCCTGA CAGACTGCCT GCCTCTATGT TTCTCTTC TTCTCTTCATG TTCTCTTCATG TTCTCATGA TATTTGTGTC CTCACATAGA TTTTCTCTTC TTCTCATGAT TATTTGTGTC CTCACATAGG TTAGTTAGTT TTTAGAGGCAAC TTAGTTAGTT	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACCTTTT TTTTTCTACG GGATTCTGAT ACAATGGAA ATGGAACATGG TCGGTTCTG AATGTATACCT TGGTTACTCT TGGTTACTCT TGGTTACTCT TGGTTACTCT TGGTTACTCT TGGTTACTCT TGGTTACTCT TTTCATCGG TCGGTTACTC TTTCATGGAC TCGTTACTG TTCTTGGAC CCTGGGTACAC	PSLIDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPPMVAP KCHELYVSPR VPKPCCAPTQ	FIHRRLESQE GGFSYPYKAV SKIPEGEAVT EGKLYFDITA FKATEVIERS DLGWQDWIIA LNAISVLYFD CAGGTTTGT GCATTTGTG GCATTTGTG GCATCATTA ACAGGTTAAA TCAGCATAGG CCATCTTTT AATTGCACTAG GCATCTTTGT TAATAATGCG AATATCGGTG GGATCCTGGT GGATCCTGGT	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TIGGGTCGGA TTTGGGTCGGA ACAGATATC CCAGGAGGGA AACAGTGGG AAGGATTGCC CAAGACAGA TGGTTCCTTG GAACTTATC CAAAGACAGA GGATTATCC CAAAGACAGA GGATTATCC CAAAGACAGA GGATTGCTC CAAAGACACG GGATTGCTC CAAAGACACG GGATTGCTC CAAAGACACG GGATTGCTC CAAAGACCCC CAAGACTCCTC GGAACGTTCCTC	120 180 240 300 360 420 60 120 180 240 300 420 480 660 720 840 900 900 1020
50 55 60 65 70	Protein Acc MHVRSLRAAA	11 PHSFVALMAP HLQGKRISAP DMYMSFVNLV RISVYQVLQE TLDGQSINPK EALEMANVAE MNATNHAIVO H 660 DNA sc d Accession ence: 211 GGCGCCCAGT AGGCAGCCTG CTGATAAAAT TTTTCTCTTC TTGAACAGCT AGGCAAAAG TTTCCTTG GTAACCCCAA AGGCAAAGT TTCTCTTG GTAACCCCAA CGGTTCCATGG TTCTCATCAT TTCTCTTCATCAT TTCTCATCAT TTCTCATCAT TTCATCATCAT TTCATCATCAT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATT ATCTCATCATCATT ATCTCATCATT ATCT	IP_001710 21 LFILLRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Quence #: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACATTGTT TTTTTCTACG GGATTCTGT TGGACATGG TCGTTTT TGGACATGG TCGTTTTCTTCTGGAC CTGGGTTACTTC TGTGGAC CCTGGCTACA TTCTGTGGAC CCTGGCTACA TGGGCTTTC	PSLDNEVHSS AVEEGGPGG YHHREPRPDL LDSRTLWASE QNKQPPMVAP KKHELYVSFR VPKPCCAPTQ 31 ACGTTCTCGT CCTATCCACC ATATTTTAGACT ATTTATAGACT GATTTTATAGCT GATTTTATGC CAGCCAGATA GTTGGCTACT AGACGATCA CTGGAGCACTAC AGACGATCA CTGGAGTACA AGACGATCA CTGGAGTACA AGACGATCA AGACGATCA AGACGATCA AGACGATCA AGACGATCA AGACGATCA AGACGATCA ATTTATATTTTTTCGGACA	FIHRRLESQE GGESYPYKAV SKIPEGEAVT EGMUVFDITA FKATEVHPRS DLGMQDMIIA LNAISVLYFD 41 GCTGGGGGGG CACAGGTTTT AAACGGAGAG TCAACTTGTC GCATTTCTC CTATAGAGGA ACAGCTAAAT ACAGCTAAAT ACAGCTAAAT ACTGCACTAGA TCAGCATAGA GCATTTTTTT ATTGCATAG GCATTTTTTT TAATAGTGA ATTGCACTAG ACTGCTTTTTT TAATAGTGA ATTGCACTAG ACTGCTTTTTT TAATAGTGA ATTGCACTAG GCATCTTTTTT TAATAATGCA ATTGCGGTG GCATCTTGT CAAAATACCT CAAAAT	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGGTCGGA ATTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC CCAGGAGGGA AACATGGGA AACATGGGAAGAACAT TGGTCCTTG GAACTATATC CAAAGACAGA GGATGACTCC CAAAGACTGCCA CAAGATTGCT CAAAGACTGCA GGATGCTCC CGAGAGTTCCT GGAAGGTTCCT GGAAGGTTCCT GTGGGGCTTC	120 180 240 300 360 420 60 120 180 240 300 360 420 480 540 660 720 780 900 900 900
50 55 60 65 70 75	Protein Acc I	11 PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP PHSFVALWAP RISVYQVLQE TLDQQSINPK 660 DNA sc. d. Accession ence: 211 660 DNA sc. d. Accession ence: 211 1	IP_001710 21 LFLLRSALAD MFMLDLYNAM EHDKEFFHPR HLGRESDLFL LAGLIGRHGP NSSDQRQAC TLVHFINPET CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGAACTTTT TTTTTCTACG GGATTCTGG TCGGTTATTGGAACATGGA CCTCTTCTGT TGGTTACTTC TTTCATGGGC TTCTGGGAC TCCTGGCTTCT TCCAGCAGCA TCCAGCAGCA	PSLDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPPMVAN KKHELYVSFR VPKPCCAPTQ	FIHRRLESQE	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TIGGGTCGGA TTTGGGTCGGA ACAGATATC CCAGGAGGGA AACAGTGGG AAGGATTGCC CAAGACAGA TGGTTCCTTG GAACTTATC CAAAGACAGA GGATTATCC CAAAGACAGA GGATTATCC CAAAGACAGA GGATTGCTC CAAAGACACG GGATTGCTC CAAAGACACG GGATTGCTC CAAAGACACG GGATTGCTC CAAAGACCCC CAAGACTCCTC GGAACGTTCCTC	120 180 300 360 420 120 180 240 300 360 420 480 6600 6600 720 780 840 950 950 1020 1020
50 55 60 65 70	Protein Acc 1	11 PHSFVALMAP HLQGKENSAP DMYMSFVNLV RISVYQVLQE TLDGQSINPK EALEMANVAE MNATNHAIVO H 660 DNA sc d Accession eence: 211 GGCGCCCAGT AGGCAGCCTG CTGATAAAAT TTTCTCTTC TTGAACAGCT TTGAACAGCT GTTTCCATG GTAACCCCA AGGCAACCCG GCCTCATGT TTCTCTCATCAT TTCTCTTCCTG TTCTCATCAT TTCTCTTCCTG GTAACCCCA TTCTCTCATCAT TTCTCTTCCTG TTCTCATCAT TTCTCTTCCTCATCAT TTCTCTTCCTCATCAT TTCTCTTCCTCATCAT TTCTCTCATCAT TTCTCTCATCAT TTCTCATCAT TTCTCAT	IP_001710 21 LFILLRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Quence \$: Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGACCTTTT TTTTTCTACG GGATTCTTG AATGTATACC TGGGTACATCG AGTAACATGG TTCTGTGGAC CCTGGCTACA TTCTGTGGAC CCTGGCTACA TGGGCTTCT TCTGGGAC CTGGCACAT TGGGCTTTC TCTGGGAC CTGGGAACATT TCGGCGACAT TGGGCTTTC TCGGCACAT TGGGCTTTC TCGGCACAT TGGGCACAT TGGGCTGAAT	PSLIDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE (MKCPELLYVSFR VPKPCCAPTO) Quence	FIHRRLESQE GGESYPYKAV SKIPEGEAVT EGMUVFDITA FKATEVHPRS DLGMQDMIIA LNAISVLYFD 41 GCTGGGGGGG GCACAGGTTTT AAACGGAGAG TCAACCTAACT GGCCCAAGG TCAACCTAACT GGCCTAACT GGCACTTCTT ATGACGTA ATGCACTAG ATGCACTAG ATTCGCTTAG ATGCACTAG GGATCCTTTT TAATAATGCA ATATCGGTG GGATCCTGGT CCAAATACCT CCAGGGCTGT AATGCACTAG ATATCGGGTG CCAAATACCT CATGGGCTGT AACATCAAGTG CCAAATACCT CATGGGCTGT TCACAATACCT TCTGAATAC TTCTGAATAC TTCTGAATAC TTCTGAATAC TTCTGAATAC	RREMOREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTGGGTCGGA ATTTTAAAAA AACAGCATA AAGAAAAAGG GCAGGGTTCT TAAAACATGG AAAGCAGAA TGGTTCCTTG GAACTATATC CAAAGACAGA GGATGCTC CTAGAGACTTCCT GGAAGGTTCCT GGAAGGTTCCT GGAAGGTTCCT GGAAGGTTCCT GGAAGGTTCCT GGAAGGTTCCT GGCACGACA GGTTACACA GGTTACAAGGTTTCT GGCACGACTA GGTTACAAGGTTT	120 180 240 300 360 420 60 120 240 300 360 420 480 540 660 720 780 960 900 910 900 910 910 910 910 910 910 91
50 55 60 65 70 75	Protein Acc 1	11 PHSFVALMAP PHSFVALMAP HLQGKHSAP DMYMSFVNLV RISVYQVLQE TLDQQSINPK EALEMANVAE MNATNHAIVQ H 660 DNA se dd Accession dence: 211 GGCGCCCAGT AGGCAGCCTG CTGATAAAAT CTCTGATAAA CTCTTGATAAC CTGATAAAAT CTTTGATAC GTAACCCCAA GGTTTCCATG GTAACCCCAA GGTTTCCATG TTCTGATGT TTCTATGT TGTAGGCAAC TTATTTGTT CTCACATG GTATCCATGT TTCTATGT TTCTAGGCAAC TTATTTCTT CTCACATGG TTCTCATCAT TTCTAGGCAAC TTATTTCTT GCTGGGGGTT ATCCGAGGTA ATCTCATCTT GCTGGGGGTT ATCTGAGGTAT ATCTCATCTT GCTGGGGGTT ATCTGAGGTAT AAAATCTGGAA	IP_001710 21 LFILLRSALAD MFMLDLYNAM EHDKEFPHPR HLGRESDLFL LAGLIGRHGP NSSSDQRQAC TLVHFINPET Quence E. Eos se 1895 21 CACTTCCTCC CTCTCCAGTC TCCTGGGTTA TGAACATGTGA ACAATGTGAA ACAGTGTAA CCATTCTTC TGTTCTCTC TGTTATTCTCT TGTTCTCTC TGTTATTCTCT TGTTCTCT TGTTATCTC TGTTATTCTC TGTTATTCTC TGTTATCTC TGTTATCTC TGTTATCTC TGTTATCTC TTTCTGTGAC CCTGGCTACA TGTGGCTTC TCCAGCACC CTGGGAACTT TCGGCACACA GACCAATGCA GACCAATGCA	PSLIDNEVHSS AVEEGGPGG YHHREPRFDL LDSRTLWASE QNKQPPMVAN KKHELYVSFR VPKPCCAPTQ 31 ACGTTCTCGT CCTATCCACC ATAITITIAA ATGATTCGAA ATAATGAAA CTCAACATCA CTCATCTGAT ATTTATGACT GAGTACTAC GAGGAGATGAC CAGCAGGATA GTTGGCTACT AGACGATGA TTGGCTACT AGACGATGA TTGGCTACA ATTATTATT ATTTTTTCGGACA TTTGTTGCAC AGTTGCTGACA TTTGTTGCAC AGTTCTGGACA TTTGTTGCAC TTTTTTCGGACA TTTGTTGCAC GTTGGCCACT GTTGGCCACT GTTGGCCACT GTTGGCCACT	FIHRRLESQE GGESYPYKAV SKIPEGEAVT EGMUVFDITA FKATEVHFRS DLGMQDMIIA LNAISVLYFD 41 GCTGGGGGGG CACAGGTTTT AAACGGAGAG GCACTTCTTC CTATAGAGGA ACAGCTTAAA ACAGCTTAAA ACAGCTTAAA ACAGCTTAAA ACTACTTAGACGA TCAACCATAG GGATCTTGT CATTCCATAG GGATCTTGT TAATAATGCA ATATCGGTG GGATCTTGT TAATAATGCA ATATCGGTG GGATCTTGT TAATAATGCA TCAACTAGAGAA TCTCAAATGC TCTAATAACCT CATGGGTG TCAAATAC TCTCAAATGC ACATCAAGGAA	RREMQREILS PSTOGPPLAS AAEFRIYKDY TSNHWVNPR IRSTGSKORS PEGYAAYYCE DSSNVILKKY 51 AGGAGCGGAT TTTGSTCGGA TTTTTAAAAA AACCAGCATA AAGAAAAAGG GCAGATTGTC CCAGGAGGGA AAGAAAAAGG GCAGATTGTC CAAAGACAGGA TGGTTCCTTG GAACTATATC CAAAGACAGA CAGATTGCT CAAAGACAGA GGATTGCTC GGAAGGATTGCT GGAAGTTGCT GGAAGATTGCT GGAAGGTTCC GGGGGCTTC GGGAGGGA GGATTTATCAA	120 180 240 300 360 420 180 240 300 360 420 480 540 660 720 780 900 950 1020 1080 1140 1260 1320

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         TICTICACT CCITICAGG TITCTITGIG TCTATCATCT ACTGCTACTG CAATGGAGAG GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCCGTGGA CTGGAAAAGG
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                                                                                                1560
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                                                                                                1740
         TCAGAGCAGG ACTGCCTGCC ACACTCTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG
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         GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA
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         Protein Accession #: Eos sequence
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                                      21
                                                    31
                                                                   41
                                                                                 51
15
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                                                                                                  480
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         SRPMESNPDT EGCOGETEDV L
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GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCCAGCTG GATTCTGATG GCACCATTAC
                                                                                                  180
                                                                                                  240
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        AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTTGTTG
GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT
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                                                                                                  420
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         CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC
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TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG
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CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT
TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA
                                                                                                1080
                                                                                                1140
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                                                                                                1320
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                                                                                                1380
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         CACOSTGACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT
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        TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC
TGGCTATGTC TGGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC
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        GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTC TCTGAATGGA
CATTTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG
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                                                                                                2040
                                                                                                2100
                                                                                                2160
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GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT
                                                                                                2280
                                                                                                2340
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                                                                                                2400
         ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC
                                                                                                2460
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TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCTTG
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         Protein Accession #: NP_005039
         MAGIGASLHV WGWLMLGSCL LARAQLDSDG TITIEEQIVL VLKAKVQCEL NITAQLQEGE
85
         GNCFPEMDGL ICMPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNFNGTWD FWHSLNKTWA
                                                                                                 120
        NYSDCLRPLQ PDISIGKQEF FERLYVMYTV GYSISPGSLA VAILIIGYPR RLHCTRNYIH
MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMODDPQ NSIEATSVDK SQYIGCKIAV
                                                                                                  180
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51

120

240

300

180

240

300

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540

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900 960

1020

WO 02/086443 Seg ID NO: 673 Protein sequence Protein Accession #: Eos sequence 5 MGYOROEPVI PROFSLYLLI KGGALSGTDT YOSLVNKTPG FRGYLLLSVL OPLYPFIAMI SYNTIAGDTL SKYFORIPGV DPENVFIGRE FLIGLSTVTF TLPLSLYRNI AKLGKVSLIS 10 TGLTTLILGI VMARAISLGP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSPLVYSSL EEPTVAKWSR LIHMSIVISV PICIFFATCG YLTPTGFTQG DLFENYCRND DLVTFGRFCY GVTVILTYPM BCFVTREVIA NVFFGGNLSS VFHIVVTVMV ITVATLVSLL IDCLGIVLBL NGVLCATPLI FIIPSACYLK LSEEPRTHSD KIMSCVMLPI GAVVMVFGFV MAITNTODCT HEQEMPYCFP DNFSLTNTSE SHVQQTTQLS TLNISIFQLE 15 Seq ID NO: 674 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1..1140 20 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTTGTATC CTTTTATAGC AATGATAAGT TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 25 CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT CTGCCTTTAT CCTTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA GGTTTAACAA CTCTGATTCT TGGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCGGG GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 30 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 35 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG
TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT GGGCAGGAAA TGTTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 40 CATGTTCAGC AGACACACA ACTTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA Seq ID NO: 675 Protein sequence Protein Accession #: Bos sequence

- 45 MGYQRQEPVI PPQVNKTPGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPGVD PENVFIGREF IIGLSTVTFT LPLSLYRNIA KLGKVSLIST GLTTLILGIV MARAISLGPH 120 IPKTEDAWVF AKPNAIOAVG VMSFAFICHH NSFLVYSSLE EFTVAKWSRL IHMSIVISVF 180 50 ICIPFATCGY LTFTGFTQGD LFENYCRNDD LVTFGRFCYG VTVILTYPME CPVTREVIAN 240 VFFGGNLSSV FEIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL SEEPRTHSDK IMSCVMLPIG AVVMVPGFVM AITNTQDCTH GQEMFYCFPD NPSLTNTSES HVOOTTOLST LNISIFOLE
- 55 Seq ID NO: 676 DNA sequence Nucleic Acid Accession #: NM_006853.1 Coding sequence: 26..874
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Protein Accession #: NP_006844.1

85 MRILQLILLA LATGLVGGET RIIKGFECKP HSQFWQAALF EKTRLLCGAT LIAPRWLLTA

5	CTTUBBLT	1.0000パリアなる(計)	EGCEQTRTAT SCLISGWGST GDSGGPLVCN	SSPOLRLPHT -	LRCANITILE	HUNCEMAIPG	120 180 240
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	ATGTGCAGCA TTCGACAAGA	GTGATGAGAA	CATCCCGGGC GGAGTGCCCC CCATTGCATC	AAGGCTAAGT	TCCGGTGCAA	TGGGTTTGAG	60 120 180
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20	CACCAGCGGA CTGCTGTCCC AATAATGGCA	AGCGGAACAA GCCTGGTGGT TCCAGTATGT	CCTCATGACG CCTGGACCAC GGCCAGCCAG	CTGCCCGTGC CCCCACCACT GCGGAGCAGA CAGAGGCCTG	GCAACGTCAC ATGCGTCGGA CGTGGTATGA	CTACAACGTC AGTAGGCTCC CCTTCCTCCA	540 600 660 720
25	COGCCCTACT CGGTCCGGGA GACACCAGCC	CTTCTGACAC GTGCCAACAG ACAGCCCGGG	GGAATCTCTG TGCCAGCTCC GCAGCCTGGC TGAAGAAGTA	AACCAAGCCG CAGGCAGCCA CCCCAGGAGG	GCAGCCTCCT	GAGCGTGGAA	780 840 900
30	Seq ID NO: Protein Acc	. 679 Prote cession #: :	in sequence Eos sequenc	е			
	1	11	21	31	41	51 1	
	MOCNERCIPO	AWOCTICE POC	 PDKSDEKECP	KAKSKCGPTF	 PPCASGIHCI	IGRPRONGPE	60
35	DONNOCHEEN	CTANDLICCT	ARVHCKNGLC	IDKSFICDGO	NNCODNSDEE	SCESSUEPGS	120 180
	TI COLUMN DU	VAVTVANUUG	IIGSSVIPVL NNGIQYVASQ	AEONASEVGS	PPSYSEALLD	OKPAMIDDE	240
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-10	Nucleic Ac	680 DNA s id Accessio uence: 12	n #: S78203	.1			
45.	1	11	21	31	41	51	
	1	.	TCACTCCAAG	GAAACTCTT	TTTCACCTGT	CTCCATTGAA	60
	CROCTROCAC	CTCCACCACC	TAGCCCTCCA	AAGAAGCCAT	CICCGACAAI	CIGIGGCICC	120
50	3 3 CM3 MCC73 C	**************************************	CITCATTGTG GATCCTGTAT	CTCAATGAAT	* TCTGCGAGCG	CITITICCIAI	180 240
30	N COMPOUND ON T	~~************************************	. ТСССТТСАСС	AGCCTCTGT	ATTITIACIO	CATCCIGGGA	300
	COLCOS TO	ALCO APPLICATION	CTTCCCAAAA	TTCAAGACAA	TCATCTATCT	CICCIIG	360 420
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	NOOCEN CENT	. ALCOHOLD AND A	י הייים דידינוריי	· ATGTTCTGG	: CTCTTTTGG/	TCAGCAGGGI	960 1020
	TCACGATGG/	CTTTGCAAG	CATCAGGATO	AATAGGAAT	TCTTCATCC	GTTGTTTGAC	1000
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		THE REPORT A CO	- CHCCCACC	\ TTTGCAGTT(3 OGGCAGCTG7	AGAGATAAAA AGTCTTGAAT	1200
		* ***********	COTCACACTO	E CTTCCCAAATT	: AAAACAATI	TUTUTIONIA	1320
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	GOGGE COMO:	MCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	יייייייייייייייייייייייייייייייייייייי	L CVCLLALCY	T ATTCTCAGG	TUCCITIAGE	1920
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80	CITGITGIG	G CACAGTTCA	G TGGCCTGGT	A CAGTGGGCC	G AATTCATTT T ACTACTATG	T TCCTGTAAAG	2100
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Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2 Coding sequence: 48..851

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			AGGATOGTAT				420
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15			CCAGGAAACA				600
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	- 4 4						
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40	Seq ID NO: Nucleic Ac: Coding sequ 1 ATGACAGGAG	688 DNA seid Accession dence: 187	equence n#: NM_009 70 21	31 AGCATCCGAT	 CCGGCGACTT	CCAAGCTCCG	60 120
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40 45	Seq ID NO: Nucleic Aci Coding sequ 1 ATGACAGGAG TTCCAGACGT TCAGCTACCG CCTACCTCCG AACGGCTCCG TACCACCAGT GAAGTGACCG AGGACTATTT	688 DNA se id Accession Dence: 18* 11 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGGAGCTA ACGGCGGGGGAGCTA ACGGCGGGGGAGCTA ATTCCAGCTT	equence 1 #: NM_009 70 21 AAGGGTCCCC GCACCATCCG CTACAGCCCT CCAGCCAAA CTACAACCGC GAGAATGGG TCAGCTGGCC	31 AGCATCCGAT TCTCAGGAAT ACCCCTACC GCTTATGCCG GTCCCAAGCG AATGGCAAAC GCATTACAGA	CCGGCGACTT CCCCGCACGG AGTATCAGTA ACTATAGCTA ACCAACCA CCAACGAAGGAAGT GAAGGTTTCA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCGAGAAA TCGTAAACCC GAAGACTCAG	120 180 240 300 360 420 480
40 45	Seq ID NO: Nucleic Act Coding sequ ATGACAGGAG TTCCAGACGT TCAGCTACCG CCTACCTCGG AACGGCTCCG TACCACCAGT GAAGTGACCG TACCACCAGT TACCTCGCCT TACCTCGCCT	688 DNA se id Accession ience: 18* 11 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CCTGCTATGG CCGGGAGCTA ACGCCGAGCTA ACGCCGAGCTA ACGCCGAGCTA ATTCCACTT TGCCGGAACCG	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCCG CTACAGCCTT CCCAGCCAAA CTACAACCGC GAGAATGGTG	31 AGCATCCGAT TCTCAGGAAT ACCGCGGGGGG AACCCCTACC GCTTATGCCG GTCCCAAGCG AATGGCAAAC GCATTACAGA GCCGCCTCGC	COGGOGACTT CGCCAACTTT CCCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAACA GAAGGTTTCA TGGGATTGAC	CCAAGCTCCG GCCCGAGTCT CTACTGCTCT TCACGGCTG CGCTAGCTCC GCCAGAGAAA TCGTAAACCC GAAGACTCAG ACAAACACAG	120 180 240 300 360 420
40 45	Seq ID NO: Nucleic Ac: Coding sequing TCAGACGT TCAGACGT TCAGACGT TCAGCTACCG CCTACCTCGG AACGGCTCCG GAACGCTCCG GAACTGACCG GAGACTATTT TACCTCGCCT GGGAAAATCT	688 DNA se id Accession zence: 18" 11	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCGG CTACAGCCTT CCCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CGCCGAGCTG	31 AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTACC GCTTATECCG GTCCCAAGCG AATGGCAAAC GCATTACAGA GCGCCCTCGC AAGATCAAGA	COGGOGACTT COCCAACTTT COCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTTCA TGGGATTGAC AGATCATGAA	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG CGCTAGCTCC GCCAGAGAAA TCGTAAACCC GAAGACTCAG ACAACACAG AAACGGGGAG	120 180 240 300 360 420 480 540
40 45 50	Seq ID NO: Nucleic Ac: Coding sequence 1 ATGACAGGAG TTCAGACGT TCAGCTACCTCGG AACGGCTCCG TACCACCAGT GAAGTGACCG AGGACTATTT TACCTCGCCT ATGCCCCCGG ATGCCCCCGG	688 DNA se id Accession sence: 18* 11 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTA ACGGCGGCGC ATTCCAGGT ATTCCAGGT ATTCCAGGT TGCCGGAACG GGTTTCAGAA AGCACAGTCC	equence 1 #: NM_005 70 21 AAGGGTCCCC GCACCATCCG CTACAGCCCT CCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGC CGCGAGCTG CCCGAGCTG CAAAGATCC CAGCTAGA	31 AGCATCCGAT TCTCAGGAAT ACGGGGGGGA AACCCTACC GCTTATECCG GTCCCAAGCG GCCCTAGCA GCATTACAGA GCCTTACAGA GCCCCTCGC AAGATCAAGA GACCCAATGG	COGGOGACTT CGCCAACTTT CCCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTTCA TGGGATTGAA CGTGTAACTC	CCAAGCTCCG GCCCGAGTCT CTACTGCTCT TCACGGCGTG GGCTAGCTCC GCCAGAGAAA TCGTAAACCC GAAGACACAG ACAAACACAG AAACGGGGAG GCCGCAGTCT	120 180 240 300 360 420 480 540 600 660
40 45	Seq ID NO: Nucleic Aci Coding sequ 1 ATGACAGGAG TTCAGCTACCG CCTACCTCGG AACGGCTCCG TACCACCAGT GAAGTGACCG GAGGACTATTT TACCTCGCCT GTGAAAATCT ATGCCCCCGG CCAGCGGTGT	688 DNA se id Accession lence: 18* 11 TGTTTGACAG CCGCAGCTAT ATTCTGACTA ACTTCTGACTA ACGGCGGGGCTA ACGCCGGGAGCTA ATTCAGCTT TGCCGGAACG GGTTTCAGAA AGCACAGTCC GGGAGCTCC	equence 1 %: NM_009 70 21 AAGGGTCCCC GCACCATCCG CTACAGCCCT CCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CGCCGAGCTG CCAGCTGGCC CAGCTGGCC CAGCTGGCC CAGCTGGCC CAGCTCGTCC	31 AGCATCCGAT TCTCAGGAAT ACCCCTACC GCTTATGCCG GTCCCAGCCG GCCCTCGC AACATCAGA GCCCCTCGC AACATCAGA GCCCCATGG GACCCAATGG CGCCTCACCCCCCCCC	CCGGGGACTT CGCCAACTTT CGCCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTTCA TGGGATTGAC AGATCATGAA AGATCATGAA AGATCATGAA GGCTCACCACCCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GGCTAGCTCC GCCAGAGAAAA TCGTAAAACA GAAGACTCAG AAAACACAG AAACGGGAG GCCGCAGTCT TCATGCCCAC	120 180 240 300 360 420 480 540 600 660 720
40 45 50	Seq ID NO: Nucleic Ac: Coding sequence 1 ATGACAGGAG TTCAGACGT TCAGCTACCTG CATACCTGG AACGGCTCCG GAAGTGACCG GAAGTGACCG TACCACAGT GAAGTGACCG TACCACCAGT TACCTCGCCT GTGAAAATCT ATGCCCCGG CCAGCGGTGT CCTCCGACCT	688 DNA se id Accession Lence: 18* 11 TOTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTA ACGGCGGGGCA AGCCCGAGGT ATTCCAGCTT TGCCGGAACG GGTTTCAGAA AGCACAGTCC CGGAGCCCCA	equence 1 8: NM_005 70 21 21 AAGGGTCCCC GCACCATAC CTACAGCCTT CAAAGCTCTC CCAGCCAAA CTACAACCGC GAGAATGGTG CCAGCTGGCC CAAAGGTCC CACAGCTCAGC CCACAGCTC CACAGCTCAGCC CAGCTCAGCC CAGCTCCAGCC CAGCTCCAGCCC CAGCTCCAGCCC CCCAGCTCC	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50	Seq ID NO: Nucleic Ac: Coding sequitation ATGACAGGAG TTCCAGACGT TCAGCTACCG CCTACCTOGG AACGGCTCCG TACCACCAGT TACCTCGCCT TACCTCGCCT AGGACTATTT TACCTCGCCCT ATGCCCCCGG CCAGCGGTGT ATGCCCCCGAC ACAGGGGGTGT ACAAGTGCAG	688 DNA se id Accession sence: 18" 11 1 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CCTTCCTATGG CCGGGAGCTA ACGGCGGGG ATTCCAGCTT TGCCGGAACCG GGTTTCAGAA AGCACAGTCC GGGAGCCCCA CCAGCTCCC CCAGCTCAAT	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCCG GCACCATCCG CTACAGCTCTC CCCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CCAGCTGCC CCAGCTCCAGCTG CCAAAGATCCCAGCTGCC CAGCTCCAGC	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720
40 45 50	Seq ID NO: Nucleic Ac: Coding sequitation ATGACAGGAG TTCCAGACGT TCAGCTACCG CCTACCTOGG AACGGCTCCG TACCACCAGT TACCTCGCCT TACCTCGCCT AGGACTATTT TACCTCGCCCT ATGCCCCCGG CCAGCGGTGT ATGCCCCCGAC ACAGGGGGTGT ACAAGTGCAG	688 DNA se id Accession Lence: 18* 11 TOTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTA ACGGCGGGGCA AGCCCGAGGT ATTCCAGCTT TGCCGGAACG GGTTTCAGAA AGCACAGTCC CGGAGCCCCA	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCCG GCACCATCCG CTACAGCTCTC CCCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CCAGCTGCC CCAGCTCCAGCTG CCAAAGATCCCAGCTGCC CAGCTCCAGC	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequence 1 ATGACAGGAG TTCAGCTACCG ACGCTCCCG AACGCTCCCG TACCACCAGT TCAGTAGAATTTT TACCTCGCCT GTGAAAATCT ATGCCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTGCAG CTGGCGCTGG CTGGCGCTGG CTGGCGCTGG	688 DNA se id Accession lence: 18* 11 TGTTTGACAG CCGCAGCTAT ATTCTGACTAT ACTGCCTATGG CCGGGAGCTA ACGCCGAGGTT ATTCAGCTT TGCCGGAACG GGTTTCAGAT ACGCGGAACG GGTTTCAGAT CGGGAGCCCCA CCAACCAGTC CCAACCAGTC CCAGCTCAAT CCTCCGGGAC	equence 1 #: NM_009 70 21 AAGGGTCCCC GCACCATCCG CTACAGCCCT CCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CACCAGCTGCC CACCAGCTGCC CACCAGCTGCC CAGCTGTCC CCAGCGTCC CCCAGCGTCC CCCAGCGTCC CCCAGCGTCC CCCAGCGTCC CCCAGCGTCC CAATTCCCAC ACTCTATTAG	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequing Tracagagagagagagagagagagagagagagagagagaga	688 DNA se id Accession sence: 18" 11 TOTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTA ACGGCGGGGG AGCCCGAGGT ATTCCAGCTT TGCCGGACG GGTTTCAGAA AGCACAGTCC CGGAGCCCA CCAACCAGTC CCACCTCAT CCTCCGGAC 689 Protei	equence 1 8: NM_005 70 21 21 AAGGGTCCCC GCACCATCCG CTACAGCCTAT CAAAGCTCTC CAAAGCTCTC CACAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CGCCGAGCTGC CCAAAGATCC CAAAAGATCC CAAAAGATCC CAAAAGATCC CAAAAGATCC CAAATCCCAC ACTCTATTAG In sequence	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50	Seq ID NO: Nucleic Ac: Coding sequing Tracagagagagagagagagagagagagagagagagagaga	688 DNA se id Accession lence: 18* 11 TGTTTGACAG CCGCAGCTAT ATTCTGACTAT ACTGCCTATGG CCGGGAGCTA ACGCCGAGGTT ATTCAGCTT TGCCGGAACG GGTTTCAGAT ACGCGGAACG GGTTTCAGAT CGGGAGCCCCA CCAACCAGTC CCAACCAGTC CCAGCTCAAT CCTCCGGGAC	equence 1 8: NM_005 70 21 21 AAGGGTCCCC GCACCATCCG CTACAGCCTAT CAAAGCTCTC CAAAGCTCTC CACAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CGCCGAGCTGC CCAAAGATCC CAAAAGATCC CAAAAGATCC CAAAAGATCC CAAAAGATCC CAAATCCCAC ACTCTATTAG In sequence	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequing Tracagagagagagagagagagagagagagagagagagaga	688 DNA se id Accession lence: 18" 11 TGTTTGACAG CCGCAGCTAT CTTCTGACTA CTTCTGACTA CTTCTGACTA ACGGCGGGCTA ACGCGGAGCTA ACGCGGACCTA ACGCGGACCT GGGTTCAGAC GGTTCAGAC CCAACCAGTC CCAGCTCAAT CCTCCGGGAC 689 Protei cession #: N	equence 1 #: NM_009 70 21 AAGGGTCCCC GCACCATCCG GCACCATCCG CTACAGCCCT CCAGCCAAA CTACAACCGC CGAGATGGG TCAGCTGGCC CAGAAAGATCC CAGCTGACC CAGCTCCAGC CAGCTCCAC CAGCTCCAC ACTCTATTAG ACTCTATTAG In sequence IP_005212.1	31 AGCATCCGAT TCTCAGGAAT ACCGCGGGGA AACCCTACC GCTTATGCCG GTCCAAGCG GCATTACAGA GCATTACAGA GCCCCTCGC AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTCG CTGCCGCCCC	CCGCGACTT CCCCGCACG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTCA TGGGATGAC GGTGTAACTC GCCACCACCC AGAACTCTGC AGACTCTGC CGGGCTCCTT	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GGCTAGCTCC GCAGAGAAA TCGTAAACCC GAAGACTCAG ACAAACACAG ACAACCACGGGAG GCCGCAGTCT TCATGCCCAC ATCCTGGTAC ACAGCACCCG	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequing Tracagagagagagagagagagagagagagagagagagaga	688 DNA se id Accession sence: 18" 11 TOTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTA ACGGCGGGGG AGCCCGAGGT ATTCCAGCTT TGCCGGACG GGTTTCAGAA AGCACAGTCC CGGAGCCCA CCAACCAGTC CCACCTCAT CCTCCGGAC 689 Protei	equence 1 8: NM_005 70 21 21 AAGGGTCCCC GCACCATCCG CTACAGCCTAT CAAAGCTCTC CAAAGCTCTC CACAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CGCCGAGCTGC CCAAAGATCC CAAAAGATCC CAAAAGATCC CAAAAGATCC CAAAAGATCC CAAATCCCAC ACTCTATTAG In sequence	31 AGCATCCGAT TCTCAGGAAT ACCGGGGGAG AACCCCTACC GCTTATCCCG GCTCCTAGCG AATGGCAAAC GCACTTACAGA GCCCCATCGA AAGATCAAGA GACCCAATGG CGCTCGCTCA AGCTACCTGG	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CAAGGAACA CAAGGAACA CAAGGATTCAC AGATCATGAA CGTGTAACTC AGACCACCC AGAACTCACCACCC AGAACTCACCACCC AGAACTCACCACCC	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACTCAG AACAGCACACAG AACGGGGAG TCATGCCCAC ATCCTGGTAC	120 180 240 300 360 420 480 540 600 660 720 780
40 45 50 55 60	Seq ID NO: Nucleic Ac: Coding sequitation ATGACAGGAG TTCCAGACGT TCAGCTACCG CCTACCTCGG AACGGCTCCG TACCACCAGT TACCTCGCCT AGGACTATTT TACCTCGCCT ATGCCCCCGG CCTACCTCGGACT ATGCCCCCGG CCTACCTCGGACT ACAGGGGTGT ACAGGGGTGT Seq ID NO: Protein Acc	688 DNA se id Accession sence: 18" 11 1 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CCTTCCTATGG CCGGGAGCTA ACCGCGGGAGCTA ACCGCGGAGCTA ACCGGGACCA GGATTCCAGCT ATTCCAGCTT CCCGGAACCA GGATTCAGAA AGCACAGTC CCAGCTCAAT CCTCCGGGAC 689 Protein cession #: N	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCCG GCACCATCCG CTACAGCTCTC CCCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CCAGCTGCC CCAGCGTCCAGC CCAGCGTCCAGCTGCC CCAGCGTCCAC ACTCTATTAG .n sequence 1P_005212.1	31 AGCATCCGAT TCTCAGGAAT TCTCAGGAG ACCCCTACC GCTTATGCCG GATTGCAGGG GATTGCAAGGG GATTACAGA GCGCCTCGC GCTCAAGGG GACCCAATGG GACCCAATGG CGCCCATCGC CTGCCGCCGC 31	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTCA TCGGATTGAC GCACCACCC AGAACTCACC AGAACTCACC CAGACTCACC CAGGCTCCTT	CCAAGCTCCG GCCCGAGTCT CTACTGCTCT TCACGGOGTG CGCTAGCTCC GCCAGAGAAA TCGTAAACCC GAAGACTCAG AAACACAG AAACACAG AAACACCAA TCCTGGTAC ATCCTGGTAC ATCCTGGTAC	120 180 240 300 360 420 480 540 660 720 780 840
40 45 50 55 60	Seq ID NO: Nucleic Ac: Coding sequence 1 ATGACAGGAG TTCCAGACGT TCAGCTACCG CCTACCACCAGT TACCACCAGT TACCACCAGT TACCACCAGT TACCACCAGT TACCACCAGG AGGACTATTT TACCTGGCCT GTGAAAATCT ATGCCCCGGACG CCAGCGGTGT CCTCCGACCT ACAAGTGCAG CTGGCGCTGG Seq ID NO: Protein Acc 1 MTGVPDRRVP	688 DNA se id Accession lence: 18* 11 1 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGGAGCTA ACCGGGAGCTA ACCGGAGGT ATTCCAGCTT TGCCGGAACC GGTTTCAGAA AGCACAGTCC CGGAGCCCA CCAACCAGTC CCAGCTCAAT CCTCCGGAC 689 Protei	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCCG GCACCATCCG CTACAGCCCT CCAGCCAAA CTACAACCGC GAGAATCGC GAGAATCGC CACCTGCC CAAATCCCC CAAATCCCC CAATCCCAC ACTCTATTAG .n sequence 1P_005212.1 21 FQTSAAMHHP	31 AGCATCCGAT TCTCAGGAAT ACGGGGGGGA AACCCTACC GCTTATECCG GTCCCAAGCG ACCCCTAGC GCATTACAGA GCATTACAGA GCACTACAGGA AAGATCAAGA AAGATCAATGG CGCCGCCTCGC AGCTACCTGG CTGCCGCCGC 31	CCGGCGACTT CCCGCACGTT CCCCGCACGT AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTTCA TGGGATTGAC GCCACCACCA AGAACTAGAA CGTGTAACTC GCCACCACCC AGAACTCTGC CGGGCTCCTT 41 SATDSDYYSP	CCAAGCTCCG GCCCGAGTCT CTACTGCTCT TCACGGCGTG GCCAGAGAAA TCGTAAACCC GAAGACACAG AAACGGGAG GCCGCAGTCT TCATGCCCAC ATCCTGGTAC ATCCTGGTAC 51 TGGAPHGYCS	120 180 240 360 420 480 660 720 780 840.
40 45 50 55	Seq ID NO: Nucleic Ac: Coding sequitary I ATGACAGGAG TTCAGACGT TCAGCTACCTG CATACCTCGG AACGGCTCCG GAAGTGACCG GAAGTGACCG GCTACCTGGCGT GAAGTGACCG TACCACAGT GAAGTGACCG TACCACAGT ATGCCCCGG CCAGCGGTGT CCTCCGACCT ACAAGTGCAG Seq ID NO: Protein Acc I MTGVPDRRVP PTSASYGKAL	688 DNA se id Accession lence: 18" 11 1 TOTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTAT ACGGCGGGGCCA AGCCCGAGGT ATTCCAGCTT TGCCGGAACG GGTTTCAGAA AGCACAGTCC CCAACCAGTC CCAACCAGTC CCAACCAGTC CCAGCTCAAT CCTCCGGGAC 1285510n #: N SIRSGDFQAP NPYQYQYHGV	Paguence 1 8: NM_005 70 21 21 3 AAGGGTCCCC GCACCATCCG CTACAGCCAAA CTACAACCGC GAGAATGGTG CCAAGCTGGCC CAAAGATCC CACCTACCAGCTCAGC CACCTACTAGCTCAGC CCACGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CAATTCCCAC ACTCTATTAG 1 Sequence 1P_005212.1 21	31 AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTACC GCTTATCCCG GTTATACCG GCATTACAGA GCATTACAGA GCACTTACAGA GCCCCATCG AAGATCAAGA GACCAATGG CGCCTCGCCA AGCTACCTGC CTGCCGCCGC 31 SQESPTLPES AYADYSYASS	COGGOGACTT COCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA ACTATGACTA GAAGGATTGAC AGATCATGAA AGATCATGAA CGTGTAACTC GCCACCACCC AGAACTCACCACCC AGAACTCACC AGACTCTGC AGAACTCTGC ACTCTGC AGAACTCTGC AGAACTCTGC AGAACTCTGC AGAACTCTGCAACTCTGC AGAACTCTGC AGAACTCTGC AGAACTCTGC AGAACTCTGC AGAACTCTGC AGAACTCTGC AG	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGCGTG CGCTAGCTCC GCCAGAGAAA TCGTAAACCC GAAGACTCAG AAACGGGAG AAACGGGAGTCT TCATGCCCAC ATCCTGGTAC ACAGCACCCG 51 TGGAPEGYCS VPSATNOPEK	120 180 240 300 360 420 540 600 660 720 780 840
40 45 50 55 60	Seq ID NO: Nucleic Ac: Coding sequitation Tracagaca Tracagaca Tracagaca Tracagaca Tracagaca Tacacagac Tacacagac Tacacagac Tacacagac Tacacagaca Aagacacagacagacagacagacagacagacacacagacacacacacacacacacacacacacacacacacacacac	688 DNA se id Accession zence: 18" 11 TOTTTGACAG CCGCAGCTAT ATTCTGACTA CTTCCTATGG CCGGAGCTAT ATTCTGACTA ACGCCGGAGCTA ATTCCAGCTT TGCCGGAAC AGCCCGAGGT ATTCCAGCTC CCGAGCCCAC AGCCCGAGGT ATTCCAGCTC CCGGAGCCCA AGCACCAGCCCAAC CCACCCGAAC CCACCCGAGT CCACCGGAC 689 Protein cession #: N SIRSGDPQAP MPYQYQYHGV NGKPKWRRP	equence 1 8: NM_005 70 21 AAGGGTCCCC GCACCATCCCC GCACCATCCCC CAAAGCTCTC CCCAGCCAAA CTACAACCGC GAGAATGGTG TCAGCTGGCC CCAAGCTACAACCGC CCAAGCTCAC CCAAGCTCAC ACTCTATTAG .n sequence 1P_005212.1 FQTSAAMHHP FQTSAAMHHP FQTSAAMHHP RGSAGSYPAK RTIYSSPQLA	31 AGCATCCGAT TCTCAGGAAT ACGGGGGGAG AACCCTACC GCTTATGCCG GTCCCAAGCG AATGGCAAAC GCATTACAGA GCCCTCGC AAGATCAAGA GACCCAATGG CGCCCACCC CTGCCGCCCGC 31 SQESPTLPES AVADYSYASS ALQRRFQKTQ	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA ACTATAGCTA CCACCAACCA CCAAGGAAGT GAAGGTTCA TCGGATTGAC AGATCATGAA AGTATCATC AGATCATCAA CGTGTAACTC CCACCACCC CGGGCTCCTT 41 SATDSDYYSP YLQYGGGAYNR YLALPERAEL	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGOSTG CGCTAGACACC GAAGACTCAG AAACACAG AAACACAG AAACACAG AAACACGAC AACACCACG AACACCACG AACACCACG ACACCACCCCG 51 TGGAPHGYCS VPSATNQPEX AASLGLTOTO	120 180 240 300 360 420 540 600 660 720 780 840.
40 45 50 55 60	Seq ID NO: Nucleic Ac: Coding sequitation ATGACAGGAG TTCCAGACGT TCAGCTACG CCTACCTCGG AACGGCTCGG AACGGCTCGG AGGACTATTT TACCTCGCCT ATGCCCCGG CCAGCGGTGC CCTCGGACT ACTAGTGCAG CCAGCGGTGC Seq ID NO: Protein Acc MTGVPDRRVP PTSASYGRAL EVTEPEVRMV VKIWFQNKRS	688 DNA se id Accession lence: 18* 11 1 TGTTTGACAG CCGCAGCTAT ATTCTGACTA CCTCCTATGG CCGGGAGCTA ACCGGGAGCTA ACCGGGAGCTA ACCGGAGCTA ACCGGAACCA GGATTCCAGAA AGCACAGTCC GGGAGCCCA CCAACCAGTC CCAGCTCAAT CCTCCGGGAC 689 Protein lession #: N SIRSGDPQAP NPYQYQYMEN NPYQYQYMEN KIKKIMNGE	Paguence 1 8: NM_005 70 21 21 3 AAGGGTCCCC GCACCATCCG CTACAGCCAAA CTACAACCGC GAGAATGGTG CCAAGCTGGCC CAAAGATCC CACCTACCAGCTCAGC CACCTACTAGCTCAGC CCACGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CCAGCTCC CAATTCCCAC ACTCTATTAG 1 Sequence 1P_005212.1 21	31 AGCATCCGAT TCTCAGGAAT TCTCAGGAAT ACGGGGGGG AACCCCTACC GCTTATGCCG GTTCCAAGCG AATGGCAAAC GCATTACAGA GCCCCTCGC GCTGCTCAAGCG CGCTGCTCAAGCG GACCCAATGG CGCTGCTCA AGCTCACTGG CTGCCGCCGC 31 SQESPTLPES AYADYSTASS ALQREPQKTQ DPMACNSPQS	CCGGCGACTT CCCGCACGG AGTATCAGTA ACTATAGCTA CCACCAACCA CAAAGAAAGT GAAGGTTCA TGGGATTGAC GCCACCACCA GAAACTCTGC GCCACCACCC AGAACTCTGC CGGGCTCCTT 41 SATDSDYYSP YHCYGGAYNR YHALPERAEL PAWWEPGGSS	CCAAGCTCCG GCCGAGTCT CTACTGCTCT TCACGGOSTG CGCTAGACACC GAAGACTCAG AAACACAG AAACACAG AAACACAG AAACACGAC AACACCACG AACACCACG AACACCACG ACAGCACCCCG 51 TGGAPHGYCS VPSATNQPEX AASLGLTOTO	120 180 240 300 360 420 540 600 660 720 780 840

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein neorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1 1. A method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a 2 3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence 4 as shown in Tables 1A-16. 2. The method of claim 1, wherein the polynucleotide selectively 1 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. 2 3. The method of claim 1, wherein the biological sample is a tissue 1 2 sample. 1 4. The method of claim 1, wherein the biological sample comprises isolated nucleic acids. 2 5. The method of claim 4, wherein the nucleic acids are mRNA. 1 6. 1 The method of claim 4, further comprising the step of amplifying 2 nucleic acids before the step of contacting the biological sample with the polynucleotide. 7. 1 The method of claim 1, wherein the polynucleotide comprises a 2 sequence as shown in Tables 1A-16. 1 8. The method of claim 1, wherein the polynucleotide is labeled. 1 9. The method of claim 8, wherein the label is a fluorescent label. 10. The method of claim 1, wherein the polynucleotide is immobilized on 1 a solid surface. 2 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic 2 regimen to treat lung cancer. 1 12. The method of claim 1, wherein the patient is suspected of having lung 2 cancer. 1 13. A method of monitoring the efficacy of a therapeutic treatment of lung 2 cancer, the method comprising the steps of:

3	WO 02/086443 PCT/US02/12476 (i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated transcript in the
6	biological sample by contacting the biological sample with a polynucleotide that selectively
7	hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
8	thereby monitoring the efficacy of the therapy.
1	14. The method of claim 13, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3	transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	15. The method of claim 13, wherein the patient is a human.
1	16. A method of monitoring the efficacy of a therapeutic treatment of lung
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated antibody in the biological
6	sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7	that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8	Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9	antibody, thereby monitoring the efficacy of the therapy.
ı	17. The method of claim 16, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3	antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
‡	treatment.
i	18. The method of claim 16, wherein the patient is a human.
l	19. A method of monitoring the efficacy of a therapeutic treatment of lung
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic
ļ	treatment; and

5	(ii) d	etermining the level of a lung cancer-associated polypeptide in the					
6	biological sample by	contacting the biological sample with an antibody, wherein the antibody					
7	specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to						
8	a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby						
9	monitoring the effic	acy of the therapy.					
1	20.	The method of claim 19, further comprising the step of: (iii) comparing					
2		cancer-associated polypeptide to a level of the lung cancer-associated					
3	_	logical sample from the patient prior to, or earlier in, the therapeutic					
4	treatment.						
1	21.	The method of claim 19, wherein the patient is a human.					
1	22.	An isolated nucleic acid molecule consisting of a polynucleotide					
2	sequence as shown i						
-		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					
1	23.	The nucleic acid molecule of claim 22, which is labeled.					
1	24.	The nucleic acid of claim 23, wherein the label is a fluorescent label					
1	25.	An expression vector comprising the nucleic acid of claim 22.					
1	26.	A host cell comprising the expression vector of claim 25.					
1	27.	An isolated polypeptide which is encoded by a nucleic acid molecule					
2	having polynucleotic	de sequence as shown in Tables 1A-16.					
1	28.	An antibody that specifically binds a polypeptide of claim 27.					
1	29.	The antibody of claim 28, further conjugated to an effector component.					
1	30.	The antibody of claim 29, wherein the effector component is a					
2	fluorescent label.						
1	31.	The antibody of claim 29, wherein the effector component is a					
2	radioisotope or a cyl						
-							
1	32.	The antibody of claim 29, which is an antibody fragment.					

1		33.	The antibody of claim 29, which is a humanized antibody
1		34.	A method of detecting a lung cancer cell in a biological sample from a
2	patient, the me	ethod co	omprising contacting the biological sample with an antibody of claim
3	28.		
1		35.	The method of claim 34, wherein the antibody is further conjugated to
2	an effector co	mponen	t.
1		36.	The method of claim 35, wherein the effector component is a
2	fluorescent lal	bel.	
1 -		37.	A method of detecting antibodies specific to lung cancer in a patient,
2	the method co	mprisin	g contacting a biological sample from the patient with a polypeptide
3	encoded by a	nucleic	acid comprises a sequence from Tables 1A-16.
1		38.	A method for identifying a compound that modulates a lung cancer-
2	associated pol	ypeptid	e, the method comprising the steps of:
3		(i) con	tacting the compound with a lung cancer-associated polypeptide, the
4	polypeptide er	ncoded l	by a polynucleotide that selectively hybridizes to a sequence at least
5	80% identical	to a seq	quence as shown in Tables 1A-16; and
6		(ii) det	termining the functional effect of the compound upon the polypeptide.
1		39.	The method of claim 38, wherein the functional effect is a physical
2	effect.		
1		40.	The method of claim 38, wherein the functional effect is a chemical
2	effect.		1
1		41.	The method of claim 38, wherein the polypeptide is expressed in a
2	eukaryotic hos	st cell o	r cell membrane.
1		42.	The method of claim 38, wherein the functional effect is determined by
2	measuring liga	and bind	ding to the polypeptide.

The method of claim 38, wherein the polypeptide is recombinant.

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43.

1	44.	A method of inhibiting proliferation of a lung cancer-associated cell to
2	treat lung cancer in	a patient, the method comprising the step of administering to the subject a
3	therapeutically effe	ctive amount of a compound identified using the method of claim 38.
1	45.	The method of claim 44, wherein the compound is an antibody.
1	46.	The method of claim 45, wherein the patient is a human.
1	47.	A drug screening assay comprising the steps of
2	(i) a	dministering a test compound to a mammal having lung cancer or a cell
3	isolated therefrom;	
4	(ii) c	comparing the level of gene expression of a polynucleotide that selectively
5	hybridizes to a sequ	nence at least 80% identical to a sequence as shown in Tables 1A-16 in a
6	treated cell or mam	mal with the level of gene expression of the polynucleotide in a control
7	cell or mammal, wi	nerein a test compound that modulates the level of expression of the
8	polynucleotide is a	candidate for the treatment of lung cancer.
1	48.	The assay of claim 47, wherein the control is a mammal with lung
2	cancer or a cell the	refrom that has not been treated with the test compound.
1	49.	The assay of claim 47, wherein the control is a normal cell or mammal
1	. 50.	A method for treating a mammal having lung cancer comprising
2	administering a cor	npound identified by the assay of claim 47.
1	51.	A pharmaceutiPcal composition for treating a mammal having lung
2	cancer, the compos	ition comprising a compound identified by the assay of claim 47 and a
3	physiologically acc	eptable excipient.